

AF

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau(43) International Publication Date
9 October 2003 (09.10.2003)

PCT

(10) International Publication Number
WO 03/083085 A2(51) International Patent Classification⁷: C12N

(21) International Application Number: PCT/US03/09797

(22) International Filing Date: 27 March 2003 (27.03.2003)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/368,840 28 March 2002 (28.03.2002) US
60/375,637 26 April 2002 (26.04.2002) US

(71) Applicant (for all designated States except US): INCYTE CORPORATION [US/US]; 3160 Porter Drive, Palo Alto, CA 94304 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): MARQUIS, Joseph, P. [US/US]; 4428 Lazy Lane, San Jose, CA 95135 (US). LEE, Soo, Y. [KR/US]; 40 Westdale Avenue, Daly City, CA 94015 (US). EMERLING, Brooke, M. [US/US]; 833 W. Buena Avenue #2108, Chicago, IL 60613 (US). HAFALIA, April, J.A. [US/US]; 15 Midvale Drive, Daly City, CA 94015 (US). KHARE, Reena [IN/US]; 12650 Orella Court, Saratoga, CA 95070 (US). KABLE, Amy, E. [US/US]; 2345 Polk Street #4, San Francisco, CA 94109 (US). RICHARDSON, Thomas, W. [US/US]; 616 Canyon Road #107, Redwood City, CA 94062 (US). SWARNAKAR, Anita [CA/US]; 8 Locksley Avenue #5D, San Francisco, CA 94122 (US). CHAWLA, Narinder, K. [US/US]; 33 Union Square, #712, Union City, CA 94587 (US). BECHA, Shanya, D. [US/US]; 1 Saint Francis #5508, San Francisco, CA 94107 (US). MASON, Patricia, M. [US/US]; 360 Clarke Lane, Morgan Hill, CA 95014 (US). ELLIOTT, Vicki, S. [US/US]; 3770 Polton Place Way, San Jose, CA 95121 (US). RAMKUMAR, Jayalaxmi [IN/US]; 34359 Maybird Circle, Fremont, CA 94555 (US). GRIFFIN, Jennifer, A. [US/US]; 33691

Mello Way, Fremont, CA 94555 (US). TRAN, Uyen, K. [US/US]; 2638 Mabury Square, San Jose, CA 95133 (US). ISON, Craig, H. [US/US]; 1242 Weathersfield Way, San Jose, CA 95118 (US). LINDQUIST, Erika, A. [US/US]; 2394 Mariner Square Drive #C-121, Alameda, CA 94501 (US). JIANG, Xin [US/US]; 14371 Elva Avenue, Saratoga, CA 95070 (US). JACKSON, Alan, A. [US/US]; 1541 Elwood Drive, Los Gatos, CA 95032 (US). WILSON, Amy, D. [US/US]; 1056 Continentals Way, #27, Belmont, CA 94002 (US). JIN, Pei [US/US]; 320 Curtner Avenue #D, Palo Alto, CA 94306 (US). CHANG, Hsin-Ru [US/US]; 326 Treasure Island Drive, Belmont, CA 94002 (US).

(74) Agents: HAMLET-COX, Diana et al.; Inycte Corporation, 3160 Porter Drive, Palo Alto, CA 94304 (US).

(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

— without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 03/083085 A2

(54) Title: TRANSPORTERS AND ION CHANNELS

(57) Abstract: Various embodiments of the invention provide human transporters and ion channels (TRICH) and polynucleotides which identify and encode TRICH. Embodiments of the invention also provide expression vectors, host cells, antibodies, agonists, and antagonists. Other embodiments provide methods for diagnosing, treating, or preventing disorders associated with aberrant expression of TRICH.

1

TRANSPORTERS AND ION CHANNELS

TECHNICAL FIELD

The invention relates to novel nucleic acids, transporters and ion channels encoded by these
5 nucleic acids, and to the use of these nucleic acids and proteins in the diagnosis, treatment, and
prevention of transport, neurological, muscle, immunological and cell proliferative disorders. The
invention also relates to the assessment of the effects of exogenous compounds on the expression of
nucleic acids and transporters and ion channels.

10

BACKGROUND OF THE INVENTION

Eukaryotic cells are surrounded and subdivided into functionally distinct organelles by
hydrophobic lipid bilayer membranes which are highly impermeable to most polar molecules. Cells and
organelles require transport proteins to import and export essential nutrients and metal ions including
K⁺, NH₄⁺, P_i, SO₄²⁻, sugars, and vitamins, as well as various metabolic waste products. Transport
15 proteins also play roles in antibiotic resistance, toxin secretion, ion balance, synaptic neurotransmission,
kidney function, intestinal absorption, tumor growth, and other diverse cell functions (Griffith, J. and C.
Sansom (1998) The Transporter Facts Book, Academic Press, San Diego CA, pp. 3-29). Transport
can occur by a passive concentration-dependent mechanism, or can be linked to an energy source
such as ATP hydrolysis or an ion gradient. Proteins that function in transport include carrier proteins,
20 which bind to a specific solute and undergo a conformational change that translocates the bound solute
across the membrane, and channel proteins, which form hydrophilic pores that allow specific solutes to
diffuse through the membrane down an electrochemical solute gradient.

Carrier proteins which transport a single solute from one side of the membrane to the other
are called uniporters. In contrast, coupled transporters link the transfer of one solute with
25 simultaneous or sequential transfer of a second solute, either in the same direction (symport) or in the
opposite direction (antiport). For example, intestinal and kidney epithelium contains a variety of
symporter systems driven by the sodium gradient that exists across the plasma membrane. Sodium
moves into the cell down its electrochemical gradient and brings the solute into the cell with it. The
sodium gradient that provides the driving force for solute uptake is maintained by the ubiquitous
30 Na⁺/K⁺ ATPase system. Sodium-coupled transporters include the mammalian glucose transporter
(SGLT1), iodide transporter (NIS), and multivitamin transporter (SMVT). All three transporters have
twelve putative transmembrane segments, extracellular glycosylation sites, and cytoplasmically-
oriented N- and C-termini. NIS plays a crucial role in the evaluation, diagnosis, and treatment of

various thyroid pathologies because it is the molecular basis for radioiodide thyroid-imaging techniques and for specific targeting of radioisotopes to the thyroid gland (Levy, O. et al. (1997) Proc. Natl. Acad. Sci. USA 94:5568-5573). SMVT is expressed in the intestinal mucosa, kidney, and placenta, and is implicated in the transport of the water-soluble vitamins, e.g., biotin and pantothenate (Prasad, P.D. et al. (1998) J. Biol. Chem. 273:7501-7506).

One of the largest families of transporters is the major facilitator superfamily (MFS), also called the uniporter-symporter-antiporter family. MFS transporters are single polypeptide carriers that transport small solutes in response to ion gradients. Members of the MFS are found in all classes of living organisms, and include transporters for sugars, oligosaccharides, phosphates, nitrates, nucleosides, monocarboxylates, and drugs. MFS transporters found in eukaryotes all have a structure comprising 12 transmembrane segments (Pao, S.S. et al. (1998) Microbiol. Molec. Biol. Rev. 62:1-34). The largest family of MFS transporters is the sugar transporter family, which includes the seven glucose transporters (GLUT1-GLUT7) found in humans that are required for the transport of glucose and other hexose sugars. These glucose transport proteins have unique tissue distributions and physiological functions. GLUT1 provides many cell types with their basal glucose requirements and transports glucose across epithelial and endothelial barrier tissues; GLUT2 facilitates glucose uptake or efflux from the liver; GLUT3 regulates glucose supply to neurons; GLUT4 is responsible for insulin-regulated glucose disposal; and GLUT5 regulates fructose uptake into skeletal muscle. Defects in glucose transporters are involved in a recently identified neurological syndrome causing infantile seizures and developmental delay, as well as glycogen storage disease, Fanconi-Bickel syndrome, and non-insulin-dependent diabetes mellitus (Mueckler, M. (1994) Eur. J. Biochem. 219:713-725; Longo, N. and L.J. Elsas (1998) Adv. Pediatr. 45:293-313).

Monocarboxylate anion transporters are proton-coupled symporters with a broad substrate specificity that includes L-lactate, pyruvate, and the ketone bodies acetate, acetoacetate, and beta-hydroxybutyrate. At least seven isoforms have been identified to date. The isoforms are predicted to have twelve transmembrane (TM) helical domains with a large intracellular loop between TM6 and TM7, and play a critical role in maintaining intracellular pH by removing the protons that are produced stoichiometrically with lactate during glycolysis. The best characterized H⁺-monocarboxylate transporter is that of the erythrocyte membrane, which transports L-lactate and a wide range of other aliphatic monocarboxylates. Other cells possess H⁺-linked monocarboxylate transporters with differing substrate and inhibitor selectivities. In particular, cardiac muscle and tumor cells have transporters that differ in their K_m values for certain substrates, including stereoselectivity for L- over D-lactate, and in their sensitivity to inhibitors. There are Na⁺-monocarboxylate

cotransporters on the luminal surface of intestinal and kidney epithelia, which allow the uptake of lactate, pyruvate, and ketone bodies in these tissues. In addition, there are specific and selective transporters for organic cations and organic anions in organs including the kidney, intestine and liver. Organic anion transporters are selective for hydrophobic, charged molecules with electron-attracting side groups. Organic cation transporters, such as the ammonium transporter, mediate the secretion of a variety of drugs and endogenous metabolites, and contribute to the maintenance of intercellular pH (Poole, R.C. and A.P. Halestrap (1993) *Am. J. Physiol.* 264:C761-C782; Price, N.T. et al. (1998) *Biochem. J.* 329:321-328; and Martinelle, K. and I. Haggstrom (1993) *J. Biotechnol.* 30:339-350).

ATP-binding cassette (ABC) transporters are members of a superfamily of membrane proteins that transport substances ranging from small molecules such as ions, sugars, amino acids, peptides, and phospholipids, to lipopeptides, large proteins, and complex hydrophobic drugs. ABC transporters consist of four modules: two nucleotide-binding domains (NBD), which hydrolyze ATP to supply the energy required for transport, and two membrane-spanning domains (MSD), each containing six putative transmembrane segments. These four modules may be encoded by a single gene, as is the case for the cystic fibrosis transmembrane regulator (CFTR), or by separate genes. When encoded by separate genes, each gene product contains a single NBD and MSD. These "half-molecules" form homo- and heterodimers, such as Tap1 and Tap2, the endoplasmic reticulum-based major histocompatibility (MHC) peptide transport system. Several genetic diseases are attributed to defects in ABC transporters, such as the following diseases and their corresponding proteins: cystic fibrosis (CFTR, an ion channel), adrenoleukodystrophy (adrenoleukodystrophy protein, ALDP), Zellweger syndrome (peroxisomal membrane protein-70, PMP70), and hyperinsulinemic hypoglycemia (sulfonylurea receptor, SUR). Overexpression of the multidrug resistance (MDR) protein, another ABC transporter, in human cancer cells makes the cells resistant to a variety of cytotoxic drugs used in chemotherapy (Taglicht, D. and S. Michaelis (1998) *Meth. Enzymol.* 292:130-162).

A number of metal ions such as iron, zinc, copper, cobalt, manganese, molybdenum, selenium, nickel, and chromium are important as cofactors for a number of enzymes. For example, copper is involved in hemoglobin synthesis, connective tissue metabolism, and bone development, by acting as a cofactor in oxidoreductases such as superoxide dismutase, ferroxidase (ceruloplasmin), and lysyl oxidase. Copper and other metal ions must be provided in the diet, and are absorbed by transporters in the gastrointestinal tract. Plasma proteins transport the metal ions to the liver and other target organs, where specific transporters move the ions into cells and cellular organelles as needed. Imbalances in metal ion metabolism have been associated with a number of disease states (Danks, D.M. (1986) *J. Med. Genet.* 23:99-106).

Transport of fatty acids across the plasma membrane can occur by diffusion, a high capacity, low affinity process. However, under normal physiological conditions a significant fraction of fatty acid transport appears to occur via a high affinity, low capacity protein-mediated transport process. Fatty acid transport protein (FATP), an integral membrane protein with four transmembrane
5 segments, is expressed in tissues exhibiting high levels of plasma membrane fatty acid flux, such as muscle, heart, and adipose. Expression of FATP is upregulated in 3T3-L1 cells during adipose conversion, and expression in COS7 fibroblasts elevates uptake of long-chain fatty acids (Hui, T.Y. et al. (1998) *J. Biol. Chem.* 273:27420-27429).

The lipocalin superfamily constitutes a phylogenetically conserved group of more than forty
10 proteins that function as extracellular ligand-binding proteins which bind and transport small hydrophobic molecules. Members of this family function as carriers of retinoids, odorants, chromophores, pheromones, allergens, and sterols, and in a variety of processes including nutrient transport, cell growth regulation, immune response, and prostaglandin synthesis. A subset of these proteins may be multifunctional, serving as either a biosynthetic enzyme or as a specific enzyme
15 inhibitor. (Tanaka, T. et al. (1997) *J. Biol. Chem.* 272:15789-15795; and van't Hof, W. et al. (1997) *J. Biol. Chem.* 272:1837-1841.)

Members of the lipocalin family display unusually low levels of overall sequence conservation. Pairwise sequence identity often falls below 20%. Sequence similarity between family members is limited to conserved cysteines which form disulfide bonds and three motifs which form a juxtaposed
20 cluster that functions as a target cell recognition site. The lipocalins share an eight stranded, anti-parallel beta-sheet which folds back on itself to form a continuously hydrogen-bonded beta-barrel. The pocket formed by the barrel functions as an internal ligand binding site. Seven loops (L1 to L7) form short beta-hairpins, except loop L1 which is a large omega loop that forms a lid to partially close the internal ligand-binding site (Flower (1996) *Biochem. J.* 318:1-14).

25 Lipocalins are important transport molecules. Each lipocalin associates with a particular ligand and delivers that ligand to appropriate target sites within the organism. Retinol-binding protein (RBP), one of the best characterized lipocalins, transports retinol from stores within the liver to target tissues. Apolipoprotein D (apo D), a component of high density lipoproteins (HDLs) and low density lipoproteins (LDLs), functions in the targeted collection and delivery of cholesterol throughout the
30 body. Lipocalins are also involved in cell regulatory processes. Apo D, which is identical to gross-cystic-disease-fluid protein (GCDFP)-24, is a progesterone/pregnenolone-binding protein expressed at high levels in breast cyst fluid. Secretion of apo D in certain human breast cancer cell lines is accompanied by reduced cell proliferation and progression of cells to a more differentiated phenotype.

Similarly, apo D and another lipocalin, α_1 -acid glycoprotein (AGP), are involved in nerve cell regeneration. AGP is also involved in anti-inflammatory and immunosuppressive activities. AGP is one of the positive acute-phase proteins (APP); circulating levels of AGP increase in response to stress and inflammatory stimulation. AGP accumulates at sites of inflammation where it inhibits platelet and neutrophil activation and inhibits phagocytosis. The immunomodulatory properties of AGP are due to glycosylation. AGP is 40% carbohydrate, making it unusually acidic and soluble. The glycosylation pattern of AGP changes during acute-phase response, and deglycosylated AGP has no immunosuppressive activity (Flower (1994) FEBS Lett. 354:7-11; Flower (1996) *supra*).

The lipocalin superfamily also includes several animal allergens, including the mouse major urinary protein (mMUP), the rat α -2-microglobulin (rA2U), the bovine β -lactoglobulin (β lg), the cockroach allergen (Bla g4), bovine dander allergen (Bos d2), and the major horse allergen, designated *Equus caballus* allergen 1 (Equ c1). Equ c1 is a powerful allergen responsible for about 80% of anti-horse IgE antibody response in patients who are chronically exposed to horse allergens. It appears that lipocalins may contain a common structure that is able to induce the IgE response (Gregoire, C. et al., (1996) J. Biol. Chem. 271:32951-32959).

Lipocalins are used as diagnostic and prognostic markers in a variety of disease states. The plasma level of AGP is monitored during pregnancy and in diagnosis and prognosis of conditions including cancer chemotherapy, renal dysfunction, myocardial infarction, arthritis, and multiple sclerosis. RBP is used clinically as a marker of tubular reabsorption in the kidney, and apo D is a marker in gross cystic breast disease (Flower (1996) *supra*). Additionally, the use of lipocalin animal allergens may help in the diagnosis of allergic reactions to horses (Gregoire *supra*), pigs, cockroaches, mice and rats.

Mitochondrial carrier proteins are transmembrane-spanning proteins which transport ions and charged metabolites between the cytosol and the mitochondrial matrix. Examples include the ADP, ATP carrier protein; the 2-oxoglutarate/malate carrier; the phosphate carrier protein; the pyruvate carrier; the dicarboxylate carrier which transports malate, succinate, fumarate, and phosphate; the tricarboxylate carrier which transports citrate and malate; and the Grave's disease carrier protein, a protein recognized by IgG in patients with active Grave's disease, an autoimmune disorder resulting in hyperthyroidism. Proteins in this family consist of three tandem repeats of an approximately 100 amino acid domain, each of which contains two transmembrane regions (Stryer, L. (1995) Biochemistry, W.H. Freeman and Company, New York NY, p. 551; PROSITE PDOC00189 Mitochondrial energy transfer proteins signature; Online Mendelian Inheritance in Man (OMIM) *275000 Graves Disease).

This class of transporters also includes the mitochondrial uncoupling proteins, which create proton leaks across the inner mitochondrial membrane, thus uncoupling oxidative phosphorylation from ATP synthesis. The result is energy dissipation in the form of heat. Mitochondrial uncoupling proteins have been implicated as modulators of thermoregulation and metabolic rate, and have been proposed as potential targets for drugs against metabolic diseases such as obesity (Ricquier, D. et al. (1999) J. Int. Med. 245:637-642).

Ion Channels

The electrical potential of a cell is generated and maintained by controlling the movement of ions across the plasma membrane. The movement of ions requires ion channels, which form ion-selective pores within the membrane. There are two basic types of ion channels, ion transporters and gated ion channels. Ion transporters utilize the energy obtained from ATP hydrolysis to actively transport an ion against the ion's concentration gradient. Gated ion channels allow passive flow of an ion down the ion's electrochemical gradient under restricted conditions. Together, these types of ion channels generate, maintain, and utilize an electrochemical gradient that is used in 1) electrical impulse conduction down the axon of a nerve cell, 2) transport of molecules into cells against concentration gradients, 3) initiation of muscle contraction, and 4) endocrine cell secretion.

Ion Transporters

Ion transporters generate and maintain the resting electrical potential of a cell. Utilizing the energy derived from ATP hydrolysis, they transport ions against the ion's concentration gradient. These transmembrane ATPases are divided into three families. The phosphorylated (P) class ion transporters, including Na⁺-K⁺ ATPase, Ca²⁺-ATPase, and H⁺-ATPase, are activated by a phosphorylation event. P-class ion transporters are responsible for maintaining resting potential distributions such that cytosolic concentrations of Na⁺ and Ca²⁺ are low and cytosolic concentration of K⁺ is high. The vacuolar (V) class of ion transporters includes H⁺ pumps on intracellular organelles, such as lysosomes and Golgi. V-class ion transporters are responsible for generating the low pH within the lumen of these organelles that is required for function. The coupling factor (F) class consists of H⁺ pumps in the mitochondria. F-class ion transporters utilize a proton gradient to generate ATP from ADP and inorganic phosphate (P_i).

The P-ATPases are hexamers of a 100 kD subunit with ten transmembrane domains and several large cytoplasmic regions that may play a role in ion binding (Scarborough, G.A. (1999) Curr. Opin. Cell Biol. 11:517-522). The V-ATPases are composed of two functional domains: the V₁ domain, a peripheral complex responsible for ATP hydrolysis; and the V₀ domain, an integral complex responsible for proton translocation across the membrane. The F-ATPases are structurally and

evolutionarily related to the V-ATPases. The F-ATPase F_0 domain contains 12 copies of the c subunit, a highly hydrophobic protein composed of two transmembrane domains and containing a single buried carboxyl group in TM2 that is essential for proton transport. The V-ATPase V_0 domain contains three types of homologous c subunits with four or five transmembrane domains and the essential carboxyl group in TM4 or TM3. Both types of complex also contain a single a subunit that may be involved in regulating the pH dependence of activity (Forgac, M. (1999) J. Biol. Chem. 274:12951-12954).

The resting potential of the cell is utilized in many processes involving carrier proteins and gated ion channels. Carrier proteins utilize the resting potential to transport molecules into and out of the cell. Amino acid and glucose transport into many cells is linked to sodium ion co-transport (symport) so that the movement of Na^+ down an electrochemical gradient drives transport of the other molecule up a concentration gradient. Similarly, cardiac muscle links transfer of Ca^{2+} out of the cell with transport of Na^+ into the cell (antiport).

Gated Ion Channels

Gated ion channels control ion flow by regulating the opening and closing of pores. The ability to control ion flux through various gating mechanisms allows ion channels to mediate such diverse signaling and homeostatic functions as neuronal and endocrine signaling, muscle contraction, fertilization, and regulation of ion and pH balance. Gated ion channels are categorized according to the manner of regulating the gating function. Mechanically-gated channels open their pores in response to mechanical stress; voltage-gated channels (e.g., Na^+ , K^+ , Ca^{2+} , and Cl^- channels) open their pores in response to changes in membrane potential; and ligand-gated channels (e.g., acetylcholine-, serotonin-, and glutamate-gated cation channels, and GABA- and glycine-gated chloride channels) open their pores in the presence of a specific ion, nucleotide, or neurotransmitter. The gating properties of a particular ion channel (i.e., its threshold for and duration of opening and closing) are sometimes modulated by association with auxiliary channel proteins and/or post translational modifications, such as phosphorylation.

Mechanically-gated or mechanosensitive ion channels act as transducers for the senses of touch, hearing, and balance, and also play important roles in cell volume regulation, smooth muscle contraction, and cardiac rhythm generation. A stretch-inactivated channel (SIC) was recently cloned from rat kidney. The SIC channel belongs to a group of channels which are activated by pressure or stress on the cell membrane and conduct both Ca^{2+} and Na^+ (Suzuki, M. et al. (1999) J. Biol. Chem. 274:6330-6335).

The pore-forming subunits of the voltage-gated cation channels form a superfamily of ion

channel proteins. The characteristic domain of these channel proteins comprises six transmembrane domains (S1-S6), a pore-forming region (P) located between S5 and S6, and intracellular amino and carboxy termini. In the Na⁺ and Ca²⁺ subfamilies, this domain is repeated four times, while in the K⁺ channel subfamily, each channel is formed from a tetramer of either identical or dissimilar subunits.

- 5 The P region contains information specifying the ion selectivity for the channel. In the case of K⁺ channels, a GYG tripeptide is involved in this selectivity (Ishii, T.M. et al. (1997) Proc. Natl. Acad. Sci. USA 94:11651-11656).

- Voltage-gated Na⁺ and K⁺ channels are necessary for the function of electrically excitable cells, such as nerve and muscle cells. Action potentials, which lead to neurotransmitter release and
 10 muscle contraction, arise from large, transient changes in the permeability of the membrane to Na⁺ and K⁺ ions. Depolarization of the membrane beyond the threshold level opens voltage-gated Na⁺ channels. Sodium ions flow into the cell, further depolarizing the membrane and opening more voltage-gated Na⁺ channels, which propagates the depolarization down the length of the cell. Depolarization also opens voltage-gated potassium channels. Consequently, potassium ions flow
 15 outward, which leads to repolarization of the membrane. Voltage-gated channels utilize charged residues in the fourth transmembrane segment (S4) to sense voltage change. The open state lasts only about 1 millisecond, at which time the channel spontaneously converts into an inactive state that cannot be opened irrespective of the membrane potential. Inactivation is mediated by the channel's N-terminus, which acts as a plug that closes the pore. The transition from an inactive to a closed state
 20 requires a return to resting potential.

- Voltage-gated Na⁺ channels are heterotrimeric complexes composed of a 260 kDa pore-forming α subunit that associates with two smaller auxiliary subunits, β 1 and β 2. The β 2 subunit is a
 integral membrane glycoprotein that contains an extracellular Ig domain, and its association with α and β 1 subunits correlates with increased functional expression of the channel, a change in its gating
 25 properties, as well as an increase in whole cell capacitance due to an increase in membrane surface area (Isom, L.L. et al. (1995) Cell 83:433-442).

- Non voltage-gated Na⁺ channels include the members of the amiloride-sensitive Na⁺ channel/degenerin (NaC/DEG) family. Channel subunits of this family are thought to consist of two
 transmembrane domains flanking a long extracellular loop, with the amino and carboxyl termini located
 30 within the cell. The NaC/DEG family includes the epithelial Na⁺ channel (ENaC) involved in Na⁺ reabsorption in epithelia including the airway, distal colon, cortical collecting duct of the kidney, and exocrine duct glands. Mutations in ENaC result in pseudohypoaldosteronism type 1 and Liddle's syndrome (pseudohyperaldosteronism). The NaC/DEG family also includes the recently characterized

H⁺-gated cation channels or acid-sensing ion channels (ASIC). ASIC subunits are expressed in the brain and form heteromultimeric Na⁺-permeable channels. These channels require acid pH fluctuations for activation. ASIC subunits show homology to the degenerins, a family of mechanically-gated channels originally isolated from *C. elegans*. Mutations in the degenerins cause

- 5 neurodegeneration. ASIC subunits may also have a role in neuronal function, or in pain perception, since tissue acidosis causes pain (Waldmann, R. and M. Lazdunski (1998) *Curr. Opin. Neurobiol.* 8:418-424; Eglen, R.M. et al. (1999) *Trends Pharmacol. Sci.* 20:337-342).

K⁺ channels are located in all cell types, and may be regulated by voltage, ATP concentration, or second messengers such as Ca²⁺ and cAMP. In non-excitabile tissue, K⁺ channels are involved in
10 protein synthesis, control of endocrine secretions, and the maintenance of osmotic equilibrium across membranes. In neurons and other excitable cells, in addition to regulating action potentials and repolarizing membranes, K⁺ channels are responsible for setting the resting membrane potential. The cytosol contains non-diffusible anions and, to balance this net negative charge, the cell contains a Na⁺-K⁺ pump and ion channels that provide the redistribution of Na⁺, K⁺, and Cl⁻. The pump actively
15 transports Na⁺ out of the cell and K⁺ into the cell in a 3:2 ratio. Ion channels in the plasma membrane allow K⁺ and Cl⁻ to flow by passive diffusion. Because of the high negative charge within the cytosol, Cl⁻ flows out of the cell. The flow of K⁺ is balanced by an electromotive force pulling K⁺ into the cell, and a K⁺ concentration gradient pushing K⁺ out of the cell. Thus, the resting membrane potential is primarily regulated by K⁺ flow (Salkoff, L. and T. Jegla (1995) *Neuron* 15:489-492).

- 20 Potassium channel subunits of the *Shaker*-like superfamily all have the characteristic six transmembrane/1 pore domain structure. Four subunits combine as homo- or heterotetramers to form functional K channels. These pore-forming subunits also associate with various cytoplasmic β subunits that alter channel inactivation kinetics. The *Shaker*-like channel family includes the voltage-gated K⁺ channels as well as the delayed rectifier type channels such as the human ether-a-go-go
25 related gene (HERG) associated with long QT, a cardiac dysrhythmia syndrome (Curran, M.E. (1998) *Curr. Opin. Biotechnol.* 9:565-572; Kaczorowski, G.J. and M.L. Garcia (1999) *Curr. Opin. Chem. Biol.* 3:448-458).

A second superfamily of K⁺ channels is composed of the inward rectifying channels (Kir). Kir channels have the property of preferentially conducting K⁺ currents in the inward direction. These
30 proteins consist of a single potassium selective pore domain and two transmembrane domains, which correspond to the fifth and sixth transmembrane domains of voltage-gated K⁺ channels. Kir subunits also associate as tetramers. The Kir family includes ROMK1, mutations in which lead to Bartter syndrome, a renal tubular disorder. Kir channels are also involved in regulation of cardiac pacemaker

activity, seizures and epilepsy, and insulin regulation (Doupnik, C.A. et al. (1995) *Curr. Opin. Neurobiol.* 5:268-277; Curran, *supra*).

The recently recognized TWIK K⁺ channel family includes the mammalian TWIK-1, TREK-1 and TASK proteins. Members of this family possess an overall structure with four transmembrane domains and two P domains. These proteins are probably involved in controlling the resting potential in a large set of cell types (Duprat, F. et al. (1997) *EMBO J* 16:5464-5471).

The voltage-gated Ca²⁺ channels have been classified into several subtypes based upon their electrophysiological and pharmacological characteristics. L-type Ca²⁺ channels are predominantly expressed in heart and skeletal muscle where they play an essential role in excitation-contraction coupling. T-type channels are important for cardiac pacemaker activity, while N-type and P/Q-type channels are involved in the control of neurotransmitter release in the central and peripheral nervous system. The L-type and N-type voltage-gated Ca²⁺ channels have been purified and, though their functions differ dramatically, they have similar subunit compositions. The channels are composed of three subunits. The α_1 subunit forms the membrane pore and voltage sensor, while the $\alpha_2\delta$ and β subunits modulate the voltage-dependence, gating properties, and the current amplitude of the channel. These subunits are encoded by at least six α_1 , one $\alpha_2\delta$, and four β genes. A fourth subunit, γ , has been identified in skeletal muscle (Walker, D. et al. (1998) *J. Biol. Chem.* 273:2361-2367; McCleskey, E.W. (1994) *Curr. Opin. Neurobiol.* 4:304-312).

The high-voltage-activated Ca²⁺ channels that have been characterized biochemically include complexes of a pore-forming α_1 subunit of approximately 190-250 kDa; a transmembrane complex of α_2 and δ subunits; an intracellular β subunit; and in some cases a transmembrane γ subunit. A variety of α_1 subunits, $\alpha_2\delta$ complexes, β subunits, and γ subunits are known. The Cav1 family of α_1 subunits conduct L-type Ca²⁺ currents, which initiate muscle contraction, endocrine secretion, and gene transcription, and are regulated primarily by second messenger-activated protein phosphorylation pathways. The Cav2 family of α_1 subunits conduct N-type, P/Q-type, and R-type Ca²⁺ currents, which initiate rapid synaptic transmission and are regulated primarily by direct interaction with G proteins and SNARE proteins and secondarily by protein phosphorylation. The Cav3 family of α_1 subunits conduct T-type Ca²⁺ currents, which are activated and inactivated more rapidly and at more negative membrane potentials than other Ca²⁺ current types. The distinct structures and patterns of regulation of these three families of Ca²⁺ channels provide an array of Ca²⁺ entry pathways in response to changes in membrane potential and a range of possibilities for regulation of Ca²⁺ entry by second messenger pathways and interacting proteins (Catterall, W.A. (2000) *Annu. Rev. Cell Dev. Biol.* 16:521-555).

The alpha-2 subunit of the voltage-gated Ca^{2+} -channel may include one or more Cache domains. An extracellular Cache domain may be fused to an intracellular catalytic domain, such as the histidine kinase, PP2C phosphatase, GGDEF (a predicted diguanylate cyclase), HD-GYP (a predicted phosphodiesterase) or adenylyl cyclase domain, or to a noncatalytic domain, like the methyl-accepting, DNA-binding winged helix-turn-helix, GAF, PAS or HAMP (a domain found in histidine kinases, adenylyl cyclases, ethyl-binding proteins and phosphatases). Small molecules are bound via the Cache domain and this signal is converted into diverse outputs depending on the intracellular domains (Anantharaman, V. and Aravind, L. (2000) Trends Biochem. Sci. 25:535-537).

The transient receptor family (Trp) of calcium ion channels are thought to mediate capacitative calcium entry (CCE). CCE is the Ca^{2+} influx into cells to resupply Ca^{2+} stores depleted by the action of inositol triphosphate (IP_3) and other agents in response to numerous hormones and growth factors. Trp and Trp-like were first cloned from *Drosophila* and have similarity to voltage gated Ca^{2+} channels in the S3 through S6 regions. This suggests that Trp and/or related proteins may form mammalian CCE channels (Zhu, X. et al. (1996) Cell 85:661-671; Boulay, G. et al. (1997) J. Biol. Chem. 272:29672-29680). Melastatin is a gene isolated in both the mouse and human, whose expression in melanoma cells is inversely correlated with melanoma aggressiveness *in vivo*. The human cDNA transcript corresponds to a 1533-amino acid protein having homology to members of the Trp family. It has been proposed that the combined use of malastatin mRNA expression status and tumor thickness might allow for the determination of subgroups of patients at both low and high risk for developing metastatic disease (Duncan, L.M. et al (2001) J. Clin. Oncol. 19:568-576).

Chloride channels are necessary in endocrine secretion and in regulation of cytosolic and organelle pH. In secretory epithelial cells, Cl^- enters the cell across a basolateral membrane through an Na^+ , K^+/Cl^- cotransporter, accumulating in the cell above its electrochemical equilibrium concentration. Secretion of Cl^- from the apical surface, in response to hormonal stimulation, leads to flow of Na^+ and water into the secretory lumen. The cystic fibrosis transmembrane conductance regulator (CFTR) is a chloride channel encoded by the gene for cystic fibrosis, a common fatal genetic disorder in humans. CFTR is a member of the ABC transporter family, and is composed of two domains each consisting of six transmembrane domains followed by a nucleotide-binding site. Loss of CFTR function decreases transepithelial water secretion and, as a result, the layers of mucus that coat the respiratory tree, pancreatic ducts, and intestine are dehydrated and difficult to clear. The resulting blockage of these sites leads to pancreatic insufficiency, "meconium ileus", and devastating "chronic obstructive pulmonary disease" (Al-Awqati, Q. et al. (1992) J. Exp. Biol. 172:245-266).

The voltage-gated chloride channels (CLC) are characterized by 10-12 transmembrane

domains, as well as two small globular domains known as CBS domains. The CLC subunits probably function as homotetramers. CLC proteins are involved in regulation of cell volume, membrane potential stabilization, signal transduction, and transepithelial transport. Mutations in CLC-1, expressed predominantly in skeletal muscle, are responsible for autosomal recessive generalized myotonia and autosomal dominant myotonia congenita, while mutations in the kidney channel CLC-5 lead to kidney stones (Jentsch, T.J. (1996) *Curr. Opin. Neurobiol.* 6:303-310).

Ligand-gated channels open their pores when an extracellular or intracellular mediator binds to the channel. Neurotransmitter-gated channels are channels that open when a neurotransmitter binds to their extracellular domain. These channels exist in the postsynaptic membrane of nerve or muscle cells. There are two types of neurotransmitter-gated channels. Sodium channels open in response to excitatory neurotransmitters, such as acetylcholine, glutamate, and serotonin. This opening causes an influx of Na^+ and produces the initial localized depolarization that activates the voltage-gated channels and starts the action potential. Chloride channels open in response to inhibitory neurotransmitters, such as γ -aminobutyric acid (GABA) and glycine, leading to hyperpolarization of the membrane and the subsequent generation of an action potential. Neurotransmitter-gated ion channels have four transmembrane domains and probably function as pentamers (Jentsch, *supra*). Amino acids in the second transmembrane domain appear to be important in determining channel permeation and selectivity (Sather, W.A. et al. (1994) *Curr. Opin. Neurobiol.* 4:313-323).

Ligand-gated channels can be regulated by intracellular second messengers. For example, calcium-activated K^+ channels are gated by internal calcium ions. In nerve cells, an influx of calcium during depolarization opens K^+ channels to modulate the magnitude of the action potential (Ishi et al., *supra*). The large conductance (BK) channel has been purified from brain and its subunit composition determined. The α subunit of the BK channel has seven rather than six transmembrane domains in contrast to voltage-gated K^+ channels. The extra transmembrane domain is located at the subunit N-terminus. A 28-amino-acid stretch in the C-terminal region of the subunit (the "calcium bowl" region) contains many negatively charged residues and is thought to be the region responsible for calcium binding. The β subunit consists of two transmembrane domains connected by a glycosylated extracellular loop, with intracellular N- and C-termini (Kaczorowski, *supra*; Vergara, C. et al. (1998) *Curr. Opin. Neurobiol.* 8:321-329).

Cyclic nucleotide-gated (CNG) channels are gated by cytosolic cyclic nucleotides. The best examples of these are the cAMP-gated Na^+ channels involved in olfaction and the cGMP-gated cation channels involved in vision. Both systems involve ligand-mediated activation of a G-protein coupled receptor which then alters the level of cyclic nucleotide within the cell. CNG channels also

represent a major pathway for Ca^{2+} entry into neurons, and play roles in neuronal development and plasticity. CNG channels are tetramers containing at least two types of subunits, an α subunit which can form functional homomeric channels, and a β subunit, which modulates the channel properties. All CNG subunits have six transmembrane domains and a pore forming region between the fifth and sixth transmembrane domains, similar to voltage-gated K^+ channels. A large C-terminal domain contains a cyclic nucleotide binding domain, while the N-terminal domain confers variation among channel subtypes (Zufall, F. et al. (1997) *Curr. Opin. Neurobiol.* 7:404-412).

The activity of other types of ion channel proteins may also be modulated by a variety of intracellular signaling proteins. Many channels have sites for phosphorylation by one or more protein kinases including protein kinase A, protein kinase C, tyrosine kinase, and casein kinase II, all of which regulate ion channel activity in cells. Kir channels are activated by the binding of the $\text{G}\beta\gamma$ subunits of heterotrimeric G-proteins (Reimann, F. and F.M. Ashcroft (1999) *Curr. Opin. Cell. Biol.* 11:503-508). Other proteins are involved in the localization of ion channels to specific sites in the cell membrane. Such proteins include the PDZ domain proteins known as MAGUKs (membrane-associated guanylate kinases) which regulate the clustering of ion channels at neuronal synapses (Craven, S.E. and D.S. Bredt (1998) *Cell* 93:495-498).

Disease Correlation

The etiology of numerous human diseases and disorders can be attributed to defects in the transport of molecules across membranes. Defects in the trafficking of membrane-bound transporters and ion channels are associated with several disorders, e.g., cystic fibrosis, glucose-galactose malabsorption syndrome, hypercholesterolemia, von Gierke disease, and certain forms of diabetes mellitus. Single-gene defect diseases resulting in an inability to transport small molecules across membranes include, e.g., cystinuria, iminoglycinuria, Hartup disease, and Fanconi disease (van't Hoff, W.G. (1996) *Exp. Nephrol.* 4:253-262; Talente, G.M. et al. (1994) *Ann. Intern. Med.* 120:218-226; and Chillon, M. et al. (1995) *New Engl. J. Med.* 332:1475-1480).

Human diseases caused by mutations in ion channel genes include disorders of skeletal muscle, cardiac muscle, and the central nervous system. Mutations in the pore-forming subunits of sodium and chloride channels cause myotonia, a muscle disorder in which relaxation after voluntary contraction is delayed. Sodium channel myotonias have been treated with channel blockers. Mutations in muscle sodium and calcium channels cause forms of periodic paralysis, while mutations in the sarcoplasmic calcium release channel, T-tubule calcium channel, and muscle sodium channel cause malignant hyperthermia. Cardiac arrhythmia disorders such as the long QT syndromes and idiopathic ventricular fibrillation are caused by mutations in potassium and sodium channels (Cooper,

E.C. and L.Y. Jan (1998) Proc. Natl. Acad. Sci. USA 96:4759-4766). All four known human idiopathic epilepsy genes code for ion channel proteins (Berkovic, S.F. and I.E. Scheffer (1999) Curr. Opin. Neurology 12:177-182). Other neurological disorders such as ataxias, hemiplegic migraine and hereditary deafness can also result from mutations in ion channel genes (Jen, J. (1999) Curr. Opin.

5 Neurobiol. 9:274-280; Cooper, *supra*).

Ion channels have been the target for many drug therapies. Neurotransmitter-gated channels have been targeted in therapies for treatment of insomnia, anxiety, depression, and schizophrenia. Voltage-gated channels have been targeted in therapies for arrhythmia, ischemic stroke, head trauma, and neurodegenerative disease (Taylor, C.P. and L.S. Narasimhan (1997) Adv. Pharmacol. 39:47-98).

10 Various classes of ion channels also play an important role in the perception of pain, and thus are potential targets for new analgesics. These include the vanilloid-gated ion channels, which are activated by the vanilloid capsaicin, as well as by noxious heat. Local anesthetics such as lidocaine and mexiletine which blockade voltage-gated Na⁺ channels have been useful in the treatment of neuropathic pain (Eglen, *supra*).

15 Ion channels in the immune system have recently been suggested as targets for immunomodulation. T-cell activation depends upon calcium signaling, and a diverse set of T-cell specific ion channels has been characterized that affect this signaling process. Channel blocking agents can inhibit secretion of lymphokines, cell proliferation, and killing of target cells. A peptide antagonist of the T-cell potassium channel Kv1.3 was found to suppress delayed-type hypersensitivity and allogenic responses in pigs, validating the idea of channel blockers as safe and efficacious immunosuppressants (Cahalan, M.D. and K.G. Chandy (1997) Curr. Opin. Biotechnol. 8:749-756).

Expression profiling

Microarrays are analytical tools used in bioanalysis. A microarray has a plurality of molecules spatially distributed over, and stably associated with, the surface of a solid support. Microarrays of 25 polypeptides, polynucleotides, and/or antibodies have been developed and find use in a variety of applications, such as gene sequencing, monitoring gene expression, gene mapping, bacterial identification, drug discovery, and combinatorial chemistry.

One area in particular in which microarrays find use is in gene expression analysis. Array technology can provide a simple way to explore the expression of a single polymorphic gene or the 30 expression profile of a large number of related or unrelated genes. When the expression of a single gene is examined, arrays are employed to detect the expression of a specific gene or its variants. When an expression profile is examined, arrays provide a platform for identifying genes that are tissue specific, are affected by a substance being tested in a toxicology assay, are part of a signaling

cascade, carry out housekeeping functions, or are specifically related to a particular genetic predisposition, condition, disease, or disorder.

Expression Profiling in Treatments for Cancer

Tumor cells stimulate the formation of stroma that secretes various mediators, such as growth factors, cytokines, and proteases, which are critical for tumor growth. For instance, serum tumor necrosis factor alpha (TNF- α) is increased in the circulation of patients with malignancy. Clinically, treatment with TNF- α , also called cachectin, in combination with Interferon-gamma (IFN- γ) may provide a successful approach to overcome the cellular heterogeneity of advanced breast tumors. TNF- α has been demonstrated to be antitumorigenic in MCF-7 cells by inducing apoptosis and inhibiting proliferation. TNF- α is produced by neutrophils, activated lymphocytes, macrophages, NK cells, LAK cells, astrocytes, endothelial cells, smooth muscle cells, and some transformed cells. TNF- α occurs as a secreted, soluble form and as a membrane-anchored form, both of which are biologically active. Two types of receptors for TNF- α have been described and virtually all cell types studied show the presence of one or both of these receptor types. TNF- α and TNF- β are extremely pleiotropic factors due to the ubiquity of their receptors, to their ability to activate multiple signal transduction pathways and to their ability to induce or suppress the expression of a wide number of genes. TNF- α and TNF- β play a critical role in mediation of the inflammatory response and in mediation of resistance to infections and tumor growth.

The cytokine interferon gamma (IFN- γ) induces growth arrest in normal human mammary epithelial cells by establishing a block during mid-G1 phase. IFN- γ inhibits the kinase activities of cdk2, cdk4 and cdk6 within 24 h of treatment. IFN- γ -mediated growth inhibition requires signal transducers and activators of transcription (STAT)-1 activation and may require induction of the cyclin-dependent kinase inhibitor p21. IFN- γ , possibly through the elevation of caspase-8 levels, sensitizes human breast tumor cells to a death receptor-mediated, mitochondria-operated pathway of apoptosis. IFN- γ , also known as Type II interferon or immune interferon, is produced primarily by T-lymphocytes and natural killer cells. IFN- γ exhibits antiproliferative, immunoregulatory and proinflammatory activities and is thus important in host defense mechanisms. IFN- γ induces the production of cytokines, and upregulates the expression of class I and II MHC antigens, Fc receptor, and leukocyte adhesion molecules. It modulates macrophage effector functions, influences isotype switching and potentiates the secretion of immunoglobulins by B cells. IFN- γ also augments TH1 cell expansion and may be required for TH1 cell differentiation. The IFN- γ receptor has been cloned and characterized, and is structurally related to the IL-10 receptor. It is present on almost all cell types except mature erythrocytes.

Breast cancer

Breast cancer is the most frequently diagnosed type of cancer in American women and the second most frequent cause of cancer death. The lifetime risk of an American woman developing breast cancer is 1 in 8, and one-third of women diagnosed with breast cancer die of the disease. A number of risk factors have been identified, including hormonal and genetic factors. One genetic defect associated with breast cancer results in a loss of heterozygosity (LOH) at multiple loci such as p53, Rb, BRCA1, and BRCA2. Another genetic defect is gene amplification involving genes such as c-myc and c-erbB2 (Her2-neu gene). Steroid and growth factor pathways are also altered in breast cancer, notably the estrogen, progesterone, and epidermal growth factor (EGF) pathways. Breast cancer evolves through a multi-step process whereby premalignant mammary epithelial cells undergo a relatively defined sequence of events leading to tumor formation. An early event in tumor development is ductal hyperplasia. Cells undergoing rapid neoplastic growth gradually progress to invasive carcinoma and become metastatic to the lung, bone, and potentially other organs. Variables that may influence the process of tumor progression and malignant transformation include genetic factors, environmental factors, growth factors, and hormones.

Lung cancer

Lung cancer is the leading cause of cancer death for men and the second leading cause of cancer death for women in the U.S. Lung cancers are divided into four histopathologically distinct groups. Three groups (squamous cell carcinoma, adenocarcinoma, and large cell carcinoma) are classified as non-small cell lung cancers (NSCLCs). The fourth group of cancers is referred to as small cell lung cancer (SCLC). Deletions on chromosome 3 are common in this disease and are thought to indicate the presence of a tumor suppressor gene in this region. Activating mutations in K-ras are commonly found in lung cancer and are the basis of one of the mouse models for the disease.

Colon cancer

While soft tissue sarcomas are relatively rare, more than 50% of new patients diagnosed with the disease will die from it. The molecular pathways leading to the development of sarcomas are relatively unknown, due to the rarity of the disease and variation in pathology. Colon cancer evolves through a multi-step process whereby pre-malignant colonocytes undergo a relatively defined sequence of events leading to tumor formation. Several factors participate in the process of tumor progression and malignant transformation including genetic factors, mutations, and selection.

To understand the nature of gene alterations in colorectal cancer, a number of studies have focused on the inherited syndromes. Familial adenomatous polyposis (FAP), is caused by mutations in the adenomatous polyposis coli gene (APC), resulting in truncated or inactive forms of the protein.

This tumor suppressor gene has been mapped to chromosome 5q. Hereditary nonpolyposis colorectal cancer (HNPCC) is caused by mutations in mis-match repair genes. Although hereditary colon cancer syndromes occur in a small percentage of the population and most colorectal cancers are considered sporadic, knowledge from studies of the hereditary syndromes can be generally applied.

- 5 For instance, somatic mutations in APC occur in at least 80% of sporadic colon tumors. APC mutations are thought to be the initiating event in the disease. Other mutations occur subsequently. Approximately 50% of colorectal cancers contain activating mutations in ras, while 85% contain inactivating mutations in p53. Changes in all of these genes lead to gene expression changes in colon cancer.

10 Osteosarcoma

- Osteosarcoma is the most common malignant bone tumor in children. Approximately 80% of patients present with non-metastatic disease. After the diagnosis is made by an initial biopsy, treatment involves the use of 3–4 courses of neoadjuvant chemotherapy before definitive surgery, followed by post-operative chemotherapy. With currently available treatment regimens, approximately
- 15 30–40% of patients with non-metastatic disease relapse after therapy. Currently, there is no prognostic factor that can be used at the time of initial diagnosis to predict which patients will have a high risk of relapse. The only significant prognostic factor predicting the outcome in a patient with non-metastatic osteosarcoma is the histopathologic response of the primary tumor resected at the time of definitive surgery. The degree of necrosis in the primary tumor is a reflection of the tumor
- 20 response to neoadjuvant chemotherapy. A higher degree of necrosis (good or favorable response) is associated with a lower risk of relapse and a better outcome. Patients with a lower degree of necrosis (poor or unfavorable response) have a much higher risk of relapse and poor outcome even after complete resection of the primary tumor. Unfortunately, poor outcome cannot be altered despite modification of post-operative chemotherapy to account for the resistance of the primary tumor to
- 25 neoadjuvant chemotherapy. Thus, there is an urgent need to identify prognostic factors that can be used at the time of diagnosis to recognize the subtypes of osteosarcomas that have various risks of relapse, so that more appropriate chemotherapy can be used at the outset to improve the outcome.

Ovarian cancer

- Ovarian cancer is the leading cause of death from a gynecologic cancer. The majority of
- 30 ovarian cancers are derived from epithelial cells, and 70% of patients with epithelial ovarian cancers present with late-stage disease. As a result, the long-term survival rates for this disease is very low. Identification of early-stage markers for ovarian cancer would significantly increase the survival rate.

Genetic variations involved in ovarian cancer development include mutation of p53 and microsatellite instability. Gene expression patterns likely vary when normal ovary is compared to ovarian tumors.

Immune response

Human peripheral blood mononuclear cells (PBMCs) can be classified into discrete cellular
 5 populations representing the major cellular components of the immune system. PBMCs contain about 52% lymphocytes (12% B lymphocytes, 40% T lymphocytes, 20% NK cells, monocytes, and 3% various cells that include dendritic cells and progenitor cells. The proportions, as well as the biology of these cellular components tend to vary slightly between healthy individuals, depending on factors such as age, gender, past medical history, and genetic background.

10 Tumor necrosis factor alpha (TNF- α), also called cachectin, is produced by neutrophils, activated lymphocytes, macrophages, NK cells, LAK cells, astrocytes, endothelial cells, smooth muscle cells, and some transformed cells. TNF- α occurs as a secreted, soluble form and a membrane-anchored form, both of which are biologically active. Two types of receptors for TNF- α have been described, and virtually all cell types studied show the presence of one or both of these
 15 receptor types. TNF- α and TNF- β are extremely pleiotropic factors due to the ubiquity of their receptors, their ability to activate multiple signal transduction pathways, and their ability to induce or suppress the expression of a wide number of genes. TNF- α and TNF- β play a critical role in mediation of the inflammatory response and in mediation of resistance to infections and tumor growth.

There is a need in the art for new compositions, including nucleic acids and proteins, for the
 20 diagnosis, prevention, and treatment of transport, neurological, muscle, immunological and cell proliferative disorders.

SUMMARY OF THE INVENTION

Various embodiments of the invention provide purified polypeptides, transporters and ion
 25 channels, referred to collectively as 'TRICH' and individually as 'TRICH-1,' 'TRICH-2,' 'TRICH-3,' 'TRICH-4,' 'TRICH-5,' 'TRICH-6,' 'TRICH-7,' 'TRICH-8,' 'TRICH-9,' 'TRICH-10,' 'TRICH-11,' 'TRICH-12,' 'TRICH-13,' 'TRICH-14,' 'TRICH-15,' 'TRICH-16,' 'TRICH-17,' 'TRICH-18,' 'TRICH-19,' 'TRICH-20,' 'TRICH-21,' 'TRICH-22,' 'TRICH-23,' 'TRICH-24,' 'TRICH-25,' 'TRICH-26,' 'TRICH-27,' 'TRICH-28,' 'TRICH-29,' 'TRICH-30,' 'TRICH-31,' 'TRICH-32,'
 30 'TRICH-33,' 'TRICH-34,' 'TRICH-35,' 'TRICH-36,' 'TRICH-37,' 'TRICH-38,' 'TRICH-39,' 'TRICH-40,' 'TRICH-41,' 'TRICH-42,' 'TRICH-43,' 'TRICH-44,' 'TRICH-45,' 'TRICH-46,' 'TRICH-47,' 'TRICH-48,' 'TRICH-49,' 'TRICH-50,' 'TRICH-51,' 'TRICH-52,' 'TRICH-53,' 'TRICH-54,' 'TRICH-55,' 'TRICH-56,' 'TRICH-57,' 'TRICH-58,' and 'TRICH-59' and

methods for using these proteins and their encoding polynucleotides for the detection, diagnosis, and treatment of diseases and medical conditions. Embodiments also provide methods for utilizing the purified transporters and ion channels and/or their encoding polynucleotides for facilitating the drug discovery process, including determination of efficacy, dosage, toxicity, and pharmacology. Related
5 embodiments provide methods for utilizing the purified transporters and ion channels and/or their encoding polynucleotides for investigating the pathogenesis of diseases and medical conditions.

An embodiment provides an isolated polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-59, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical or at
10 least about 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-59, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-59, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-59. Another embodiment provides an isolated polypeptide comprising an amino acid sequence of SEQ ID NO:1-59.

15 Still another embodiment provides an isolated polynucleotide encoding a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-59, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical or at least about 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-59, c) a biologically active fragment of a polypeptide
20 having an amino acid sequence selected from the group consisting of SEQ ID NO:1-59, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-59. In another embodiment, the polynucleotide encodes a polypeptide selected from the group consisting of SEQ ID NO:1-59. In an alternative embodiment, the polynucleotide is selected from the group consisting of SEQ ID NO:60-118.

25 Still another embodiment provides a recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide encoding a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-59, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical or at least about 90% identical to an amino acid sequence selected from the group
30 consisting of SEQ ID NO:1-59, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-59, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-59.

Another embodiment provides a cell transformed with the recombinant polynucleotide. Yet another embodiment provides a transgenic organism comprising the recombinant polynucleotide.

Another embodiment provides a method for producing a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-59, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical or at least about 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-59, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-59, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-59.

10 The method comprises a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell is transformed with a recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide encoding the polypeptide, and b) recovering the polypeptide so expressed.

Yet another embodiment provides an isolated antibody which specifically binds to a

15 polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-59, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical or at least about 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-59, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-59, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-59.

20

Still yet another embodiment provides an isolated polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:60-118, b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical or at least about 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:60-118, c) a polynucleotide complementary to the polynucleotide of a), d) a polynucleotide complementary to the polynucleotide of b), and e) an RNA equivalent of a)-d). In other embodiments, the polynucleotide can comprise at least about 20, 30, 40, 60, 80, or 100 contiguous nucleotides.

25

Yet another embodiment provides a method for detecting a target polynucleotide in a sample, said target polynucleotide being selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:60-118, b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical or at least about 90%

30

identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:60-118, c) a polynucleotide complementary to the polynucleotide of a), d) a polynucleotide complementary to the polynucleotide of b), and e) an RNA equivalent of a)-d). The method comprises a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence

- 5 complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and b) detecting the presence or absence of said hybridization complex. In a related embodiment, the method can include detecting the amount of the hybridization complex. In still other embodiments, the probe can comprise at least about 20, 30,
10 40, 60, 80, or 100 contiguous nucleotides.

Still yet another embodiment provides a method for detecting a target polynucleotide in a sample, said target polynucleotide being selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:60-118, b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical or at
15 least about 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:60-118, c) a polynucleotide complementary to the polynucleotide of a), d) a polynucleotide complementary to the polynucleotide of b), and e) an RNA equivalent of a)-d). The method comprises a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and b) detecting the presence or absence of said amplified target polynucleotide
20 or fragment thereof. In a related embodiment, the method can include detecting the amount of the amplified target polynucleotide or fragment thereof.

Another embodiment provides a composition comprising an effective amount of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-59, b) a polypeptide comprising a naturally occurring
25 amino acid sequence at least 90% identical or at least about 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-59, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-59, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-59, and a pharmaceutically acceptable excipient. In one
30 embodiment, the composition can comprise an amino acid sequence selected from the group consisting of SEQ ID NO:1-59. Other embodiments provide a method of treating a disease or condition associated with decreased or abnormal expression of functional TRICH, comprising administering to a patient in need of such treatment the composition.

Yet another embodiment provides a method for screening a compound for effectiveness as an agonist of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-59, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical or at least about 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-59, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-59, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-59. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting agonist activity in the sample. Another embodiment provides a composition comprising an agonist compound identified by the method and a pharmaceutically acceptable excipient. Yet another embodiment provides a method of treating a disease or condition associated with decreased expression of functional TRICH, comprising administering to a patient in need of such treatment the composition.

Still yet another embodiment provides a method for screening a compound for effectiveness as an antagonist of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-59, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical or at least about 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-59, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-59, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-59. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting antagonist activity in the sample. Another embodiment provides a composition comprising an antagonist compound identified by the method and a pharmaceutically acceptable excipient. Yet another embodiment provides a method of treating a disease or condition associated with overexpression of functional TRICH, comprising administering to a patient in need of such treatment the composition.

Another embodiment provides a method of screening for a compound that specifically binds to a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-59, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical or at least about 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-59, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-59, and d) an immunogenic fragment of a polypeptide having an amino acid sequence

selected from the group consisting of SEQ ID NO:1-59. The method comprises a) combining the polypeptide with at least one test compound under suitable conditions, and b) detecting binding of the polypeptide to the test compound, thereby identifying a compound that specifically binds to the polypeptide.

5 Yet another embodiment provides a method of screening for a compound that modulates the activity of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-59, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical or at least about 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-59, c) a biologically active
10 fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-59, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-59. The method comprises a) combining the polypeptide with at least one test compound under conditions permissive for the activity of the polypeptide, b) assessing the activity of the polypeptide in the presence of the test compound, and c)
15 comparing the activity of the polypeptide in the presence of the test compound with the activity of the polypeptide in the absence of the test compound, wherein a change in the activity of the polypeptide in the presence of the test compound is indicative of a compound that modulates the activity of the polypeptide.

Still yet another embodiment provides a method for screening a compound for effectiveness in
20 altering expression of a target polynucleotide, wherein said target polynucleotide comprises a polynucleotide sequence selected from the group consisting of SEQ ID NO:60-118, the method comprising a) exposing a sample comprising the target polynucleotide to a compound, b) detecting altered expression of the target polynucleotide, and c) comparing the expression of the target polynucleotide in the presence of varying amounts of the compound and in the absence of the
25 compound.

Another embodiment provides a method for assessing toxicity of a test compound, said method comprising a) treating a biological sample containing nucleic acids with the test compound; b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide selected from the group consisting of i) a polynucleotide
30 comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:60-118, ii) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical or at least about 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID

NO:60-118, iii) a polynucleotide having a sequence complementary to i), iv) a polynucleotide complementary to the polynucleotide of ii), and v) an RNA equivalent of i)-iv). Hybridization occurs under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide selected from the group consisting of

5 i) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:60-118, ii) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical or at least about 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:60-118, iii) a polynucleotide complementary to the polynucleotide of i), iv) a polynucleotide complementary to the polynucleotide of ii), and v) an RNA equivalent of i)-iv).

10 Alternatively, the target polynucleotide can comprise a fragment of a polynucleotide selected from the group consisting of i)-v) above; c) quantifying the amount of hybridization complex; and d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

15

BRIEF DESCRIPTION OF THE TABLES

Table 1 summarizes the nomenclature for full length polynucleotide and polypeptide embodiments of the invention.

20 Table 2 shows the GenBank identification number and annotation of the nearest GenBank homolog, and the PROTEOME database identification numbers and annotations of PROTEOME database homologs, for polypeptide embodiments of the invention. The probability scores for the matches between each polypeptide and its homolog(s) are also shown.

25 Table 3 shows structural features of polypeptide embodiments, including predicted motifs and domains, along with the methods, algorithms, and searchable databases used for analysis of the polypeptides.

Table 4 lists the cDNA and/or genomic DNA fragments which were used to assemble polynucleotide embodiments, along with selected fragments of the polynucleotides.

Table 5 shows representative cDNA libraries for polynucleotide embodiments.

30 Table 6 provides an appendix which describes the tissues and vectors used for construction of the cDNA libraries shown in Table 5.

Table 7 shows the tools, programs, and algorithms used to analyze polynucleotides and polypeptides, along with applicable descriptions, references, and threshold parameters.

Table 8 shows single nucleotide polymorphisms found in polynucleotide sequences of the invention, along with allele frequencies in different human populations.

DESCRIPTION OF THE INVENTION

5 Before the present proteins, nucleic acids, and methods are described, it is understood that embodiments of the invention are not limited to the particular machines, instruments, materials, and methods described, as these may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the invention.

10 As used herein and in the appended claims, the singular forms “a,” “an,” and “the” include plural reference unless the context clearly dictates otherwise. Thus, for example, a reference to “a host cell” includes a plurality of such host cells, and a reference to “an antibody” is a reference to one or more antibodies and equivalents thereof known to those skilled in the art, and so forth.

Unless defined otherwise, all technical and scientific terms used herein have the same
15 meanings as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any machines, materials, and methods similar or equivalent to those described herein can be used to practice or test the present invention, the preferred machines, materials and methods are now described. All publications mentioned herein are cited for the purpose of describing and disclosing the cell lines, protocols, reagents and vectors which are reported in the publications and which might be
20 used in connection with various embodiments of the invention. Nothing herein is to be construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention.

DEFINITIONS

“TRICH” refers to the amino acid sequences of substantially purified TRICH obtained from any species, particularly a mammalian species, including bovine, ovine, porcine, murine, equine, and
25 human, and from any source, whether natural, synthetic, semi-synthetic, or recombinant.

The term “agonist” refers to a molecule which intensifies or mimics the biological activity of TRICH. Agonists may include proteins, nucleic acids, carbohydrates, small molecules, or any other compound or composition which modulates the activity of TRICH either by directly interacting with TRICH or by acting on components of the biological pathway in which TRICH participates.

30 An “allelic variant” is an alternative form of the gene encoding TRICH. Allelic variants may result from at least one mutation in the nucleic acid sequence and may result in altered mRNAs or in polypeptides whose structure or function may or may not be altered. A gene may have none, one, or

many allelic variants of its naturally occurring form. Common mutational changes which give rise to allelic variants are generally ascribed to natural deletions, additions, or substitutions of nucleotides. Each of these types of changes may occur alone, or in combination with the others, one or more times in a given sequence.

5 “Altered” nucleic acid sequences encoding TRICH include those sequences with deletions, insertions, or substitutions of different nucleotides, resulting in a polypeptide the same as TRICH or a polypeptide with at least one functional characteristic of TRICH. Included within this definition are polymorphisms which may or may not be readily detectable using a particular oligonucleotide probe of the polynucleotide encoding TRICH, and improper or unexpected hybridization to allelic variants, with
10 a locus other than the normal chromosomal locus for the polynucleotide encoding TRICH. The encoded protein may also be “altered,” and may contain deletions, insertions, or substitutions of amino acid residues which produce a silent change and result in a functionally equivalent TRICH. Deliberate amino acid substitutions may be made on the basis of one or more similarities in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues, as long as the
15 biological or immunological activity of TRICH is retained. For example, negatively charged amino acids may include aspartic acid and glutamic acid, and positively charged amino acids may include lysine and arginine. Amino acids with uncharged polar side chains having similar hydrophilicity values may include: asparagine and glutamine; and serine and threonine. Amino acids with uncharged side chains having similar hydrophilicity values may include: leucine, isoleucine, and valine; glycine and
20 alanine; and phenylalanine and tyrosine.

The terms “amino acid” and “amino acid sequence” can refer to an oligopeptide, a peptide, a polypeptide, or a protein sequence, or a fragment of any of these, and to naturally occurring or synthetic molecules. Where “amino acid sequence” is recited to refer to a sequence of a naturally occurring protein molecule, “amino acid sequence” and like terms are not meant to limit the amino acid
25 sequence to the complete native amino acid sequence associated with the recited protein molecule.

“Amplification” relates to the production of additional copies of a nucleic acid. Amplification may be carried out using polymerase chain reaction (PCR) technologies or other nucleic acid amplification technologies well known in the art.

The term “antagonist” refers to a molecule which inhibits or attenuates the biological activity
30 of TRICH. Antagonists may include proteins such as antibodies, anticalins, nucleic acids, carbohydrates, small molecules, or any other compound or composition which modulates the activity of

TRICH either by directly interacting with TRICH or by acting on components of the biological pathway in which TRICH participates.

The term "antibody" refers to intact immunoglobulin molecules as well as to fragments thereof, such as Fab, F(ab')₂, and Fv fragments, which are capable of binding an epitopic determinant.

5 Antibodies that bind TRICH polypeptides can be prepared using intact polypeptides or using fragments containing small peptides of interest as the immunizing antigen. The polypeptide or oligopeptide used to immunize an animal (e.g., a mouse, a rat, or a rabbit) can be derived from the translation of RNA, or synthesized chemically, and can be conjugated to a carrier protein if desired. Commonly used carriers that are chemically coupled to peptides include bovine serum albumin, thyroglobulin, and

10 keyhole limpet hemocyanin (KLH). The coupled peptide is then used to immunize the animal.

The term "antigenic determinant" refers to that region of a molecule (i.e., an epitope) that makes contact with a particular antibody. When a protein or a fragment of a protein is used to immunize a host animal, numerous regions of the protein may induce the production of antibodies which bind specifically to antigenic determinants (particular regions or three-dimensional structures on the protein). An antigenic determinant may compete with the intact antigen (i.e., the immunogen used to elicit the immune response) for binding to an antibody.

15

The term "aptamer" refers to a nucleic acid or oligonucleotide molecule that binds to a specific molecular target. Aptamers are derived from an *in vitro* evolutionary process (e.g., SELEX (Systematic Evolution of Ligands by EXponential Enrichment), described in U.S. Patent No. 5,270,163), which selects for target-specific aptamer sequences from large combinatorial libraries.

20 Aptamer compositions may be double-stranded or single-stranded, and may include deoxyribonucleotides, ribonucleotides, nucleotide derivatives, or other nucleotide-like molecules. The nucleotide components of an aptamer may have modified sugar groups (e.g., the 2'-OH group of a ribonucleotide may be replaced by 2'-F or 2'-NH₂), which may improve a desired property, e.g.,

25 resistance to nucleases or longer lifetime in blood. Aptamers may be conjugated to other molecules, e.g., a high molecular weight carrier to slow clearance of the aptamer from the circulatory system. Aptamers may be specifically cross-linked to their cognate ligands, e.g., by photo-activation of a cross-linker (Brody, E.N. and L. Gold (2000) J. Biotechnol. 74:5-13).

The term "intramer" refers to an aptamer which is expressed *in vivo*. For example, a

30 vaccinia virus-based RNA expression system has been used to express specific RNA aptamers at high levels in the cytoplasm of leukocytes (Blind, M. et al. (1999) Proc. Natl. Acad. Sci. USA 96:3606-3610).

The term "spiegelmer" refers to an aptamer which includes L-DNA, L-RNA, or other left-handed nucleotide derivatives or nucleotide-like molecules. Aptamers containing left-handed nucleotides are resistant to degradation by naturally occurring enzymes, which normally act on substrates containing right-handed nucleotides.

5 The term "antisense" refers to any composition capable of base-pairing with the "sense" (coding) strand of a polynucleotide having a specific nucleic acid sequence. Antisense compositions may include DNA; RNA; peptide nucleic acid (PNA); oligonucleotides having modified backbone linkages such as phosphorothioates, methylphosphonates, or benzylphosphonates; oligonucleotides having modified sugar groups such as 2'-methoxyethyl sugars or 2'-methoxyethoxy sugars; or
10 oligonucleotides having modified bases such as 5-methyl cytosine, 2'-deoxyuracil, or 7-deaza-2'-deoxyguanosine. Antisense molecules may be produced by any method including chemical synthesis or transcription. Once introduced into a cell, the complementary antisense molecule base-pairs with a naturally occurring nucleic acid sequence produced by the cell to form duplexes which block either transcription or translation. The designation "negative" or "minus" can refer to the antisense strand,
15 and the designation "positive" or "plus" can refer to the sense strand of a reference DNA molecule.

 The term "biologically active" refers to a protein having structural, regulatory, or biochemical functions of a naturally occurring molecule. Likewise, "immunologically active" or "immunogenic" refers to the capability of the natural, recombinant, or synthetic TRICH, or of any oligopeptide thereof, to induce a specific immune response in appropriate animals or cells and to bind with specific
20 antibodies.

 "Complementary" describes the relationship between two single-stranded nucleic acid sequences that anneal by base-pairing. For example, 5'-AGT-3' pairs with its complement, 3'-TCA-5'.

 A "composition comprising a given polynucleotide" and a "composition comprising a given
25 polypeptide" can refer to any composition containing the given polynucleotide or polypeptide. The composition may comprise a dry formulation or an aqueous solution. Compositions comprising polynucleotides encoding TRICH or fragments of TRICH may be employed as hybridization probes. The probes may be stored in freeze-dried form and may be associated with a stabilizing agent such as a carbohydrate. In hybridizations, the probe may be deployed in an aqueous solution containing salts
30 (e.g., NaCl), detergents (e.g., sodium dodecyl sulfate; SDS), and other components (e.g., Denhardt's solution, dry milk, salmon sperm DNA, etc.).

“Consensus sequence” refers to a nucleic acid sequence which has been subjected to repeated DNA sequence analysis to resolve uncalled bases, extended using the XL-PCR kit (Applied Biosystems, Foster City CA) in the 5' and/or the 3' direction, and resequenced, or which has been assembled from one or more overlapping cDNA, EST, or genomic DNA fragments using a computer program for fragment assembly, such as the GELVIEW fragment assembly system (Accelrys, Burlington MA) or Phrap (University of Washington, Seattle WA). Some sequences have been both extended and assembled to produce the consensus sequence.

“Conservative amino acid substitutions” are those substitutions that are predicted to least interfere with the properties of the original protein, i.e., the structure and especially the function of the protein is conserved and not significantly changed by such substitutions. The table below shows amino acids which may be substituted for an original amino acid in a protein and which are regarded as conservative amino acid substitutions.

	Original Residue	Conservative Substitution
15	Ala	Gly, Ser
	Arg	His, Lys
	Asn	Asp, Gln, His
	Asp	Asn, Glu
	Cys	Ala, Ser
	Gln	Asn, Glu, His
20	Glu	Asp, Gln, His
	Gly	Ala
	His	Asn, Arg, Gln, Glu
	Ile	Leu, Val
	Leu	Ile, Val
25	Lys	Arg, Gln, Glu
	Met	Leu, Ile
	Phe	His, Met, Leu, Trp, Tyr
	Ser	Cys, Thr
	Thr	Ser, Val
30	Trp	Phe, Tyr
	Tyr	His, Phe, Trp
	Val	Ile, Leu, Thr

Conservative amino acid substitutions generally maintain (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a beta sheet or alpha helical conformation, (b) the charge or hydrophobicity of the molecule at the site of the substitution, and/or (c) the bulk of the side chain.

A “deletion” refers to a change in the amino acid or nucleotide sequence that results in the absence of one or more amino acid residues or nucleotides.

The term "derivative" refers to a chemically modified polynucleotide or polypeptide.

Chemical modifications of a polynucleotide can include, for example, replacement of hydrogen by an alkyl, acyl, hydroxyl, or amino group. A derivative polynucleotide encodes a polypeptide which retains at least one biological or immunological function of the natural molecule. A derivative polypeptide is
5 one modified by glycosylation, pegylation, or any similar process that retains at least one biological or immunological function of the polypeptide from which it was derived.

A "detectable label" refers to a reporter molecule or enzyme that is capable of generating a measurable signal and is covalently or noncovalently joined to a polynucleotide or polypeptide.

"Differential expression" refers to increased or upregulated; or decreased, downregulated, or
10 absent gene or protein expression, determined by comparing at least two different samples. Such comparisons may be carried out between, for example, a treated and an untreated sample, or a diseased and a normal sample.

"Exon shuffling" refers to the recombination of different coding regions (exons). Since an exon may represent a structural or functional domain of the encoded protein, new proteins may be
15 assembled through the novel reassortment of stable substructures, thus allowing acceleration of the evolution of new protein functions.

A "fragment" is a unique portion of TRICH or a polynucleotide encoding TRICH which can be identical in sequence to, but shorter in length than, the parent sequence. A fragment may comprise up to the entire length of the defined sequence, minus one nucleotide/amino acid residue. For
20 example, a fragment may comprise from about 5 to about 1000 contiguous nucleotides or amino acid residues. A fragment used as a probe, primer, antigen, therapeutic molecule, or for other purposes, may be at least 5, 10, 15, 16, 20, 25, 30, 40, 50, 60, 75, 100, 150, 250 or at least 500 contiguous nucleotides or amino acid residues in length. Fragments may be preferentially selected from certain regions of a molecule. For example, a polypeptide fragment may comprise a certain length of
25 contiguous amino acids selected from the first 250 or 500 amino acids (or first 25% or 50%) of a polypeptide as shown in a certain defined sequence. Clearly these lengths are exemplary, and any length that is supported by the specification, including the Sequence Listing, tables, and figures, may be encompassed by the present embodiments.

A fragment of SEQ ID NO:60-118 can comprise a region of unique polynucleotide sequence
30 that specifically identifies SEQ ID NO:60-118, for example, as distinct from any other sequence in the genome from which the fragment was obtained. A fragment of SEQ ID NO:60-118 can be employed in one or more embodiments of methods of the invention, for example, in hybridization and

amplification technologies and in analogous methods that distinguish SEQ ID NO:60-118 from related polynucleotides. The precise length of a fragment of SEQ ID NO:60-118 and the region of SEQ ID NO:60-118 to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

5 A fragment of SEQ ID NO:1-59 is encoded by a fragment of SEQ ID NO:60-118. A fragment of SEQ ID NO:1-59 can comprise a region of unique amino acid sequence that specifically identifies SEQ ID NO:1-59. For example, a fragment of SEQ ID NO:1-59 can be used as an immunogenic peptide for the development of antibodies that specifically recognize SEQ ID NO:1-59. The precise length of a fragment of SEQ ID NO:1-59 and the region of SEQ ID NO:1-59 to which
10 the fragment corresponds can be determined based on the intended purpose for the fragment using one or more analytical methods described herein or otherwise known in the art.

A "full length" polynucleotide is one containing at least a translation initiation codon (e.g., methionine) followed by an open reading frame and a translation termination codon. A "full length" polynucleotide sequence encodes a "full length" polypeptide sequence.

15 "Homology" refers to sequence similarity or, alternatively, sequence identity, between two or more polynucleotide sequences or two or more polypeptide sequences.

The terms "percent identity" and "% identity," as applied to polynucleotide sequences, refer to the percentage of identical nucleotide matches between at least two polynucleotide sequences aligned using a standardized algorithm. Such an algorithm may insert, in a standardized and reproducible way,
20 gaps in the sequences being compared in order to optimize alignment between two sequences, and therefore achieve a more meaningful comparison of the two sequences.

Percent identity between polynucleotide sequences may be determined using one or more computer algorithms or programs known in the art or described herein. For example, percent identity can be determined using the default parameters of the CLUSTAL V algorithm as incorporated into
25 the MEGALIGN version 3.12e sequence alignment program. This program is part of the LASERGENE software package, a suite of molecular biological analysis programs (DNASTAR, Madison WI). CLUSTAL V is described in Higgins, D.G. and P.M. Sharp (1989; CABIOS 5:151-153) and in Higgins, D.G. et al. (1992; CABIOS 8:189-191). For pairwise alignments of polynucleotide sequences, the default parameters are set as follows: Ktuple=2, gap penalty=5,
30 window=4, and "diagonals saved"=4. The "weighted" residue weight table is selected as the default.

Alternatively, a suite of commonly used and freely available sequence comparison algorithms which can be used is provided by the National Center for Biotechnology Information (NCBI) Basic

Local Alignment Search Tool (BLAST) (Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410), which is available from several sources, including the NCBI, Bethesda, MD, and on the Internet at <http://www.ncbi.nlm.nih.gov/BLAST/>. The BLAST software suite includes various sequence analysis programs including "blastn," that is used to align a known polynucleotide sequence with other polynucleotide sequences from a variety of databases. Also available is a tool called "BLAST 2 Sequences" that is used for direct pairwise comparison of two nucleotide sequences. "BLAST 2 Sequences" can be accessed and used interactively at <http://www.ncbi.nlm.nih.gov/gorf/bl2.html>. The "BLAST 2 Sequences" tool can be used for both blastn and blastp (discussed below). BLAST programs are commonly used with gap and other parameters set to default settings. For example, to compare two nucleotide sequences, one may use blastn with the "BLAST 2 Sequences" tool Version 2.0.12 (April-21-2000) set at default parameters. Such default parameters may be, for example:

Matrix: BLOSUM62

Reward for match: 1

Penalty for mismatch: -2

Open Gap: 5 and Extension Gap: 2 penalties

Gap x drop-off: 50

Expect: 10

Word Size: 11

Filter: on

Percent identity may be measured over the length of an entire defined sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined sequence, for instance, a fragment of at least 20, at least 30, at least 40, at least 50, at least 70, at least 100, or at least 200 contiguous nucleotides. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in the tables, figures, or Sequence Listing, may be used to describe a length over which percentage identity may be measured.

Nucleic acid sequences that do not show a high degree of identity may nevertheless encode similar amino acid sequences due to the degeneracy of the genetic code. It is understood that changes in a nucleic acid sequence can be made using this degeneracy to produce multiple nucleic acid sequences that all encode substantially the same protein.

The phrases "percent identity" and "% identity," as applied to polypeptide sequences, refer to the percentage of identical residue matches between at least two polypeptide sequences aligned using

a standardized algorithm. Methods of polypeptide sequence alignment are well-known. Some alignment methods take into account conservative amino acid substitutions. Such conservative substitutions, explained in more detail above, generally preserve the charge and hydrophobicity at the site of substitution, thus preserving the structure (and therefore function) of the polypeptide. The phrases “percent similarity” and “% similarity,” as applied to polypeptide sequences, refer to the percentage of residue matches, including identical residue matches and conservative substitutions, between at least two polypeptide sequences aligned using a standardized algorithm. In contrast, conservative substitutions are not included in the calculation of percent identity between polypeptide sequences.

Percent identity between polypeptide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment program (described and referenced above). For pairwise alignments of polypeptide sequences using CLUSTAL V, the default parameters are set as follows: Ktuple=1, gap penalty=3, window=5, and “diagonals saved”=5. The PAM250 matrix is selected as the default residue weight table.

Alternatively the NCBI BLAST software suite may be used. For example, for a pairwise comparison of two polypeptide sequences, one may use the “BLAST 2 Sequences” tool Version 2.0.12 (April-21-2000) with blastp set at default parameters. Such default parameters may be, for example:

Matrix: BLOSUM62
Open Gap: 11 and Extension Gap: 1 penalties
Gap x drop-off: 50
Expect: 10
Word Size: 3
Filter: on

Percent identity may be measured over the length of an entire defined polypeptide sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined polypeptide sequence, for instance, a fragment of at least 15, at least 20, at least 30, at least 40, at least 50, at least 70 or at least 150 contiguous residues. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in the tables, figures or Sequence Listing, may be used to describe a length over which percentage identity may be measured.

“Human artificial chromosomes” (HACs) are linear microchromosomes which may contain DNA sequences of about 6 kb to 10 Mb in size and which contain all of the elements required for chromosome replication, segregation and maintenance.

The term “humanized antibody” refers to an antibody molecule in which the amino acid
5 sequence in the non-antigen binding regions has been altered so that the antibody more closely resembles a human antibody, and still retains its original binding ability.

“Hybridization” refers to the process by which a polynucleotide strand anneals with a complementary strand through base pairing under defined hybridization conditions. Specific hybridization is an indication that two nucleic acid sequences share a high degree of complementarity.
10 Specific hybridization complexes form under permissive annealing conditions and remain hybridized after the “washing” step(s). The washing step(s) is particularly important in determining the stringency of the hybridization process, with more stringent conditions allowing less non-specific binding, i.e., binding between pairs of nucleic acid strands that are not perfectly matched. Permissive conditions for annealing of nucleic acid sequences are routinely determinable by one of ordinary skill in
15 the art and may be consistent among hybridization experiments, whereas wash conditions may be varied among experiments to achieve the desired stringency, and therefore hybridization specificity. Permissive annealing conditions occur, for example, at 68°C in the presence of about 6 x SSC, about 1% (w/v) SDS, and about 100 µg/ml sheared, denatured salmon sperm DNA.

Generally, stringency of hybridization is expressed, in part, with reference to the temperature
20 under which the wash step is carried out. Such wash temperatures are typically selected to be about 5°C to 20°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. An equation for calculating T_m and conditions for nucleic acid hybridization are well known and can be found in Sambrook, J. and D.W.
25 Russell (2001; Molecular Cloning: A Laboratory Manual, 3rd ed., vol. 1-3, Cold Spring Harbor Press, Cold Spring Harbor NY, ch. 9).

High stringency conditions for hybridization between polynucleotides of the present invention include wash conditions of 68°C in the presence of about 0.2 x SSC and about 0.1% SDS, for 1 hour. Alternatively, temperatures of about 65°C, 60°C, 55°C, or 42°C may be used. SSC concentration may
30 be varied from about 0.1 to 2 x SSC, with SDS being present at about 0.1%. Typically, blocking reagents are used to block non-specific hybridization. Such blocking reagents include, for instance, sheared and denatured salmon sperm DNA at about 100-200 µg/ml. Organic solvent, such as

formamide at a concentration of about 35-50% v/v, may also be used under particular circumstances, such as for RNA:DNA hybridizations. Useful variations on these wash conditions will be readily apparent to those of ordinary skill in the art. Hybridization, particularly under high stringency conditions, may be suggestive of evolutionary similarity between the nucleotides. Such similarity is
5 strongly indicative of a similar role for the nucleotides and their encoded polypeptides.

The term "hybridization complex" refers to a complex formed between two nucleic acids by virtue of the formation of hydrogen bonds between complementary bases. A hybridization complex may be formed in solution (e.g., C_0t or R_0t analysis) or formed between one nucleic acid present in solution and another nucleic acid immobilized on a solid support (e.g., paper, membranes, filters, chips,
10 pins or glass slides, or any other appropriate substrate to which cells or their nucleic acids have been fixed).

The words "insertion" and "addition" refer to changes in an amino acid or polynucleotide sequence resulting in the addition of one or more amino acid residues or nucleotides, respectively.

"Immune response" can refer to conditions associated with inflammation, trauma, immune
15 disorders, or infectious or genetic disease, etc. These conditions can be characterized by expression of various factors, e.g., cytokines, chemokines, and other signaling molecules, which may affect cellular and systemic defense systems.

An "immunogenic fragment" is a polypeptide or oligopeptide fragment of TRICH which is capable of eliciting an immune response when introduced into a living organism, for example, a
20 mammal. The term "immunogenic fragment" also includes any polypeptide or oligopeptide fragment of TRICH which is useful in any of the antibody production methods disclosed herein or known in the art.

The term "microarray" refers to an arrangement of a plurality of polynucleotides, polypeptides, antibodies, or other chemical compounds on a substrate.

25 The terms "element" and "array element" refer to a polynucleotide, polypeptide, antibody, or other chemical compound having a unique and defined position on a microarray.

The term "modulate" refers to a change in the activity of TRICH. For example, modulation may cause an increase or a decrease in protein activity, binding characteristics, or any other biological, functional, or immunological properties of TRICH.

30 The phrases "nucleic acid" and "nucleic acid sequence" refer to a nucleotide, oligonucleotide, polynucleotide, or any fragment thereof. These phrases also refer to DNA or RNA of genomic or

synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA), or to any DNA-like or RNA-like material.

“Operably linked” refers to the situation in which a first nucleic acid sequence is placed in a functional relationship with a second nucleic acid sequence. For instance, a promoter is operably
5 linked to a coding sequence if the promoter affects the transcription or expression of the coding sequence. Operably linked DNA sequences may be in close proximity or contiguous and, where necessary to join two protein coding regions, in the same reading frame.

“Peptide nucleic acid” (PNA) refers to an antisense molecule or anti-gene agent which comprises an oligonucleotide of at least about 5 nucleotides in length linked to a peptide backbone of
10 amino acid residues ending in lysine. The terminal lysine confers solubility to the composition. PNAs preferentially bind complementary single stranded DNA or RNA and stop transcript elongation, and may be pegylated to extend their lifespan in the cell.

“Post-translational modification” of an TRICH may involve lipidation, glycosylation, phosphorylation, acetylation, racemization, proteolytic cleavage, and other modifications known in the
15 art. These processes may occur synthetically or biochemically. Biochemical modifications will vary by cell type depending on the enzymatic milieu of TRICH.

“Probe” refers to nucleic acids encoding TRICH, their complements, or fragments thereof, which are used to detect identical, allelic or related nucleic acids. Probes are isolated oligonucleotides or polynucleotides attached to a detectable label or reporter molecule. Typical labels include
20 radioactive isotopes, ligands, chemiluminescent agents, and enzymes. “Primers” are short nucleic acids, usually DNA oligonucleotides, which may be annealed to a target polynucleotide by complementary base-pairing. The primer may then be extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification (and identification) of a nucleic acid, e.g., by the polymerase chain reaction (PCR).

25 Probes and primers as used in the present invention typically comprise at least 15 contiguous nucleotides of a known sequence. In order to enhance specificity, longer probes and primers may also be employed, such as probes and primers that comprise at least 20, 25, 30, 40, 50, 60, 70, 80, 90, 100, or at least 150 consecutive nucleotides of the disclosed nucleic acid sequences. Probes and primers may be considerably longer than these examples, and it is understood that any length supported by the
30 specification, including the tables, figures, and Sequence Listing, may be used.

Methods for preparing and using probes and primers are described in, for example, Sambrook, J. and D.W. Russell (2001; Molecular Cloning: A Laboratory Manual, 3rd ed., vol. 1-3, Cold Spring

Harbor Press, Cold Spring Harbor NY), Ausubel, F.M. et al. (1999; Short Protocols in Molecular Biology, 4th ed., John Wiley & Sons, New York NY), and Innis, M. et al. (1990; PCR Protocols, A Guide to Methods and Applications, Academic Press, San Diego CA). PCR primer pairs can be derived from a known sequence, for example, by using computer programs intended for that purpose
5 such as Primer (Version 0.5, 1991, Whitehead Institute for Biomedical Research, Cambridge MA).

Oligonucleotides for use as primers are selected using software known in the art for such purpose. For example, OLIGO 4.06 software is useful for the selection of PCR primer pairs of up to 100 nucleotides each, and for the analysis of oligonucleotides and larger polynucleotides of up to 5,000 nucleotides from an input polynucleotide sequence of up to 32 kilobases. Similar primer selection
10 programs have incorporated additional features for expanded capabilities. For example, the PrimOU primer selection program (available to the public from the Genome Center at University of Texas South West Medical Center, Dallas TX) is capable of choosing specific primers from megabase sequences and is thus useful for designing primers on a genome-wide scope. The Primer3 primer selection program (available to the public from the Whitehead Institute/MIT Center for Genome
15 Research, Cambridge MA) allows the user to input a "mispriming library," in which sequences to avoid as primer binding sites are user-specified. Primer3 is useful, in particular, for the selection of oligonucleotides for microarrays. (The source code for the latter two primer selection programs may also be obtained from their respective sources and modified to meet the user's specific needs.) The PrimeGen program (available to the public from the UK Human Genome Mapping Project Resource
20 Centre, Cambridge UK) designs primers based on multiple sequence alignments, thereby allowing selection of primers that hybridize to either the most conserved or least conserved regions of aligned nucleic acid sequences. Hence, this program is useful for identification of both unique and conserved oligonucleotides and polynucleotide fragments. The oligonucleotides and polynucleotide fragments identified by any of the above selection methods are useful in hybridization technologies, for example,
25 as PCR or sequencing primers, microarray elements, or specific probes to identify fully or partially complementary polynucleotides in a sample of nucleic acids. Methods of oligonucleotide selection are not limited to those described above.

A "recombinant nucleic acid" is a nucleic acid that is not naturally occurring or has a sequence that is made by an artificial combination of two or more otherwise separated segments of
30 sequence. This artificial combination is often accomplished by chemical synthesis or, more commonly, by the artificial manipulation of isolated segments of nucleic acids, e.g., by genetic engineering techniques such as those described in Sambrook and Russell (*supra*). The term recombinant includes

nucleic acids that have been altered solely by addition, substitution, or deletion of a portion of the nucleic acid. Frequently, a recombinant nucleic acid may include a nucleic acid sequence operably linked to a promoter sequence. Such a recombinant nucleic acid may be part of a vector that is used, for example, to transform a cell.

- 5 Alternatively, such recombinant nucleic acids may be part of a viral vector, e.g., based on a vaccinia virus, that could be used to vaccinate a mammal wherein the recombinant nucleic acid is expressed, inducing a protective immunological response in the mammal.

 A "regulatory element" refers to a nucleic acid sequence usually derived from untranslated regions of a gene and includes enhancers, promoters, introns, and 5' and 3' untranslated regions
10 (UTRs). Regulatory elements interact with host or viral proteins which control transcription, translation, or RNA stability.

 "Reporter molecules" are chemical or biochemical moieties used for labeling a nucleic acid, amino acid, or antibody. Reporter molecules include radionuclides; enzymes; fluorescent, chemiluminescent, or chromogenic agents; substrates; cofactors; inhibitors; magnetic particles; and
15 other moieties known in the art.

 An "RNA equivalent," in reference to a DNA molecule, is composed of the same linear sequence of nucleotides as the reference DNA molecule with the exception that all occurrences of the nitrogenous base thymine are replaced with uracil, and the sugar backbone is composed of ribose instead of deoxyribose.

- 20 The term "sample" is used in its broadest sense. A sample suspected of containing TRICH, nucleic acids encoding TRICH, or fragments thereof may comprise a bodily fluid; an extract from a cell, chromosome, organelle, or membrane isolated from a cell; a cell; genomic DNA, RNA, or cDNA, in solution or bound to a substrate; a tissue; a tissue print; etc.

 The terms "specific binding" and "specifically binding" refer to that interaction between a
25 protein or peptide and an agonist, an antibody, an antagonist, a small molecule, or any natural or synthetic binding composition. The interaction is dependent upon the presence of a particular structure of the protein, e.g., the antigenic determinant or epitope, recognized by the binding molecule. For example, if an antibody is specific for epitope "A," the presence of a polypeptide comprising the epitope A, or the presence of free unlabeled A, in a reaction containing free labeled A and the
30 antibody will reduce the amount of labeled A that binds to the antibody.

 The term "substantially purified" refers to nucleic acid or amino acid sequences that are removed from their natural environment and are isolated or separated, and are at least about 60%

free, preferably at least about 75% free, and most preferably at least about 90% free from other components with which they are naturally associated.

A "substitution" refers to the replacement of one or more amino acid residues or nucleotides by different amino acid residues or nucleotides, respectively.

5 "Substrate" refers to any suitable rigid or semi-rigid support including membranes, filters, chips, slides, wafers, fibers, magnetic or nonmagnetic beads, gels, tubing, plates, polymers, microparticles and capillaries. The substrate can have a variety of surface forms, such as wells, trenches, pins, channels and pores, to which polynucleotides or polypeptides are bound.

10 A "transcript image" or "expression profile" refers to the collective pattern of gene expression by a particular cell type or tissue under given conditions at a given time.

"Transformation" describes a process by which exogenous DNA is introduced into a recipient cell. Transformation may occur under natural or artificial conditions according to various methods well known in the art, and may rely on any known method for the insertion of foreign nucleic acid sequences into a prokaryotic or eukaryotic host cell. The method for transformation is selected based
15 on the type of host cell being transformed and may include, but is not limited to, bacteriophage or viral infection, electroporation, heat shock, lipofection, and particle bombardment. The term "transformed cells" includes stably transformed cells in which the inserted DNA is capable of replication either as an autonomously replicating plasmid or as part of the host chromosome, as well as transiently transformed cells which express the inserted DNA or RNA for limited periods of time.

20 A "transgenic organism," as used herein, is any organism, including but not limited to animals and plants, in which one or more of the cells of the organism contains heterologous nucleic acid introduced by way of human intervention, such as by transgenic techniques well known in the art. The nucleic acid is introduced into the cell, directly or indirectly by introduction into a precursor of the cell, by way of deliberate genetic manipulation, such as by microinjection or by infection with a
25 recombinant virus. In another embodiment, the nucleic acid can be introduced by infection with a recombinant viral vector, such as a lentiviral vector (Lois, C. et al. (2002) Science 295:868-872). The term genetic manipulation does not include classical cross-breeding, or *in vitro* fertilization, but rather is directed to the introduction of a recombinant DNA molecule. The transgenic organisms contemplated in accordance with the present invention include bacteria, cyanobacteria, fungi, plants
30 and animals. The isolated DNA of the present invention can be introduced into the host by methods known in the art, for example infection, transfection, transformation or transconjugation. Techniques

for transferring the DNA of the present invention into such organisms are widely known and provided in references such as Sambrook and Russell (*supra*).

A "variant" of a particular nucleic acid sequence is defined as a nucleic acid sequence having at least 40% sequence identity to the particular nucleic acid sequence over a certain length of one of the nucleic acid sequences using blastn with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such a pair of nucleic acids may show, for example, at least 50%, at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% or greater sequence identity over a certain defined length. A variant may be described as, for example, an "allelic" (as defined above), "splice," "species," or "polymorphic" variant. A splice variant may have significant identity to a reference molecule, but will generally have a greater or lesser number of polynucleotides due to alternate splicing during mRNA processing. The corresponding polypeptide may possess additional functional domains or lack domains that are present in the reference molecule. Species variants are polynucleotides that vary from one species to another. The resulting polypeptides will generally have significant amino acid identity relative to each other. A polymorphic variant is a variation in the polynucleotide sequence of a particular gene between individuals of a given species. Polymorphic variants also may encompass "single nucleotide polymorphisms" (SNPs) in which the polynucleotide sequence varies by one nucleotide base. The presence of SNPs may be indicative of, for example, a certain population, a disease state, or a propensity for a disease state.

A "variant" of a particular polypeptide sequence is defined as a polypeptide sequence having at least 40% sequence identity or sequence similarity to the particular polypeptide sequence over a certain length of one of the polypeptide sequences using blastp with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such a pair of polypeptides may show, for example, at least 50%, at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% or greater sequence identity or sequence similarity over a certain defined length of one of the polypeptides.

THE INVENTION

Various embodiments of the invention include new human transporters and ion channels (TRICH), the polynucleotides encoding TRICH, and the use of these compositions for the diagnosis,

treatment, or prevention of transport, neurological, muscle, immunological and cell proliferative disorders.

Table 1 summarizes the nomenclature for the full length polynucleotide and polypeptide embodiments of the invention. Each polynucleotide and its corresponding polypeptide are correlated to a single Incyte project identification number (Incyte Project ID). Each polypeptide sequence is denoted by both a polypeptide sequence identification number (Polypeptide SEQ ID NO:) and an Incyte polypeptide sequence number (Incyte Polypeptide ID) as shown. Each polynucleotide sequence is denoted by both a polynucleotide sequence identification number (Polynucleotide SEQ ID NO:) and an Incyte polynucleotide consensus sequence number (Incyte Polynucleotide ID) as shown. Column 6 shows the Incyte ID numbers of physical, full length clones corresponding to the polypeptide and polynucleotide sequences of the invention. The full length clones encode polypeptides which have at least 95% sequence identity to the polypeptide sequences shown in column 3.

Table 2 shows sequences with homology to polypeptide embodiments of the invention as identified by BLAST analysis against the GenBank protein (genpept) database and the PROTEOME database. Columns 1 and 2 show the polypeptide sequence identification number (Polypeptide SEQ ID NO:) and the corresponding Incyte polypeptide sequence number (Incyte Polypeptide ID) for polypeptides of the invention. Column 3 shows the GenBank identification number (GenBank ID NO:) of the nearest GenBank homolog and the PROTEOME database identification numbers (PROTEOME ID NO:) of the nearest PROTEOME database homologs. Column 4 shows the probability scores for the matches between each polypeptide and its homolog(s). Column 5 shows the annotation of the GenBank and PROTEOME database homolog(s) along with relevant citations where applicable, all of which are expressly incorporated by reference herein.

Table 3 shows various structural features of the polypeptides of the invention. Columns 1 and 2 show the polypeptide sequence identification number (SEQ ID NO:) and the corresponding Incyte polypeptide sequence number (Incyte Polypeptide ID) for each polypeptide of the invention. Column 3 shows the number of amino acid residues in each polypeptide. Column 4 shows potential phosphorylation sites, and column 5 shows potential glycosylation sites, as determined by the MOTIFS program of the GCG sequence analysis software package (Accelrys, Burlington MA). Column 6 shows amino acid residues comprising signature sequences, domains, and motifs. Column 7 shows analytical methods for protein structure/function analysis and in some cases, searchable databases to which the analytical methods were applied.

Together, Tables 2 and 3 summarize the properties of polypeptides of the invention, and these properties establish that the claimed polypeptides are transporters and ion channels. For example, SEQ ID NO:7 is 99% identical, from residue M1 to residue E300, to human acetylcholine receptor beta-subunit preprotein (GenBank ID g560155) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is $1.9e-199$, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:7 also has homology to the cholinergic receptor (nicotinic) beta 1 subunit, as determined by BLAST analysis using the PROTEOME database. SEQ ID NO:7 also contains a neurotransmitter-gated ion-channel ligand binding domain and a neurotransmitter-gated ion-channel transmembrane region as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM database of conserved protein families/domains, and a cation transporter family protein domain as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based TIGRFAM database of conserved protein families/domains. (See Table 3.) Data from BLIMPS, MOTIFS, and PROFILESCAN analyses provide further corroborative evidence that SEQ ID NO:7 is a cholinergic receptor subunit. In an alternative example, SEQ ID NO:41 is 97% identical, from residue M1 to residue T241, to human gamma-aminobutyric acidA receptor alpha 2 subunit (GenBank ID g386422) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is $5.4e-215$, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:41 also has homology to the alpha 2 subunit of the GABA-A receptor, a chloride channel that is the major inhibitory neurotransmitter receptor in the brain as determined by BLAST analysis using the PROTEOME database. SEQ ID NO:41 also contains a neurotransmitter-gated ion channel ligand binding domain and a neurotransmitter-gated ion channel transmembrane domain, as well as a cation transporter family protein domain, as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM and TIGRFAM databases of conserved protein families/domains. (See Table 3.) Data from BLIMPS, MOTIFS, and PROFILESCAN analyses, and BLAST analyses against the PRODOM and DOMO databases, provide further corroborative evidence that SEQ ID NO:41 is a GABA receptor. SEQ ID NO:1-6, SEQ ID NO:8-40, and SEQ ID NO:42-59 were analyzed and annotated in a similar manner. The algorithms and parameters for the analysis of SEQ ID NO:1-59 are described in Table 7.

As shown in Table 4, the full length polynucleotide embodiments were assembled using cDNA sequences or coding (exon) sequences derived from genomic DNA, or any combination of these two

types of sequences. Column 1 lists the polynucleotide sequence identification number (Polynucleotide SEQ ID NO:), the corresponding Incyte polynucleotide consensus sequence number (Incyte ID) for each polynucleotide of the invention, and the length of each polynucleotide sequence in basepairs.

Column 2 shows the nucleotide start (5') and stop (3') positions of the cDNA and/or genomic

- 5 sequences used to assemble the full length polynucleotide embodiments, and of fragments of the polynucleotides which are useful, for example, in hybridization or amplification technologies that identify SEQ ID NO:60-118 or that distinguish between SEQ ID NO:60-118 and related polynucleotides.

- The polynucleotide fragments described in Column 2 of Table 4 may refer specifically, for
 10 example, to Incyte cDNAs derived from tissue-specific cDNA libraries or from pooled cDNA libraries. Alternatively, the polynucleotide fragments described in column 2 may refer to GenBank cDNAs or ESTs which contributed to the assembly of the full length polynucleotides. In addition, the polynucleotide fragments described in column 2 may identify sequences derived from the ENSEMBL (The Sanger Centre, Cambridge, UK) database (*i.e.*, those sequences including the designation
 15 "ENST"). Alternatively, the polynucleotide fragments described in column 2 may be derived from the NCBI RefSeq Nucleotide Sequence Records Database (*i.e.*, those sequences including the designation "NM" or "NT") or the NCBI RefSeq Protein Sequence Records (*i.e.*, those sequences including the designation "NP"). Alternatively, the polynucleotide fragments described in column 2 may refer to assemblages of both cDNA and Genscan-predicted exons brought together by an "exon
 20 stitching" algorithm. For example, a polynucleotide sequence identified as FL_XXXXXXX_N₁_N₂_YYYYY_N₃_N₄ represents a "stitched" sequence in which XXXXXX is the identification number of the cluster of sequences to which the algorithm was applied, and YYYYY is the number of the prediction generated by the algorithm, and N_{1,2,3...}, if present, represent specific exons that may have been manually edited during analysis (See Example V). Alternatively, the
 25 polynucleotide fragments in column 2 may refer to assemblages of exons brought together by an "exon-stretching" algorithm. For example, a polynucleotide sequence identified as FLXXXXXX_gAAAAA_gBBBBB_1_N is a "stretched" sequence, with XXXXXX being the Incyte project identification number, gAAAAA being the GenBank identification number of the human genomic sequence to which the "exon-stretching" algorithm was applied, gBBBBB being the GenBank
 30 identification number or NCBI RefSeq identification number of the nearest GenBank protein homolog, and N referring to specific exons (See Example V). In instances where a RefSeq sequence was used

as a protein homolog for the "exon-stretching" algorithm, a RefSeq identifier (denoted by "NM," "NP," or "NT") may be used in place of the GenBank identifier (*i.e.*, *gBBBBB*).

Alternatively, a prefix identifies component sequences that were hand-edited, predicted from genomic DNA sequences, or derived from a combination of sequence analysis methods. The following Table lists examples of component sequence prefixes and corresponding sequence analysis methods associated with the prefixes (see Example IV and Example V).

Prefix	Type of analysis and/or examples of programs
GNN, GFG, ENST	Exon prediction from genomic sequences using, for example, GENSCAN (Stanford University, CA, USA) or FGENES (Computer Genomics Group, The Sanger Centre, Cambridge, UK).
GBI	Hand-edited analysis of genomic sequences.
FL	Stitched or stretched genomic sequences (see Example V).
INCY	Full length transcript and exon prediction from mapping of EST sequences to the genome. Genomic location and EST composition data are combined to predict the exons and resulting transcript.

In some cases, Incyte cDNA coverage redundant with the sequence coverage shown in Table 4 was obtained to confirm the final consensus polynucleotide sequence, but the relevant Incyte cDNA identification numbers are not shown.

Table 5 shows the representative cDNA libraries for those full length polynucleotides which were assembled using Incyte cDNA sequences. The representative cDNA library is the Incyte cDNA library which is most frequently represented by the Incyte cDNA sequences which were used to assemble and confirm the above polynucleotides. The tissues and vectors which were used to construct the cDNA libraries shown in Table 5 are described in Table 6.

Table 8 shows single nucleotide polymorphisms (SNPs) found in polynucleotide sequences of the invention, along with allele frequencies in different human populations. Columns 1 and 2 show the polynucleotide sequence identification number (SEQ ID NO:) and the corresponding Incyte project identification number (PID) for polynucleotides of the invention. Column 3 shows the Incyte identification number for the EST in which the SNP was detected (EST ID), and column 4 shows the identification number for the SNP (SNP ID). Column 5 shows the position within the EST sequence at which the SNP is located (EST SNP), and column 6 shows the position of the SNP within the full-length polynucleotide sequence (CB1 SNP). Column 7 shows the allele found in the EST sequence.

Columns 8 and 9 show the two alleles found at the SNP site. Column 10 shows the amino acid encoded by the codon including the SNP site, based upon the allele found in the EST. Columns 11-14 show the frequency of allele 1 in four different human populations. An entry of n/d (not detected) indicates that the frequency of allele 1 in the population was too low to be detected, while n/a (not available) indicates that the allele frequency was not determined for the population.

The invention also encompasses TRICH variants. Various embodiments of TRICH variants can have at least about 80%, at least about 90%, or at least about 95% amino acid sequence identity to the TRICH amino acid sequence, and can contain at least one functional or structural characteristic of TRICH.

Various embodiments also encompass polynucleotides which encode TRICH. In a particular embodiment, the invention encompasses a polynucleotide sequence comprising a sequence selected from the group consisting of SEQ ID NO:60-118, which encodes TRICH. The polynucleotide sequences of SEQ ID NO:60-118, as presented in the Sequence Listing, embrace the equivalent RNA sequences, wherein occurrences of the nitrogenous base thymine are replaced with uracil, and the sugar backbone is composed of ribose instead of deoxyribose.

The invention also encompasses variants of a polynucleotide encoding TRICH. In particular, such a variant polynucleotide will have at least about 70%, or alternatively at least about 85%, or even at least about 95% polynucleotide sequence identity to a polynucleotide encoding TRICH. A particular aspect of the invention encompasses a variant of a polynucleotide comprising a sequence selected from the group consisting of SEQ ID NO:60-118 which has at least about 70%, or alternatively at least about 85%, or even at least about 95% polynucleotide sequence identity to a nucleic acid sequence selected from the group consisting of SEQ ID NO:60-118. Any one of the polynucleotide variants described above can encode a polypeptide which contains at least one functional or structural characteristic of TRICH.

In addition, or in the alternative, a polynucleotide variant of the invention is a splice variant of a polynucleotide encoding TRICH. A splice variant may have portions which have significant sequence identity to a polynucleotide encoding TRICH, but will generally have a greater or lesser number of polynucleotides due to additions or deletions of blocks of sequence arising from alternate splicing during mRNA processing. A splice variant may have less than about 70%, or alternatively less than about 60%, or alternatively less than about 50% polynucleotide sequence identity to a polynucleotide encoding TRICH over its entire length; however, portions of the splice variant will have at least about 70%, or alternatively at least about 85%, or alternatively at least about 95%, or alternatively 100%

polynucleotide sequence identity to portions of the polynucleotide encoding TRICH. For example, a polynucleotide comprising a sequence of SEQ ID NO:63 is a splice variant of a polynucleotide comprising a sequence of SEQ ID NO:66; and a polynucleotide comprising a sequence of SEQ ID NO:64 is a splice variant of a polynucleotide comprising a sequence of SEQ ID NO:68. In an
5 alternative example, a polynucleotide comprising a sequence of SEQ ID NO:97, a polynucleotide comprising a sequence of SEQ ID NO:98, a polynucleotide comprising a sequence of SEQ ID NO:99, a polynucleotide comprising a sequence of SEQ ID NO:100, a polynucleotide comprising a sequence of SEQ ID NO:101, a polynucleotide comprising a sequence of SEQ ID NO:102, and a polynucleotide comprising a sequence of SEQ ID NO:114 are all splice variants of each other. In a further example,
10 a polynucleotide comprising a sequence of SEQ ID NO:93 is a splice variant of a polynucleotide comprising a sequence of SEQ ID NO:94, a polynucleotide comprising a sequence of SEQ ID NO:106 is a splice variant of a polynucleotide comprising a sequence of SEQ ID NO:107, and a polynucleotide comprising a sequence of SEQ ID NO:116 is a splice variant of a polynucleotide comprising a sequence of SEQ ID NO:117. In addition, a polynucleotide comprising a sequence of SEQ ID NO:60
15 is a splice variant of a polynucleotide comprising a sequence of SEQ ID NO:79, a polynucleotide comprising a sequence of SEQ ID NO:67 is a splice variant of a polynucleotide comprising a sequence of SEQ ID NO:84, a polynucleotide comprising a sequence of SEQ ID NO:71 is a splice variant of a polynucleotide comprising a sequence of SEQ ID NO:75, and a polynucleotide comprising a sequence of SEQ ID NO:73 is a splice variant of a polynucleotide comprising a sequence of SEQ ID NO:81.
20 Any one of the splice variants described above can encode a polypeptide which contains at least one functional or structural characteristic of TRICH.

It will be appreciated by those skilled in the art that as a result of the degeneracy of the genetic code, a multitude of polynucleotide sequences encoding TRICH, some bearing minimal similarity to the polynucleotide sequences of any known and naturally occurring gene, may be
25 produced. Thus, the invention contemplates each and every possible variation of polynucleotide sequence that could be made by selecting combinations based on possible codon choices. These combinations are made in accordance with the standard triplet genetic code as applied to the polynucleotide sequence of naturally occurring TRICH, and all such variations are to be considered as being specifically disclosed.

30 Although polynucleotides which encode TRICH and its variants are generally capable of hybridizing to polynucleotides encoding naturally occurring TRICH under appropriately selected conditions of stringency, it may be advantageous to produce polynucleotides encoding TRICH or its

derivatives possessing a substantially different codon usage, e.g., inclusion of non-naturally occurring codons. Codons may be selected to increase the rate at which expression of the peptide occurs in a particular prokaryotic or eukaryotic host in accordance with the frequency with which particular codons are utilized by the host. Other reasons for substantially altering the nucleotide sequence
5 encoding TRICH and its derivatives without altering the encoded amino acid sequences include the production of RNA transcripts having more desirable properties, such as a greater half-life, than transcripts produced from the naturally occurring sequence.

The invention also encompasses production of polynucleotides which encode TRICH and TRICH derivatives, or fragments thereof, entirely by synthetic chemistry. After production, the
10 synthetic polynucleotide may be inserted into any of the many available expression vectors and cell systems using reagents well known in the art. Moreover, synthetic chemistry may be used to introduce mutations into a polynucleotide encoding TRICH or any fragment thereof.

Embodiments of the invention can also include polynucleotides that are capable of hybridizing to the claimed polynucleotides, and, in particular, to those having the sequences shown in SEQ ID
15 NO:60-118 and fragments thereof, under various conditions of stringency (Wahl, G.M. and S.L. Berger (1987) *Methods Enzymol.* 152:399-407; Kimmel, A.R. (1987) *Methods Enzymol.* 152:507-511). Hybridization conditions, including annealing and wash conditions, are described in "Definitions."

Methods for DNA sequencing are well known in the art and may be used to practice any of the embodiments of the invention. The methods may employ such enzymes as the Klenow fragment
20 of DNA polymerase I, SEQUENASE (US Biochemical, Cleveland OH), Taq polymerase (Applied Biosystems), thermostable T7 polymerase (Amersham Biosciences, Piscataway NJ), or combinations of polymerases and proofreading exonucleases such as those found in the ELONGASE amplification system (Invitrogen, Carlsbad CA). Preferably, sequence preparation is automated with machines such as the MICROLAB 2200 liquid transfer system (Hamilton, Reno NV), PTC200 thermal cycler
25 (MJ Research, Watertown MA) and ABI CATALYST 800 thermal cycler (Applied Biosystems). Sequencing is then carried out using either the ABI 373 or 377 DNA sequencing system (Applied Biosystems), the MEGABACE 1000 DNA sequencing system (Amersham Biosciences), or other systems known in the art. The resulting sequences are analyzed using a variety of algorithms which are well known in the art (Ausubel et al., *supra*, ch. 7; Meyers, R.A. (1995) Molecular Biology and
30 Biotechnology, Wiley VCH, New York NY, pp. 856-853).

The nucleic acids encoding TRICH may be extended utilizing a partial nucleotide sequence and employing various PCR-based methods known in the art to detect upstream sequences, such as

promoters and regulatory elements. For example, one method which may be employed, restriction-site PCR, uses universal and nested primers to amplify unknown sequence from genomic DNA within a cloning vector (Sarkar, G. (1993) PCR Methods Applic. 2:318-322). Another method, inverse PCR, uses primers that extend in divergent directions to amplify unknown sequence from a circularized
5 template. The template is derived from restriction fragments comprising a known genomic locus and surrounding sequences (Triglia, T. et al. (1988) Nucleic Acids Res. 16:8186). A third method, capture PCR, involves PCR amplification of DNA fragments adjacent to known sequences in human and yeast artificial chromosome DNA (Lagerstrom, M. et al. (1991) PCR Methods Applic. 1:111-119). In this method, multiple restriction enzyme digestions and ligations may be used to insert an engineered
10 double-stranded sequence into a region of unknown sequence before performing PCR. Other methods which may be used to retrieve unknown sequences are known in the art (Parker, J.D. et al. (1991) Nucleic Acids Res. 19:3055-3060). Additionally, one may use PCR, nested primers, and PROMOTERFINDER libraries (Clontech, Palo Alto CA) to walk genomic DNA. This procedure avoids the need to screen libraries and is useful in finding intron/exon junctions. For all PCR-based
15 methods, primers may be designed using commercially available software, such as OLIGO 4.06 primer analysis software (National Biosciences, Plymouth MN) or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the template at temperatures of about 68°C to 72°C.

When screening for full-length cDNAs, it is preferable to use libraries that have been
20 size-selected to include larger cDNAs. In addition, random-primed libraries, which often include sequences containing the 5' regions of genes, are preferable for situations in which an oligo d(T) library does not yield a full-length cDNA. Genomic libraries may be useful for extension of sequence into 5' non-transcribed regulatory regions.

Capillary electrophoresis systems which are commercially available may be used to analyze
25 the size or confirm the nucleotide sequence of sequencing or PCR products. In particular, capillary sequencing may employ flowable polymers for electrophoretic separation, four different nucleotide-specific, laser-stimulated fluorescent dyes, and a charge coupled device camera for detection of the emitted wavelengths. Output/light intensity may be converted to electrical signal using appropriate software (e.g., GENOTYPER and SEQUENCE NAVIGATOR, Applied Biosystems), and the entire
30 process from loading of samples to computer analysis and electronic data display may be computer controlled. Capillary electrophoresis is especially preferable for sequencing small DNA fragments which may be present in limited amounts in a particular sample.

In another embodiment of the invention, polynucleotides or fragments thereof which encode TRICH may be cloned in recombinant DNA molecules that direct expression of TRICH, or fragments or functional equivalents thereof, in appropriate host cells. Due to the inherent degeneracy of the genetic code, other polynucleotides which encode substantially the same or a functionally equivalent polypeptides may be produced and used to express TRICH.

The polynucleotides of the invention can be engineered using methods generally known in the art in order to alter TRICH-encoding sequences for a variety of purposes including, but not limited to, modification of the cloning, processing, and/or expression of the gene product. DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. For example, oligonucleotide-mediated site-directed mutagenesis may be used to introduce mutations that create new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, and so forth.

The nucleotides of the present invention may be subjected to DNA shuffling techniques such as MOLECULARBREEDING (Maxygen Inc., Santa Clara CA; described in U.S. Patent No. 5,837,458; Chang, C.-C. et al. (1999) Nat. Biotechnol. 17:793-797; Christians, F.C. et al. (1999) Nat. Biotechnol. 17:259-264; and Crameri, A. et al. (1996) Nat. Biotechnol. 14:315-319) to alter or improve the biological properties of TRICH, such as its biological or enzymatic activity or its ability to bind to other molecules or compounds. DNA shuffling is a process by which a library of gene variants is produced using PCR-mediated recombination of gene fragments. The library is then subjected to selection or screening procedures that identify those gene variants with the desired properties. These preferred variants may then be pooled and further subjected to recursive rounds of DNA shuffling and selection/screening. Thus, genetic diversity is created through "artificial" breeding and rapid molecular evolution. For example, fragments of a single gene containing random point mutations may be recombined, screened, and then reshuffled until the desired properties are optimized. Alternatively, fragments of a given gene may be recombined with fragments of homologous genes in the same gene family, either from the same or different species, thereby maximizing the genetic diversity of multiple naturally occurring genes in a directed and controllable manner.

In another embodiment, polynucleotides encoding TRICH may be synthesized, in whole or in part, using one or more chemical methods well known in the art (Caruthers, M.H. et al. (1980) Nucleic Acids Symp. Ser. 7:215-223; Horn, T. et al. (1980) Nucleic Acids Symp. Ser. 7:225-232). Alternatively, TRICH itself or a fragment thereof may be synthesized using chemical methods known in the art. For example, peptide synthesis can be performed using various solution-phase or

solid-phase techniques (Creighton, T. (1984) Proteins, Structures and Molecular Properties, WH Freeman, New York NY, pp. 55-60; Roberge, J.Y. et al. (1995) *Science* 269:202-204). Automated synthesis may be achieved using the ABI 431A peptide synthesizer (Applied Biosystems).

Additionally, the amino acid sequence of TRICH, or any part thereof, may be altered during direct
5 synthesis and/or combined with sequences from other proteins, or any part thereof, to produce a variant polypeptide or a polypeptide having a sequence of a naturally occurring polypeptide.

The peptide may be substantially purified by preparative high performance liquid chromatography (Chiez, R.M. and F.Z. Regnier (1990) *Methods Enzymol.* 182:392-421). The composition of the synthetic peptides may be confirmed by amino acid analysis or by sequencing
10 (Creighton, *supra*, pp. 28-53).

In order to express a biologically active TRICH, the polynucleotides encoding TRICH or derivatives thereof may be inserted into an appropriate expression vector, i.e., a vector which contains the necessary elements for transcriptional and translational control of the inserted coding sequence in a suitable host. These elements include regulatory sequences, such as enhancers, constitutive and
15 inducible promoters, and 5' and 3' untranslated regions in the vector and in polynucleotides encoding TRICH. Such elements may vary in their strength and specificity. Specific initiation signals may also be used to achieve more efficient translation of polynucleotides encoding TRICH. Such signals include the ATG initiation codon and adjacent sequences, e.g. the Kozak sequence. In cases where a polynucleotide sequence encoding TRICH and its initiation codon and upstream regulatory sequences
20 are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a fragment thereof, is inserted, exogenous translational control signals including an in-frame ATG initiation codon should be provided by the vector. Exogenous translational elements and initiation codons may be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of
25 enhancers appropriate for the particular host cell system used (Scharf, D. et al. (1994) *Results Probl. Cell Differ.* 20:125-162).

Methods which are well known to those skilled in the art may be used to construct expression vectors containing polynucleotides encoding TRICH and appropriate transcriptional and translational control elements. These methods include *in vitro* recombinant DNA techniques, synthetic techniques,
30 and *in vivo* genetic recombination (Sambrook and Russell, *supra*, ch. 1-4, and 8; Ausubel et al., *supra*, ch. 1, 3, and 15).

A variety of expression vector/host systems may be utilized to contain and express polynucleotides encoding TRICH. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with viral expression
 5 vectors (e.g., baculovirus); plant cell systems transformed with viral expression vectors (e.g., cauliflower mosaic virus, CaMV, or tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or animal cell systems (Sambrook and Russell, *supra*; Ausubel et al., *supra*; Van Heeke, G. and S.M. Schuster (1989) J. Biol. Chem. 264:5503-5509; Engelhard, E.K. et al. (1994) Proc. Natl. Acad. Sci. USA 91:3224-3227; Sandig, V. et al. (1996) Hum. Gene Ther. 7:1937-
 10 1945; Takamatsu, N. (1987) EMBO J. 6:307-311; The McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York NY, pp. 191-196; Logan, J. and T. Shenk (1984) Proc. Natl. Acad. Sci. USA 81:3655-3659; Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355). Expression vectors derived from retroviruses, adenoviruses, or herpes or vaccinia viruses, or from various bacterial plasmids, may be used for delivery of polynucleotides to the targeted organ, tissue, or
 15 cell population (Di Nicola, M. et al. (1998) Cancer Gen. Ther. 5:350-356; Yu, M. et al. (1993) Proc. Natl. Acad. Sci. USA 90:6340-6344; Buller, R.M. et al. (1985) Nature 317:813-815; McGregor, D.P. et al. (1994) Mol. Immunol. 31:219-226; Verma, I.M. and N. Somia (1997) Nature 389:239-242). The invention is not limited by the host cell employed.

In bacterial systems, a number of cloning and expression vectors may be selected depending
 20 upon the use intended for polynucleotides encoding TRICH. For example, routine cloning, subcloning, and propagation of polynucleotides encoding TRICH can be achieved using a multifunctional *E. coli* vector such as PBLUESCRIPT (Stratagene, La Jolla CA) or PSPORT1 plasmid (Invitrogen). Ligation of polynucleotides encoding TRICH into the vector's multiple cloning site disrupts the *lacZ* gene, allowing a colorimetric screening procedure for identification of transformed bacteria containing
 25 recombinant molecules. In addition, these vectors may be useful for *in vitro* transcription, dideoxy sequencing, single strand rescue with helper phage, and creation of nested deletions in the cloned sequence (Van Heeke, G. and S.M. Schuster (1989) J. Biol. Chem. 264:5503-5509). When large quantities of TRICH are needed, e.g. for the production of antibodies, vectors which direct high level expression of TRICH may be used. For example, vectors containing the strong, inducible SP6 or T7
 30 bacteriophage promoter may be used.

Yeast expression systems may be used for production of TRICH. A number of vectors containing constitutive or inducible promoters, such as alpha factor, alcohol oxidase, and PGH

promoters, may be used in the yeast *Saccharomyces cerevisiae* or *Pichia pastoris*. In addition, such vectors direct either the secretion or intracellular retention of expressed proteins and enable integration of foreign polynucleotide sequences into the host genome for stable propagation (Ausubel et al., *supra*; Bitter, G.A. et al. (1987) *Methods Enzymol.* 153:516-544; Scorer, C.A. et al. (1994)

5 Bio/Technology 12:181-184).

Plant systems may also be used for expression of TRICH. Transcription of polynucleotides encoding TRICH may be driven by viral promoters, e.g., the 35S and 19S promoters of CaMV used alone or in combination with the omega leader sequence from TMV (Takamatsu, N. (1987) *EMBO J.* 6:307-311). Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock
10 promoters may be used (Coruzzi, G. et al. (1984) *EMBO J.* 3:1671-1680; Broglie, R. et al. (1984) *Science* 224:838-843; Winter, J. et al. (1991) *Results Probl. Cell Differ.* 17:85-105). These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection (The McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York NY, pp. 191-196).

15 In mammalian cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, polynucleotides encoding TRICH may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to obtain infective virus which expresses TRICH in host cells (Logan, J. and T. Shenk (1984) *Proc. Natl. Acad.*
20 *Sci. USA* 81:3655-3659). In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells. SV40 or EBV-based vectors may also be used for high-level protein expression.

Human artificial chromosomes (HACs) may also be employed to deliver larger fragments of DNA than can be contained in and expressed from a plasmid. HACs of about 6 kb to 10 Mb are
25 constructed and delivered via conventional delivery methods (liposomes, polycationic amino polymers, or vesicles) for therapeutic purposes (Harrington, J.J. et al. (1997) *Nat. Genet.* 15:345-355).

For long term production of recombinant proteins in mammalian systems, stable expression of TRICH in cell lines is preferred. For example, polynucleotides encoding TRICH can be transformed into cell lines using expression vectors which may contain viral origins of replication and/or
30 endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells may be allowed to grow for about 1 to 2 days in enriched media before being switched to selective media. The purpose of the selectable marker is to confer

resistance to a selective agent, and its presence allows growth and recovery of cells which successfully express the introduced sequences. Resistant clones of stably transformed cells may be propagated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These
5 include, but are not limited to, the herpes simplex virus thymidine kinase and adenine
phosphoribosyltransferase genes, for use in *tk* and *ap^r* cells, respectively (Wigler, M. et al. (1977)
Cell 11:223-232; Lowy, I. et al. (1980) Cell 22:817-823). Also, antimetabolite, antibiotic, or herbicide
resistance can be used as the basis for selection. For example, *dhfr* confers resistance to
methotrexate; *neo* confers resistance to the aminoglycosides neomycin and G-418; and *als* and *pat*
10 confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively (Wigler, M. et al.
(1980) Proc. Natl. Acad. Sci. USA 77:3567-3570; Colbere-Garapin, F. et al. (1981) J. Mol. Biol.
150:1-14). Additional selectable genes have been described, e.g., *trpB* and *hisD*, which alter cellular
requirements for metabolites (Hartman, S.C. and R.C. Mulligan (1988) Proc. Natl. Acad. Sci. USA
85:8047-8051). Visible markers, e.g., anthocyanins, green fluorescent proteins (GFP; Clontech), β -
15 glucuronidase and its substrate β -glucuronide, or luciferase and its substrate luciferin may be used.
These markers can be used not only to identify transformants, but also to quantify the amount of
transient or stable protein expression attributable to a specific vector system (Rhodes, C.A. (1995)
Methods Mol. Biol. 55:121-131).

Although the presence/absence of marker gene expression suggests that the gene of interest
20 is also present, the presence and expression of the gene may need to be confirmed. For example, if
the sequence encoding TRICH is inserted within a marker gene sequence, transformed cells
containing polynucleotides encoding TRICH can be identified by the absence of marker gene function.
Alternatively, a marker gene can be placed in tandem with a sequence encoding TRICH under the
control of a single promoter. Expression of the marker gene in response to induction or selection
25 usually indicates expression of the tandem gene as well.

In general, host cells that contain the polynucleotide encoding TRICH and that express
TRICH may be identified by a variety of procedures known to those of skill in the art. These
procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations, PCR
amplification, and protein bioassay or immunoassay techniques which include membrane, solution, or
30 chip based technologies for the detection and/or quantification of nucleic acid or protein sequences.

Immunological methods for detecting and measuring the expression of TRICH using either
specific polyclonal or monoclonal antibodies are known in the art. Examples of such techniques

include enzyme-linked immunosorbent assays (ELISAs), radioimmunoassays (RIAs), and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on TRICH is preferred, but a competitive binding assay may be employed. These and other assays are well known in the art

5 (Hampton, R. et al. (1990) Serological Methods, a Laboratory Manual, APS Press, St. Paul MN, Sect. IV; Coligan, J.E. et al. (1997) Current Protocols in Immunology, Greene Pub. Associates and Wiley-Interscience, New York NY; Pound, J.D. (1998) Immunochemical Protocols, Humana Press, Totowa NJ).

A wide variety of labels and conjugation techniques are known by those skilled in the art and

10 may be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides encoding TRICH include oligolabeling, nick translation, end-labeling, or PCR amplification using a labeled nucleotide. . . .

Alternatively, polynucleotides encoding TRICH, or any fragments thereof, may be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available,

15 and may be used to synthesize RNA probes *in vitro* by addition of an appropriate RNA polymerase such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted using a variety of commercially available kits, such as those provided by Amersham Biosciences, Promega (Madison WI), and US Biochemical. Suitable reporter molecules or labels which may be used for ease of detection include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents, as

20 well as substrates, cofactors, inhibitors, magnetic particles, and the like.

Host cells transformed with polynucleotides encoding TRICH may be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a transformed cell may be secreted or retained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing

25 polynucleotides which encode TRICH may be designed to contain signal sequences which direct secretion of TRICH through a prokaryotic or eukaryotic cell membrane.

In addition, a host cell strain may be chosen for its ability to modulate expression of the inserted polynucleotides or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation,

30 phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" or "pro" form of the protein may also be used to specify protein targeting, folding, and/or activity. Different host cells which have specific cellular machinery and characteristic mechanisms for

post-translational activities (e.g., CHO, HeLa, MDCK, HEK293, and WI38) are available from the American Type Culture Collection (ATCC, Manassas VA) and may be chosen to ensure the correct modification and processing of the foreign protein.

In another embodiment of the invention, natural, modified, or recombinant polynucleotides
5 encoding TRICH may be ligated to a heterologous sequence resulting in translation of a fusion protein in any of the aforementioned host systems. For example, a chimeric TRICH protein containing a heterologous moiety that can be recognized by a commercially available antibody may facilitate the screening of peptide libraries for inhibitors of TRICH activity. Heterologous protein and peptide moieties may also facilitate purification of fusion proteins using commercially available affinity
10 matrices. Such moieties include, but are not limited to, glutathione S-transferase (GST), maltose binding protein (MBP), thioredoxin (Trx), calmodulin binding peptide (CBP), 6-His, FLAG, *c-myc*, and hemagglutinin (HA). GST, MBP, Trx, CBP, and 6-His enable purification of their cognate fusion proteins on immobilized glutathione, maltose, phenylarsine oxide, calmodulin, and metal-chelate resins, respectively. FLAG, *c-myc*, and hemagglutinin (HA) enable immunoaffinity purification of fusion
15 proteins using commercially available monoclonal and polyclonal antibodies that specifically recognize these epitope tags. A fusion protein may also be engineered to contain a proteolytic cleavage site located between the TRICH encoding sequence and the heterologous protein sequence, so that TRICH may be cleaved away from the heterologous moiety following purification. Methods for fusion protein expression and purification are discussed in Ausubel et al. (*supra*, ch. 10 and 16). A
20 variety of commercially available kits may also be used to facilitate expression and purification of fusion proteins.

In another embodiment, synthesis of radiolabeled TRICH may be achieved *in vitro* using the TNT rabbit reticulocyte lysate or wheat germ extract system (Promega). These systems couple
transcription and translation of protein-coding sequences operably associated with the T7, T3, or SP6
25 promoters. Translation takes place in the presence of a radiolabeled amino acid precursor, for example, ³⁵S-methionine.

TRICH, fragments of TRICH, or variants of TRICH may be used to screen for compounds that specifically bind to TRICH. One or more test compounds may be screened for specific binding to TRICH. In various embodiments, 1, 2, 3, 4, 5, 10, 20, 50, 100, or 200 test compounds can be screened
30 for specific binding to TRICH. Examples of test compounds can include antibodies, anticalins, oligonucleotides, proteins (e.g., ligands or receptors), or small molecules.

In related embodiments, variants of TRICH can be used to screen for binding of test compounds, such as antibodies, to TRICH, a variant of TRICH, or a combination of TRICH and/or one or more variants TRICH. In an embodiment, a variant of TRICH can be used to screen for compounds that bind to a variant of TRICH, but not to TRICH having the exact sequence of a
5 sequence of SEQ ID NO:1-59. TRICH variants used to perform such screening can have a range of about 50% to about 99% sequence identity to TRICH, with various embodiments having 60%, 70%, 75%, 80%, 85%, 90%, and 95% sequence identity.

In an embodiment, a compound identified in a screen for specific binding to TRICH can be closely related to the natural ligand of TRICH, e.g., a ligand or fragment thereof, a natural substrate, a
10 structural or functional mimetic, or a natural binding partner (Coligan, J.E. et al. (1991) Current Protocols in Immunology 1(2):Chapter 5). In another embodiment, the compound thus identified can be a natural ligand of a receptor TRICH (Howard, A.D. et al. (2001) *Trends Pharmacol. Sci.* 22:132-140; Wise, A. et al. (2002) *Drug Discovery Today* 7:235-246).

In other embodiments, a compound identified in a screen for specific binding to TRICH can be
15 closely related to the natural receptor to which TRICH binds, at least a fragment of the receptor, or a fragment of the receptor including all or a portion of the ligand binding site or binding pocket. For example, the compound may be a receptor for TRICH which is capable of propagating a signal, or a decoy receptor for TRICH which is not capable of propagating a signal (Ashkenazi, A. and V.M. Divit (1999) *Curr. Opin. Cell Biol.* 11:255-260; Mantovani, A. et al. (2001) *Trends Immunol.* 22:328-
20 336). The compound can be rationally designed using known techniques. Examples of such techniques include those used to construct the compound etanercept (ENBREL; Amgen Inc., Thousand Oaks CA), which is efficacious for treating rheumatoid arthritis in humans. Etanercept is an engineered p75 tumor necrosis factor (TNF) receptor dimer linked to the Fc portion of human IgG₁ (Taylor, P.C. et al. (2001) *Curr. Opin. Immunol.* 13:611-616).

25 In one embodiment, two or more antibodies having similar or, alternatively, different specificities can be screened for specific binding to TRICH, fragments of TRICH, or variants of TRICH. The binding specificity of the antibodies thus screened can thereby be selected to identify particular fragments or variants of TRICH. In one embodiment, an antibody can be selected such that its binding specificity allows for preferential identification of specific fragments or variants of TRICH.
30 In another embodiment, an antibody can be selected such that its binding specificity allows for preferential diagnosis of a specific disease or condition having increased, decreased, or otherwise abnormal production of TRICH.

In an embodiment, anticalins can be screened for specific binding to TRICH, fragments of TRICH, or variants of TRICH. Anticalins are ligand-binding proteins that have been constructed based on a lipocalin scaffold (Weiss, G.A. and H.B. Lowman (2000) Chem. Biol. 7:R177-R184; Skerra, A. (2001) J. Biotechnol. 74:257-275). The protein architecture of lipocalins can include a
5 beta-barrel having eight antiparallel beta-strands, which supports four loops at its open end. These loops form the natural ligand-binding site of the lipocalins, a site which can be re-engineered *in vitro* by amino acid substitutions to impart novel binding specificities. The amino acid substitutions can be made using methods known in the art or described herein, and can include conservative substitutions (e.g., substitutions that do not alter binding specificity) or substitutions that modestly, moderately, or
10 significantly alter binding specificity.

In one embodiment, screening for compounds which specifically bind to, stimulate, or inhibit TRICH involves producing appropriate cells which express TRICH, either as a secreted protein or on the cell membrane. Preferred cells can include cells from mammals, yeast, *Drosophila*, or *E. coli*. Cells expressing TRICH or cell membrane fractions which contain TRICH are then contacted with a
15 test compound and binding, stimulation, or inhibition of activity of either TRICH or the compound is analyzed.

An assay may simply test binding of a test compound to the polypeptide, wherein binding is detected by a fluorophore, radioisotope, enzyme conjugate, or other detectable label. For example, the assay may comprise the steps of combining at least one test compound with TRICH, either in solution
20 or affixed to a solid support, and detecting the binding of TRICH to the compound. Alternatively, the assay may detect or measure binding of a test compound in the presence of a labeled competitor. Additionally, the assay may be carried out using cell-free preparations, chemical libraries, or natural product mixtures, and the test compound(s) may be free in solution or affixed to a solid support.

An assay can be used to assess the ability of a compound to bind to its natural ligand and/or to
25 inhibit the binding of its natural ligand to its natural receptors. Examples of such assays include radio-labeling assays such as those described in U.S. Patent No. 5,914,236 and U.S. Patent No. 6,372,724. In a related embodiment, one or more amino acid substitutions can be introduced into a polypeptide compound (such as a receptor) to improve or alter its ability to bind to its natural ligands (Matthews, D.J. and J.A. Wells. (1994) Chem. Biol. 1:25-30). In another related embodiment, one or more amino
30 acid substitutions can be introduced into a polypeptide compound (such as a ligand) to improve or alter its ability to bind to its natural receptors (Cunningham, B.C. and J.A. Wells (1991) Proc. Natl. Acad. Sci. USA 88:3407-3411; Lowman, H.B. et al. (1991) J. Biol. Chem. 266:10982-10988).

TRICH, fragments of TRICH, or variants of TRICH may be used to screen for compounds that modulate the activity of TRICH. Such compounds may include agonists, antagonists, or partial or inverse agonists. In one embodiment, an assay is performed under conditions permissive for TRICH activity, wherein TRICH is combined with at least one test compound, and the activity of TRICH in the presence of a test compound is compared with the activity of TRICH in the absence of the test compound. A change in the activity of TRICH in the presence of the test compound is indicative of a compound that modulates the activity of TRICH. Alternatively, a test compound is combined with an *in vitro* or cell-free system comprising TRICH under conditions suitable for TRICH activity, and the assay is performed. In either of these assays, a test compound which modulates the activity of TRICH may do so indirectly and need not come in direct contact with the test compound. At least one and up to a plurality of test compounds may be screened.

In another embodiment, polynucleotides encoding TRICH or their mammalian homologs may be "knocked out" in an animal model system using homologous recombination in embryonic stem (ES) cells. Such techniques are well known in the art and are useful for the generation of animal models of human disease (see, e.g., U.S. Patent No. 5,175,383 and U.S. Patent No. 5,767,337). For example, mouse ES cells, such as the mouse 129/SvJ cell line, are derived from the early mouse embryo and grown in culture. The ES cells are transformed with a vector containing the gene of interest disrupted by a marker gene, e.g., the neomycin phosphotransferase gene (*neo*; Capecchi, M.R. (1989) Science 244:1288-1292). The vector integrates into the corresponding region of the host genome by homologous recombination. Alternatively, homologous recombination takes place using the Cre-loxP system to knockout a gene of interest in a tissue- or developmental stage-specific manner (Marth, J.D. (1996) Clin. Invest. 97:1999-2002; Wagner, K.U. et al. (1997) Nucleic Acids Res. 25:4323-4330). Transformed ES cells are identified and microinjected into mouse cell blastocysts such as those from the C57BL/6 mouse strain. The blastocysts are surgically transferred to pseudopregnant dams, and the resulting chimeric progeny are genotyped and bred to produce heterozygous or homozygous strains. Transgenic animals thus generated may be tested with potential therapeutic or toxic agents.

Polynucleotides encoding TRICH may also be manipulated *in vitro* in ES cells derived from human blastocysts. Human ES cells have the potential to differentiate into at least eight separate cell lineages including endoderm, mesoderm, and ectodermal cell types. These cell lineages differentiate into, for example, neural cells, hematopoietic lineages, and cardiomyocytes (Thomson, J.A. et al. (1998) Science 282:1145-1147).

Polynucleotides encoding TRICH can also be used to create "knockin" humanized animals (pigs) or transgenic animals (mice or rats) to model human disease. With knockin technology, a region of a polynucleotide encoding TRICH is injected into animal ES cells, and the injected sequence integrates into the animal cell genome. Transformed cells are injected into blastulae, and the blastulae
 5 are implanted as described above. Transgenic progeny or inbred lines are studied and treated with potential pharmaceutical agents to obtain information on treatment of a human disease. Alternatively, a mammal inbred to overexpress TRICH, e.g., by secreting TRICH in its milk, may also serve as a convenient source of that protein (Janne, J. et al. (1998) *Biotechnol. Annu. Rev.* 4:55-74).

THERAPEUTICS

10 Chemical and structural similarity, e.g., in the context of sequences and motifs, exists between regions of TRICH and transporters and ion channels. In addition, examples of tissues expressing TRICH can be found in Table 6 and can also be found in Example XI. Therefore, TRICH appears to play a role in transport, neurological, muscle, immunological and cell proliferative disorders. In the treatment of disorders associated with increased TRICH expression or activity, it is desirable to
 15 decrease the expression or activity of TRICH. In the treatment of disorders associated with decreased TRICH expression or activity, it is desirable to increase the expression or activity of TRICH.

Therefore, in one embodiment, TRICH or a fragment or derivative thereof may be administered to a subject to treat or prevent a disorder associated with decreased expression or
 20 activity of TRICH. Examples of such disorders include, but are not limited to, a transport disorder such as akinesia, amyotrophic lateral sclerosis, ataxia telangiectasia, cystic fibrosis, Becker's muscular dystrophy, Bell's palsy, Charcot-Marie Tooth disease, diabetes mellitus, diabetes insipidus, diabetic neuropathy, Duchenne muscular dystrophy, hyperkalemic periodic paralysis, normokalemic periodic paralysis, Parkinson's disease, malignant hyperthermia, multidrug resistance, myasthenia gravis,
 25 myotonic dystrophy, catatonia, tardive dyskinesia, dystonias, peripheral neuropathy, cerebral neoplasms, prostate cancer, cardiac disorders associated with transport, e.g., angina, bradyarrhythmia, tachyarrhythmia, hypertension, Long QT syndrome, myocarditis, cardiomyopathy, nemaline myopathy, centronuclear myopathy, lipid myopathy, mitochondrial myopathy, thyrotoxic myopathy, ethanol myopathy, dermatomyositis, inclusion body myositis, infectious myositis, polymyositis, neurological
 30 disorders associated with transport, e.g., Alzheimer's disease, amnesia, bipolar disorder, dementia, depression, epilepsy, Tourette's disorder, paranoid psychoses, and schizophrenia, and other disorders associated with transport, e.g., neurofibromatosis, postherpetic neuralgia, trigeminal neuropathy,

sarcoidosis, sickle cell anemia, Wilson's disease, cataracts, infertility, pulmonary artery stenosis, sensorineural autosomal deafness, hyperglycemia, hypoglycemia, Grave's disease, goiter, Cushing's disease, Addison's disease, glucose-galactose malabsorption syndrome, glycogen storage disease, hypercholesterolemia, adrenoleukodystrophy, Zellweger syndrome, Menkes disease, occipital horn syndrome, von Gierke disease, pseudohypoaldosteronism type 1, Liddle's syndrome, cystinuria, iminoglycinuria, Hartup disease, Fanconi disease, and Bartter syndrome; a neurological disorder such as epilepsy, ischemic cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's disease, Pick's disease, Huntington's disease, dementia, Parkinson's disease and other extrapyramidal disorders, amyotrophic lateral sclerosis and other motor neuron disorders, progressive neural muscular atrophy, retinitis pigmentosa, hereditary ataxias, multiple sclerosis and other demyelinating diseases, bacterial and viral meningitis, brain abscess, subdural empyema, epidural abscess, suppurative intracranial thrombophlebitis, myelitis and radiculitis, viral central nervous system disease, prion diseases including kuru, Creutzfeldt-Jakob disease, and Gerstmann-Straussler-Scheinker syndrome, fatal familial insomnia, nutritional and metabolic diseases of the nervous system, neurofibromatosis, tuberous sclerosis, cerebelloretinal hemangioblastomatosis, encephalotrigeminal syndrome, mental retardation and other developmental disorders of the central nervous system including Down syndrome, cerebral palsy, neuroskeletal disorders, autonomic nervous system disorders, cranial nerve disorders, spinal cord diseases, muscular dystrophy and other neuromuscular disorders, peripheral nervous system disorders, dermatomyositis and polymyositis, inherited, metabolic, endocrine, and toxic myopathies, myasthenia gravis, periodic paralysis, mental disorders including mood, anxiety, and schizophrenic disorders, seasonal affective disorder (SAD), akathisia, amnesia, catatonia, diabetic neuropathy, hemiplegic migraine, tardive dyskinesia, dystonias, paranoid psychoses, postherpetic neuralgia, Tourette's disorder, progressive supranuclear palsy, corticobasal degeneration, and familial frontotemporal dementia; a muscle disorder such as cardiomyopathy, myocarditis, Duchenne's muscular dystrophy, Becker's muscular dystrophy, myotonic dystrophy, central core disease, nemaline myopathy, centronuclear myopathy, lipid myopathy, mitochondrial myopathy, infectious myositis, polymyositis, dermatomyositis, inclusion body myositis, thyrotoxic myopathy, ethanol myopathy, angina, anaphylactic shock, arrhythmias, asthma, cardiovascular shock, Cushing's syndrome, hypertension, hypoglycemia, myocardial infarction, migraine, pheochromocytoma, and myopathies including encephalopathy, epilepsy, Kearns-Sayre syndrome, lactic acidosis, myoclonic disorder, ophthalmoplegia, acid maltase deficiency (AMD, also known as Pompe's disease), generalized myotonia, and myotonia congenita; an immunological disorder such as acquired immunodeficiency syndrome (AIDS), Addison's disease,

adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy (APECED), bronchitis, cholecystitis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, and trauma; and a cell proliferative disorder such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, colon, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus.

20 In another embodiment, a vector capable of expressing TRICH or a fragment or derivative thereof may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of TRICH including, but not limited to, those described above.

In a further embodiment, a composition comprising a substantially purified TRICH in conjunction with a suitable pharmaceutical carrier may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of TRICH including, but not limited to, those provided above.

In still another embodiment, an agonist which modulates the activity of TRICH may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of TRICH including, but not limited to, those listed above.

30 In a further embodiment, an antagonist of TRICH may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of TRICH. Examples of such disorders include, but are not limited to, those transport, neurological, muscle, immunological and cell

proliferative disorders described above. In one aspect, an antibody which specifically binds TRICH may be used directly as an antagonist or indirectly as a targeting or delivery mechanism for bringing a pharmaceutical agent to cells or tissues which express TRICH.

In an additional embodiment, a vector expressing the complement of the polynucleotide
5 encoding TRICH may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of TRICH including, but not limited to, those described above.

In other embodiments, any protein, agonist, antagonist, antibody, complementary sequence, or vector embodiments may be administered in combination with other appropriate therapeutic agents. Selection of the appropriate agents for use in combination therapy may be made by one of ordinary
10 skill in the art, according to conventional pharmaceutical principles. The combination of therapeutic agents may act synergistically to effect the treatment or prevention of the various disorders described above. Using this approach, one may be able to achieve therapeutic efficacy with lower dosages of each agent, thus reducing the potential for adverse side effects.

An antagonist of TRICH may be produced using methods which are generally known in the
15 art. In particular, purified TRICH may be used to produce antibodies or to screen libraries of pharmaceutical agents to identify those which specifically bind TRICH. Antibodies to TRICH may also be generated using methods that are well known in the art. Such antibodies may include, but are not limited to, polyclonal, monoclonal, chimeric, and single chain antibodies, Fab fragments, and fragments produced by a Fab expression library. In an embodiment, neutralizing antibodies (i.e., those
20 which inhibit dimer formation) can be used therapeutically. Single chain antibodies (e.g., from camels or llamas) may be potent enzyme inhibitors and may have application in the design of peptide mimetics, and in the development of immuno-adsorbents and biosensors (Muyldermans, S. (2001) J. Biotechnol. 74:277-302).

For the production of antibodies, various hosts including goats, rabbits, rats, mice, camels,
25 dromedaries, llamas, humans, and others may be immunized by injection with TRICH or with any fragment or oligopeptide thereof which has immunogenic properties. Depending on the host species, various adjuvants may be used to increase immunological response. Such adjuvants include, but are not limited to, Freund's, mineral gels such as aluminum hydroxide, and surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, KLH, and dinitrophenol. Among
30 adjuvants used in humans, BCG (bacilli Calmette-Guerin) and *Corynebacterium parvum* are especially preferable.

It is preferred that the oligopeptides, peptides, or fragments used to induce antibodies to TRICH have an amino acid sequence consisting of at least about 5 amino acids, and generally will consist of at least about 10 amino acids. It is also preferable that these oligopeptides, peptides, or fragments are substantially identical to a portion of the amino acid sequence of the natural protein.

5 Short stretches of TRICH amino acids may be fused with those of another protein, such as KLH, and antibodies to the chimeric molecule may be produced.

Monoclonal antibodies to TRICH may be prepared using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These include, but are not limited to, the hybridoma technique, the human B-cell hybridoma technique, and the EBV-hybridoma

10 technique (Kohler, G. et al. (1975) Nature 256:495-497; Kozbor, D. et al. (1985) J. Immunol. Methods 81:31-42; Cote, R.J. et al. (1983) Proc. Natl. Acad. Sci. USA 80:2026-2030; Cole, S.P. et al. (1984) Mol. Cell Biol. 62:109-120).

In addition, techniques developed for the production of "chimeric antibodies," such as the splicing of mouse antibody genes to human antibody genes to obtain a molecule with appropriate

15 antigen specificity and biological activity, can be used (Morrison, S.L. et al. (1984) Proc. Natl. Acad. Sci. USA 81:6851-6855; Neuberger, M.S. et al. (1984) Nature 312:604-608; Takeda, S. et al. (1985) Nature 314:452-454). Alternatively, techniques described for the production of single chain antibodies may be adapted, using methods known in the art, to produce TRICH-specific single chain antibodies. Antibodies with related specificity, but of distinct idiotypic composition, may be generated by chain

20 shuffling from random combinatorial immunoglobulin libraries (Burton, D.R. (1991) Proc. Natl. Acad. Sci. USA 88:10134-10137).

Antibodies may also be produced by inducing *in vivo* production in the lymphocyte population or by screening immunoglobulin libraries or panels of highly specific binding reagents as disclosed in the literature (Orlandi, R. et al. (1989) Proc. Natl. Acad. Sci. USA 86:3833-3837; Winter, G. et al.

25 (1991) Nature 349:293-299).

Antibody fragments which contain specific binding sites for TRICH may also be generated. For example, such fragments include, but are not limited to, F(ab')₂ fragments produced by pepsin digestion of the antibody molecule and Fab fragments generated by reducing the disulfide bridges of the F(ab')₂ fragments. Alternatively, Fab expression libraries may be constructed to allow rapid and

30 easy identification of monoclonal Fab fragments with the desired specificity (Huse, W.D. et al. (1989) Science 246:1275-1281).

Various immunoassays may be used for screening to identify antibodies having the desired specificity. Numerous protocols for competitive binding or immunoradiometric assays using either polyclonal or monoclonal antibodies with established specificities are well known in the art. Such immunoassays typically involve the measurement of complex formation between TRICH and its
5 specific antibody. A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering TRICH epitopes is generally used, but a competitive binding assay may also be employed (Pound, *supra*).

Various methods such as Scatchard analysis in conjunction with radioimmunoassay techniques may be used to assess the affinity of antibodies for TRICH. Affinity is expressed as an association
10 constant, K_a , which is defined as the molar concentration of TRICH-antibody complex divided by the molar concentrations of free antigen and free antibody under equilibrium conditions. The K_a determined for a preparation of polyclonal antibodies, which are heterogeneous in their affinities for multiple TRICH epitopes, represents the average affinity, or avidity, of the antibodies for TRICH. The K_a determined for a preparation of monoclonal antibodies, which are monospecific for a particular
15 TRICH epitope, represents a true measure of affinity. High-affinity antibody preparations with K_a ranging from about 10^9 to 10^{12} L/mole are preferred for use in immunoassays in which the TRICH-antibody complex must withstand rigorous manipulations. Low-affinity antibody preparations with K_a ranging from about 10^6 to 10^7 L/mole are preferred for use in immunopurification and similar procedures which ultimately require dissociation of TRICH, preferably in active form, from the
20 antibody (Catty, D. (1988) Antibodies, Volume I: A Practical Approach, IRL Press, Washington DC; Liddell, J.E. and A. Cryer (1991) A Practical Guide to Monoclonal Antibodies, John Wiley & Sons, New York NY).

The titer and avidity of polyclonal antibody preparations may be further evaluated to determine the quality and suitability of such preparations for certain downstream applications. For example, a
25 polyclonal antibody preparation containing at least 1-2 mg specific antibody/ml, preferably 5-10 mg specific antibody/ml, is generally employed in procedures requiring precipitation of TRICH-antibody complexes. Procedures for evaluating antibody specificity, titer, and avidity, and guidelines for antibody quality and usage in various applications, are generally available (Catty, *supra*; Coligan et al., *supra*).

30 In another embodiment of the invention, polynucleotides encoding TRICH, or any fragment or complement thereof, may be used for therapeutic purposes. In one aspect, modifications of gene expression can be achieved by designing complementary sequences or antisense molecules (DNA,

RNA, PNA, or modified oligonucleotides) to the coding or regulatory regions of the gene encoding TRICH. Such technology is well known in the art, and antisense oligonucleotides or larger fragments can be designed from various locations along the coding or control regions of sequences encoding TRICH (Agrawal, S., ed. (1996) Antisense Therapeutics, Humana Press, Totawa NJ).

5 In therapeutic use, any gene delivery system suitable for introduction of the antisense sequences into appropriate target cells can be used. Antisense sequences can be delivered intracellularly in the form of an expression plasmid which, upon transcription, produces a sequence complementary to at least a portion of the cellular sequence encoding the target protein (Slater, J.E. et al. (1998) *J. Allergy Clin. Immunol.* 102:469-475; Scanlon, K.J. et al. (1995) 9:1288-1296). Antisense
10 sequences can also be introduced intracellularly through the use of viral vectors, such as retrovirus and adeno-associated virus vectors (Miller, A.D. (1990) *Blood* 76:271; Ausubel et al., *supra*; Uckert, W. and W. Walther (1994) *Pharmacol. Ther.* 63:323-347). Other gene delivery mechanisms include liposome-derived systems, artificial viral envelopes, and other systems known in the art (Rossi, J.J. (1995) *Br. Med. Bull.* 51:217-225; Boado, R.J. et al. (1998) *J. Pharm. Sci.* 87:1308-1315; Morris,
15 M.C. et al. (1997) *Nucleic Acids Res.* 25:2730-2736).

In another embodiment of the invention, polynucleotides encoding TRICH may be used for somatic or germline gene therapy. Gene therapy may be performed to (i) correct a genetic deficiency (e.g., in the cases of severe combined immunodeficiency (SCID)-X1 disease characterized by X-linked inheritance (Cavazzana-Calvo, M. et al. (2000) *Science* 288:669-672), severe combined
20 immunodeficiency syndrome associated with an inherited adenosine deaminase (ADA) deficiency (Blaese, R.M. et al. (1995) *Science* 270:475-480; Bordignon, C. et al. (1995) *Science* 270:470-475), cystic fibrosis (Zabner, J. et al. (1993) *Cell* 75:207-216; Crystal, R.G. et al. (1995) *Hum. Gene Therapy* 6:643-666; Crystal, R.G. et al. (1995) *Hum. Gene Therapy* 6:667-703), thalassemias, familial hypercholesterolemia, and hemophilia resulting from Factor VIII or Factor IX deficiencies (Crystal,
25 R.G. (1995) *Science* 270:404-410; Verma, I.M. and N. Somia (1997) *Nature* 389:239-242)), (ii) express a conditionally lethal gene product (e.g., in the case of cancers which result from unregulated cell proliferation), or (iii) express a protein which affords protection against intracellular parasites (e.g., against human retroviruses, such as human immunodeficiency virus (HIV) (Baltimore, D. (1988) *Nature* 335:395-396; Poeschla, E. et al. (1996) *Proc. Natl. Acad. Sci. USA* 93:11395-11399), hepatitis
30 B or C virus (HBV, HCV); fungal parasites, such as *Candida albicans* and *Paracoccidioides brasiliensis*; and protozoan parasites such as *Plasmodium falciparum* and *Trypanosoma cruzi*). In the case where a genetic deficiency in TRICH expression or regulation causes disease, the expression

of TRICH from an appropriate population of transduced cells may alleviate the clinical manifestations caused by the genetic deficiency.

In a further embodiment of the invention, diseases or disorders caused by deficiencies in TRICH are treated by constructing mammalian expression vectors encoding TRICH and introducing
5 these vectors by mechanical means into TRICH-deficient cells. Mechanical transfer technologies for use with cells *in vivo* or *ex vitro* include (i) direct DNA microinjection into individual cells, (ii) ballistic gold particle delivery, (iii) liposome-mediated transfection, (iv) receptor-mediated gene transfer, and (v) the use of DNA transposons (Morgan, R.A. and W.F. Anderson (1993) *Annu. Rev. Biochem.* 62:191-217; Ivics, Z. (1997) *Cell* 91:501-510; Boulay, J.-L. and H. Récipon (1998) *Curr. Opin.*
10 *Biotechnol.* 9:445-450).

Expression vectors that may be effective for the expression of TRICH include, but are not limited to, the PCDNA 3.1, EPITAG, PRCCMV2, PREP, PVAX, PCR2-TOPOTA vectors (Invitrogen, Carlsbad CA), PCMV-SCRIPT, PCMV-TAG, PEGSH/PERV (Stratagene, La Jolla CA), and PTET-OFF, PTET-ON, PTRE2, PTRE2-LUC, PTK-HYG (Clontech, Palo Alto CA). TRICH
15 may be expressed using (i) a constitutively active promoter, (e.g., from cytomegalovirus (CMV), Rous sarcoma virus (RSV), SV40 virus, thymidine kinase (TK), or β -actin genes), (ii) an inducible promoter (e.g., the tetracycline-regulated promoter (Gossen, M. and H. Bujard (1992) *Proc. Natl. Acad. Sci. USA* 89:5547-5551; Gossen, M. et al. (1995) *Science* 268:1766-1769; Rossi, F.M.V. and H.M. Blau (1998) *Curr. Opin. Biotechnol.* 9:451-456), commercially available in the T-REX plasmid (Invitrogen));
20 the ecdysone-inducible promoter (available in the plasmids PVGRXR and PIND; Invitrogen); the FK506/rapamycin inducible promoter; or the RU486/mifepristone inducible promoter (Rossi, F.M.V. and H.M. Blau, *supra*), or (iii) a tissue-specific promoter or the native promoter of the endogenous gene encoding TRICH from a normal individual.

Commercially available liposome transformation kits (e.g., the PERFECT LIPID
25 TRANSFECTION KIT, available from Invitrogen) allow one with ordinary skill in the art to deliver polynucleotides to target cells in culture and require minimal effort to optimize experimental parameters. In the alternative, transformation is performed using the calcium phosphate method (Graham, F.L. and A.J. Eb (1973) *Virology* 52:456-467), or by electroporation (Neumann, E. et al. (1982) *EMBO J.* 1:841-845). The introduction of DNA to primary cells requires modification of these
30 standardized mammalian transfection protocols.

In another embodiment of the invention, diseases or disorders caused by genetic defects with respect to TRICH expression are treated by constructing a retrovirus vector consisting of (i) the

polynucleotide encoding TRICH under the control of an independent promoter or the retrovirus long terminal repeat (LTR) promoter, (ii) appropriate RNA packaging signals, and (iii) a Rev-responsive element (RRE) along with additional retrovirus *cis*-acting RNA sequences and coding sequences required for efficient vector propagation. Retrovirus vectors (e.g., PFB and PFBNEO) are commercially available (Stratagene) and are based on published data (Riviere, I. et al. (1995) Proc. Natl. Acad. Sci. USA 92:6733-6737), incorporated by reference herein. The vector is propagated in an appropriate vector producing cell line (VPCL) that expresses an envelope gene with a tropism for receptors on the target cells or a promiscuous envelope protein such as VSVg (Armentano, D. et al. (1987) J. Virol. 61:1647-1650; Bender, M.A. et al. (1987) J. Virol. 61:1639-1646; Adam, M.A. and A.D. Miller (1988) J. Virol. 62:3802-3806; Dull, T. et al. (1998) J. Virol. 72:8463-8471; Zufferey, R. et al. (1998) J. Virol. 72:9873-9880). U.S. Patent No. 5,910,434 to Rigg ("Method for obtaining retrovirus packaging cell lines producing high transducing efficiency retroviral supernatant") discloses a method for obtaining retrovirus packaging cell lines and is hereby incorporated by reference. Propagation of retrovirus vectors, transduction of a population of cells (e.g., CD4⁺ T-cells), and the return of transduced cells to a patient are procedures well known to persons skilled in the art of gene therapy and have been well documented (Ranga, U. et al. (1997) J. Virol. 71:7020-7029; Bauer, G. et al. (1997) Blood 89:2259-2267; Bonyhadi, M.L. (1997) J. Virol. 71:4707-4716; Ranga, U. et al. (1998) Proc. Natl. Acad. Sci. USA 95:1201-1206; Su, L. (1997) Blood 89:2283-2290).

In an embodiment, an adenovirus-based gene therapy delivery system is used to deliver polynucleotides encoding TRICH to cells which have one or more genetic abnormalities with respect to the expression of TRICH. The construction and packaging of adenovirus-based vectors are well known to those with ordinary skill in the art. Replication defective adenovirus vectors have proven to be versatile for importing genes encoding immunoregulatory proteins into intact islets in the pancreas (Csete, M.E. et al. (1995) Transplantation 27:263-268). Potentially useful adenoviral vectors are described in U.S. Patent No. 5,707,618 to Armentano ("Adenovirus vectors for gene therapy"), hereby incorporated by reference. For adenoviral vectors, see also Antinozzi, P.A. et al. (1999; Annu. Rev. Nutr. 19:511-544) and Verma, I.M. and N. Somia (1997; Nature 18:389:239-242).

In another embodiment, a herpes-based, gene therapy delivery system is used to deliver polynucleotides encoding TRICH to target cells which have one or more genetic abnormalities with respect to the expression of TRICH. The use of herpes simplex virus (HSV)-based vectors may be especially valuable for introducing TRICH to cells of the central nervous system, for which HSV has a tropism. The construction and packaging of herpes-based vectors are well known to those with

ordinary skill in the art. A replication-competent herpes simplex virus (HSV) type 1-based vector has been used to deliver a reporter gene to the eyes of primates (Liu, X. et al. (1999) Exp. Eye Res. 169:385-395). The construction of a HSV-1 virus vector has also been disclosed in detail in U.S. Patent No. 5,804,413 to DeLuca ("Herpes simplex virus strains for gene transfer"), which is hereby
5 incorporated by reference. U.S. Patent No. 5,804,413 teaches the use of recombinant HSV d92 which consists of a genome containing at least one exogenous gene to be transferred to a cell under the control of the appropriate promoter for purposes including human gene therapy. Also taught by this patent are the construction and use of recombinant HSV strains deleted for ICP4, ICP27 and ICP22. For HSV vectors, see also Goins, W.F. et al. (1999; J. Virol. 73:519-532) and Xu, H. et al.
10 (1994; Dev. Biol. 163:152-161). The manipulation of cloned herpesvirus sequences, the generation of recombinant virus following the transfection of multiple plasmids containing different segments of the large herpesvirus genomes, the growth and propagation of herpesvirus, and the infection of cells with herpesvirus are techniques well known to those of ordinary skill in the art.

In another embodiment, an alphavirus (positive, single-stranded RNA virus) vector is used to
15 deliver polynucleotides encoding TRICH to target cells. The biology of the prototypic alphavirus, Semliki Forest Virus (SFV), has been studied extensively and gene transfer vectors have been based on the SFV genome (Garoff, H. and K.-J. Li (1998) Curr. Opin. Biotechnol. 9:464-469). During alphavirus RNA replication, a subgenomic RNA is generated that normally encodes the viral capsid proteins. This subgenomic RNA replicates to higher levels than the full length genomic RNA,
20 resulting in the overproduction of capsid proteins relative to the viral proteins with enzymatic activity (e.g., protease and polymerase). Similarly, inserting the coding sequence for TRICH into the alphavirus genome in place of the capsid-coding region results in the production of a large number of TRICH-coding RNAs and the synthesis of high levels of TRICH in vector transduced cells. While alphavirus infection is typically associated with cell lysis within a few days, the ability to establish a
25 persistent infection in hamster normal kidney cells (BHK-21) with a variant of Sindbis virus (SIN) indicates that the lytic replication of alphaviruses can be altered to suit the needs of the gene therapy application (Dryga, S.A. et al. (1997) Virology 228:74-83). The wide host range of alphaviruses will allow the introduction of TRICH into a variety of cell types. The specific transduction of a subset of cells in a population may require the sorting of cells prior to transduction. The methods of
30 manipulating infectious cDNA clones of alphaviruses, performing alphavirus cDNA and RNA transfections, and performing alphavirus infections, are well known to those with ordinary skill in the art.

Oligonucleotides derived from the transcription initiation site, e.g., between about positions -10 and +10 from the start site, may also be employed to inhibit gene expression. Similarly, inhibition can be achieved using triple helix base-pairing methodology. Triple helix pairing is useful because it causes inhibition of the ability of the double helix to open sufficiently for the binding of polymerases,

5 transcription factors, or regulatory molecules. Recent therapeutic advances using triplex DNA have been described in the literature (Gee, J.E. et al. (1994) in Huber, B.E. and B.I. Carr, Molecular and Immunologic Approaches, Futura Publishing, Mt. Kisco NY, pp. 163-177). A complementary sequence or antisense molecule may also be designed to block translation of mRNA by preventing the transcript from binding to ribosomes.

10 Ribozymes, enzymatic RNA molecules, may also be used to catalyze the specific cleavage of RNA. The mechanism of ribozyme action involves sequence-specific hybridization of the ribozyme molecule to complementary target RNA, followed by endonucleolytic cleavage. For example, engineered hammerhead motif ribozyme molecules may specifically and efficiently catalyze endonucleolytic cleavage of RNA molecules encoding TRICH.

15 Specific ribozyme cleavage sites within any potential RNA target are initially identified by scanning the target molecule for ribozyme cleavage sites, including the following sequences: GUA, GUU, and GUC. Once identified, short RNA sequences of between 15 and 20 ribonucleotides, corresponding to the region of the target gene containing the cleavage site, may be evaluated for secondary structural features which may render the oligonucleotide inoperable. The suitability of candidate targets may also be evaluated by testing accessibility to hybridization with complementary oligonucleotides using ribonuclease protection assays.

Complementary ribonucleic acid molecules and ribozymes may be prepared by any method known in the art for the synthesis of nucleic acid molecules. These include techniques for chemically synthesizing oligonucleotides such as solid phase phosphoramidite chemical synthesis. Alternatively, 25 RNA molecules may be generated by *in vitro* and *in vivo* transcription of DNA molecules encoding TRICH. Such DNA sequences may be incorporated into a wide variety of vectors with suitable RNA polymerase promoters such as T7 or SP6. Alternatively, these cDNA constructs that synthesize complementary RNA, constitutively or inducibly, can be introduced into cell lines, cells, or tissues.

RNA molecules may be modified to increase intracellular stability and half-life. Possible 30 modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends of the molecule, or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages within the backbone of the molecule. This concept is inherent in the production of PNAs and can be

extended in all of these molecules by the inclusion of nontraditional bases such as inosine, queosine, and wybutosine, as well as acetyl-, methyl-, thio-, and similarly modified forms of adenine, cytidine, guanine, thymine, and uridine which are not as easily recognized by endogenous endonucleases.

In other embodiments of the invention, the expression of one or more selected polynucleotides of the present invention can be altered, inhibited, decreased, or silenced using RNA interference (RNAi) or post-transcriptional gene silencing (PTGS) methods known in the art. RNAi is a post-transcriptional mode of gene silencing in which double-stranded RNA (dsRNA) introduced into a targeted cell specifically suppresses the expression of the homologous gene (i.e., the gene bearing the sequence complementary to the dsRNA). This effectively knocks out or substantially reduces the expression of the targeted gene. PTGS can also be accomplished by use of DNA or DNA fragments as well. RNAi methods are described by Fire, A. et al. (1998; Nature 391:806-811) and Gura, T. (2000; Nature 404:804-808). PTGS can also be initiated by introduction of a complementary segment of DNA into the selected tissue using gene delivery and/or viral vector delivery methods described herein or known in the art.

RNAi can be induced in mammalian cells by the use of small interfering RNA also known as siRNA. SiRNA are shorter segments of dsRNA (typically about 21 to 23 nucleotides in length) that result *in vivo* from cleavage of introduced dsRNA by the action of an endogenous ribonuclease. SiRNA appear to be the mediators of the RNAi effect in mammals. The most effective siRNAs appear to be 21 nucleotide dsRNAs with 2 nucleotide 3' overhangs. The use of siRNA for inducing RNAi in mammalian cells is described by Elbashir, S.M. et al. (2001; Nature 411:494-498).

SiRNA can either be generated indirectly by introduction of dsRNA into the targeted cell, or directly by mammalian transfection methods and agents described herein or known in the art (such as liposome-mediated transfection, viral vector methods, or other polynucleotide delivery/introductory methods). Suitable SiRNAs can be selected by examining a transcript of the target polynucleotide (e.g., mRNA) for nucleotide sequences downstream from the AUG start codon and recording the occurrence of each nucleotide and the 3' adjacent 19 to 23 nucleotides as potential siRNA target sites, with sequences having a 21 nucleotide length being preferred. Regions to be avoided for target siRNA sites include the 5' and 3' untranslated regions (UTRs) and regions near the start codon (within 75 bases), as these may be richer in regulatory protein binding sites. UTR-binding proteins and/or translation initiation complexes may interfere with binding of the siRNP endonuclease complex. The selected target sites for siRNA can then be compared to the appropriate genome database (e.g., human, etc.) using BLAST or other sequence comparison algorithms known in the art. Target

sequences with significant homology to other coding sequences can be eliminated from consideration. The selected SiRNAs can be produced by chemical synthesis methods known in the art or by *in vitro* transcription using commercially available methods and kits such as the SILENCER siRNA construction kit (Ambion, Austin TX).

5 In alternative embodiments, long-term gene silencing and/or RNAi effects can be induced in selected tissue using expression vectors that continuously express siRNA. This can be accomplished using expression vectors that are engineered to express hairpin RNAs (shRNAs) using methods known in the art (see, e.g., Brummelkamp, T.R. et al. (2002) Science 296:550-553; and Paddison, P.J. et al. (2002) Genes Dev. 16:948-958). In these and related embodiments, shRNAs can be delivered to
10 target cells using expression vectors known in the art. An example of a suitable expression vector for delivery of siRNA is the PSILENCER1.0-U6 (circular) plasmid (Ambion). Once delivered to the target tissue, shRNAs are processed *in vivo* into siRNA-like molecules capable of carrying out gene-specific silencing.

In various embodiments, the expression levels of genes targeted by RNAi or PTGS methods
15 can be determined by assays for mRNA and/or protein analysis. Expression levels of the mRNA of a targeted gene, can be determined by northern analysis methods using, for example, the NORTHERNMAX-GLY kit (Ambion); by microarray methods; by PCR methods; by real time PCR methods; and by other RNA/polynucleotide assays known in the art or described herein. Expression levels of the protein encoded by the targeted gene can be determined by Western analysis using
20 standard techniques known in the art.

An additional embodiment of the invention encompasses a method for screening for a compound which is effective in altering expression of a polynucleotide encoding TRICH. Compounds which may be effective in altering expression of a specific polynucleotide may include, but are not limited to, oligonucleotides, antisense oligonucleotides, triple helix-forming oligonucleotides,
25 transcription factors and other polypeptide transcriptional regulators, and non-macromolecular chemical entities which are capable of interacting with specific polynucleotide sequences. Effective compounds may alter polynucleotide expression by acting as either inhibitors or promoters of polynucleotide expression. Thus, in the treatment of disorders associated with increased TRICH expression or activity, a compound which specifically inhibits expression of the polynucleotide
30 encoding TRICH may be therapeutically useful, and in the treatment of disorders associated with decreased TRICH expression or activity, a compound which specifically promotes expression of the polynucleotide encoding TRICH may be therapeutically useful.

In various embodiments, one or more test compounds may be screened for effectiveness in altering expression of a specific polynucleotide. A test compound may be obtained by any method commonly known in the art, including chemical modification of a compound known to be effective in altering polynucleotide expression; selection from an existing, commercially-available or proprietary library of naturally-occurring or non-natural chemical compounds; rational design of a compound based on chemical and/or structural properties of the target polynucleotide; and selection from a library of chemical compounds created combinatorially or randomly. A sample comprising a polynucleotide encoding TRICH is exposed to at least one test compound thus obtained. The sample may comprise, for example, an intact or permeabilized cell, or an *in vitro* cell-free or reconstituted biochemical system. Alterations in the expression of a polynucleotide encoding TRICH are assayed by any method commonly known in the art. Typically, the expression of a specific nucleotide is detected by hybridization with a probe having a nucleotide sequence complementary to the sequence of the polynucleotide encoding TRICH. The amount of hybridization may be quantified, thus forming the basis for a comparison of the expression of the polynucleotide both with and without exposure to one or more test compounds. Detection of a change in the expression of a polynucleotide exposed to a test compound indicates that the test compound is effective in altering the expression of the polynucleotide. A screen for a compound effective in altering expression of a specific polynucleotide can be carried out, for example, using a *Schizosaccharomyces pombe* gene expression system (Atkins, D. et al. (1999) U.S. Patent No. 5,932,435; Arndt, G.M. et al. (2000) Nucleic Acids Res. 28:E15) or a human cell line such as HeLa cell (Clarke, M.L. et al. (2000) Biochem. Biophys. Res. Commun. 268:8-13). A particular embodiment of the present invention involves screening a combinatorial library of oligonucleotides (such as deoxyribonucleotides, ribonucleotides, peptide nucleic acids, and modified oligonucleotides) for antisense activity against a specific polynucleotide sequence (Bruce, T.W. et al. (1997) U.S. Patent No. 5,686,242; Bruce, T.W. et al. (2000) U.S. Patent No. 6,022,691).

Many methods for introducing vectors into cells or tissues are available and equally suitable for use *in vivo*, *in vitro*, and *ex vivo*. For *ex vivo* therapy, vectors may be introduced into stem cells taken from the patient and clonally propagated for autologous transplant back into that same patient. Delivery by transfection, by liposome injections, or by polycationic amino polymers may be achieved using methods which are well known in the art (Goldman, C.K. et al. (1997) Nat. Biotechnol. 15:462-466).

Any of the therapeutic methods described above may be applied to any subject in need of such therapy, including, for example, mammals such as humans, dogs, cats, cows, horses, rabbits, and monkeys.

5 An additional embodiment of the invention relates to the administration of a composition which generally comprises an active ingredient formulated with a pharmaceutically acceptable excipient. Excipients may include, for example, sugars, starches, celluloses, gums, and proteins. Various formulations are commonly known and are thoroughly discussed in the latest edition of Remington's Pharmaceutical Sciences (Maack Publishing, Easton PA). Such compositions may consist of TRICH, antibodies to TRICH, and mimetics, agonists, antagonists, or inhibitors of TRICH.

10 In various embodiments, the compositions described herein, such as pharmaceutical compositions, may be administered by any number of routes including, but not limited to, oral, intravenous, intramuscular, intra-arterial, intramedullary, intrathecal, intraventricular, pulmonary, transdermal, subcutaneous, intraperitoneal, intranasal, enteral, topical, sublingual, or rectal means.

Compositions for pulmonary administration may be prepared in liquid or dry powder form. 15 These compositions are generally aerosolized immediately prior to inhalation by the patient. In the case of small molecules (e.g. traditional low molecular weight organic drugs), aerosol delivery of fast-acting formulations is well-known in the art. In the case of macromolecules (e.g. larger peptides and proteins), recent developments in the field of pulmonary delivery via the alveolar region of the lung have enabled the practical delivery of drugs such as insulin to blood circulation (see, e.g., Patton, J.S. 20 et al.; U.S. Patent No. 5,997,848). Pulmonary delivery allows administration without needle injection, and obviates the need for potentially toxic penetration enhancers.

Compositions suitable for use in the invention include compositions wherein the active ingredients are contained in an effective amount to achieve the intended purpose. The determination of an effective dose is well within the capability of those skilled in the art.

25 Specialized forms of compositions may be prepared for direct intracellular delivery of macromolecules comprising TRICH or fragments thereof. For example, liposome preparations containing a cell-impermeable macromolecule may promote cell fusion and intracellular delivery of the macromolecule. Alternatively, TRICH or a fragment thereof may be joined to a short cationic N-terminal portion from the HIV Tat-1 protein. Fusion proteins thus generated have been found to 30 transduce into the cells of all tissues, including the brain, in a mouse model system (Schwarze, S.R. et al. (1999) Science 285:1569-1572).

For any compound, the therapeutically effective dose can be estimated initially either in cell culture assays, e.g., of neoplastic cells, or in animal models such as mice, rats, rabbits, dogs, monkeys, or pigs. An animal model may also be used to determine the appropriate concentration range and route of administration. Such information can then be used to determine useful doses and routes for administration in humans.

A therapeutically effective dose refers to that amount of active ingredient, for example TRICH or fragments thereof, antibodies of TRICH, and agonists, antagonists or inhibitors of TRICH, which ameliorates the symptoms or condition. Therapeutic efficacy and toxicity may be determined by standard pharmaceutical procedures in cell cultures or with experimental animals, such as by calculating the ED_{50} (the dose therapeutically effective in 50% of the population) or LD_{50} (the dose lethal to 50% of the population) statistics. The dose ratio of toxic to therapeutic effects is the therapeutic index, which can be expressed as the LD_{50}/ED_{50} ratio. Compositions which exhibit large therapeutic indices are preferred. The data obtained from cell culture assays and animal studies are used to formulate a range of dosage for human use. The dosage contained in such compositions is preferably within a range of circulating concentrations that includes the ED_{50} with little or no toxicity. The dosage varies within this range depending upon the dosage form employed, the sensitivity of the patient, and the route of administration.

The exact dosage will be determined by the practitioner, in light of factors related to the subject requiring treatment. Dosage and administration are adjusted to provide sufficient levels of the active moiety or to maintain the desired effect. Factors which may be taken into account include the severity of the disease state, the general health of the subject, the age, weight, and gender of the subject, time and frequency of administration, drug combination(s), reaction sensitivities, and response to therapy. Long-acting compositions may be administered every 3 to 4 days, every week, or biweekly depending on the half-life and clearance rate of the particular formulation.

Normal dosage amounts may vary from about 0.1 μg to 100,000 μg , up to a total dose of about 1 gram, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature and generally available to practitioners in the art. Those skilled in the art will employ different formulations for nucleotides than for proteins or their inhibitors. Similarly, delivery of polynucleotides or polypeptides will be specific to particular cells, conditions, locations, etc.

DIAGNOSTICS

In another embodiment, antibodies which specifically bind TRICH may be used for the diagnosis of disorders characterized by expression of TRICH, or in assays to monitor patients being treated with TRICH or agonists, antagonists, or inhibitors of TRICH. Antibodies useful for diagnostic purposes may be prepared in the same manner as described above for therapeutics. Diagnostic
5 assays for TRICH include methods which utilize the antibody and a label to detect TRICH in human body fluids or in extracts of cells or tissues. The antibodies may be used with or without modification, and may be labeled by covalent or non-covalent attachment of a reporter molecule. A wide variety of reporter molecules, several of which are described above, are known in the art and may be used.

A variety of protocols for measuring TRICH, including ELISAs, RIAs, and FACS, are known
10 in the art and provide a basis for diagnosing altered or abnormal levels of TRICH expression. Normal or standard values for TRICH expression are established by combining body fluids or cell extracts taken from normal mammalian subjects, for example, human subjects, with antibodies to TRICH under conditions suitable for complex formation. The amount of standard complex formation may be quantitated by various methods, such as photometric means. Quantities of TRICH expressed in
15 subject, control, and disease samples from biopsied tissues are compared with the standard values. Deviation between standard and subject values establishes the parameters for diagnosing disease.

In another embodiment of the invention, polynucleotides encoding TRICH may be used for diagnostic purposes. The polynucleotides which may be used include oligonucleotides, complementary RNA and DNA molecules, and PNAs. The polynucleotides may be used to detect and quantify gene
20 expression in biopsied tissues in which expression of TRICH may be correlated with disease. The diagnostic assay may be used to determine absence, presence, and excess expression of TRICH, and to monitor regulation of TRICH levels during therapeutic intervention.

In one aspect, hybridization with PCR probes which are capable of detecting polynucleotides, including genomic sequences, encoding TRICH or closely related molecules may be used to identify
25 nucleic acid sequences which encode TRICH. The specificity of the probe, whether it is made from a highly specific region, e.g., the 5' regulatory region, or from a less specific region, e.g., a conserved motif, and the stringency of the hybridization or amplification will determine whether the probe identifies only naturally occurring sequences encoding TRICH, allelic variants, or related sequences.

Probes may also be used for the detection of related sequences, and may have at least 50%
30 sequence identity to any of the TRICH encoding sequences. The hybridization probes of the subject invention may be DNA or RNA and may be derived from the sequence of SEQ ID NO:60-118 or from genomic sequences including promoters, enhancers, and introns of the TRICH gene.

Means for producing specific hybridization probes for polynucleotides encoding TRICH include the cloning of polynucleotides encoding TRICH or TRICH derivatives into vectors for the production of mRNA probes. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes *in vitro* by means of the addition of the appropriate RNA

5 polymerases and the appropriate labeled nucleotides. Hybridization probes may be labeled by a variety of reporter groups, for example, by radionuclides such as ^{32}P or ^{35}S , or by enzymatic labels, such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems, and the like.

Polynucleotides encoding TRICH may be used for the diagnosis of disorders associated with expression of TRICH. Examples of such disorders include, but are not limited to, a transport disorder
 10 such as akinesia, amyotrophic lateral sclerosis, ataxia telangiectasia, cystic fibrosis, Becker's muscular dystrophy, Bell's palsy, Charcot-Marie Tooth disease, diabetes mellitus, diabetes insipidus, diabetic neuropathy, Duchenne muscular dystrophy, hyperkalemic periodic paralysis, normokalemic periodic paralysis, Parkinson's disease, malignant hyperthermia, multidrug resistance, myasthenia gravis, myotonic dystrophy, catatonia, tardive dyskinesia, dystonias, peripheral neuropathy, cerebral
 15 neoplasms, prostate cancer, cardiac disorders associated with transport, e.g., angina, bradyarrhythmia, tachyarrhythmia, hypertension, Long QT syndrome, myocarditis, cardiomyopathy, nemaline myopathy, centronuclear myopathy, lipid myopathy, mitochondrial myopathy, thyrotoxic myopathy, ethanol myopathy, dermatomyositis, inclusion body myositis, infectious myositis, polymyositis, neurological disorders associated with transport, e.g., Alzheimer's disease, amnesia, bipolar disorder, dementia,
 20 depression, epilepsy, Tourette's disorder, paranoid psychoses, and schizophrenia, and other disorders associated with transport, e.g., neurofibromatosis, postherpetic neuralgia, trigeminal neuropathy, sarcoidosis, sickle cell anemia, Wilson's disease, cataracts, infertility, pulmonary artery stenosis, sensorineural autosomal deafness, hyperglycemia, hypoglycemia, Grave's disease, goiter, Cushing's disease, Addison's disease, glucose-galactose malabsorption syndrome, glycogen storage disease,
 25 hypercholesterolemia, adrenoleukodystrophy, Zellweger syndrome, Menkes disease, occipital horn syndrome, von Gierke disease, pseudohypoaldosteronism type 1, Liddle's syndrome, cystinuria, iminoglycinuria, Hartup disease, Fanconi disease, and Bartter syndrome; a neurological disorder such as epilepsy, ischemic cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's disease, Pick's disease, Huntington's disease, dementia, Parkinson's disease and other extrapyramidal disorders,
 30 amyotrophic lateral sclerosis and other motor neuron disorders, progressive neural muscular atrophy, retinitis pigmentosa, hereditary ataxias, multiple sclerosis and other demyelinating diseases, bacterial and viral meningitis, brain abscess, subdural empyema, epidural abscess, suppurative intracranial

thrombophlebitis, myelitis and radiculitis, viral central nervous system disease, prion diseases including kuru, Creutzfeldt-Jakob disease, and Gerstmann-Straussler-Scheinker syndrome, fatal familial insomnia, nutritional and metabolic diseases of the nervous system, neurofibromatosis, tuberous sclerosis, cerebelloretinal hemangioblastomatosis, encephalotrigeminal syndrome, mental retardation

5 and other developmental disorders of the central nervous system including Down syndrome, cerebral palsy, neuroskeletal disorders, autonomic nervous system disorders, cranial nerve disorders, spinal cord diseases, muscular dystrophy and other neuromuscular disorders, peripheral nervous system disorders, dermatomyositis and polymyositis, inherited, metabolic, endocrine, and toxic myopathies, myasthenia gravis, periodic paralysis, mental disorders including mood, anxiety, and schizophrenic disorders,

10 seasonal affective disorder (SAD), akathisia, amnesia, catatonia, diabetic neuropathy, hemiplegic migraine, tardive dyskinesia, dystonias, paranoid psychoses, postherpetic neuralgia, Tourette's disorder, progressive supranuclear palsy, corticobasal degeneration, and familial frontotemporal dementia; a muscle disorder such as cardiomyopathy, myocarditis, Duchenne's muscular dystrophy, Becker's muscular dystrophy, myotonic dystrophy, central core disease, nemaline myopathy, centronuclear

15 myopathy, lipid myopathy, mitochondrial myopathy, infectious myositis, polymyositis, dermatomyositis, inclusion body myositis, thyrotoxic myopathy, ethanol myopathy, angina, anaphylactic shock, arrhythmias, asthma, cardiovascular shock, Cushing's syndrome, hypertension, hypoglycemia, myocardial infarction, migraine, pheochromocytoma, and myopathies including encephalopathy, epilepsy, Kearns-Sayre syndrome, lactic acidosis, myoclonic disorder, ophthalmoplegia, acid maltase

20 deficiency (AMD, also known as Pompe's disease), generalized myotonia, and myotonia congenita; an immunological disorder such as acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy (APECED), bronchitis, cholecystitis, contact

25 dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter's

30 syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial,

5 fungal, parasitic, protozoal, and helminthic infections, and trauma; and a cell proliferative disorder such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, colon, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus. Polynucleotides encoding TRICH may be used in Southern or northern analysis, dot blot, or other membrane-based technologies; in PCR technologies; in dipstick, pin, and multiformat ELISA-like assays; and in microarrays utilizing fluids or tissues from patients to detect altered TRICH expression. Such qualitative or quantitative methods are well known in the art.

In a particular embodiment, polynucleotides encoding TRICH may be used in assays that detect the presence of associated disorders, particularly those mentioned above. Polynucleotides complementary to sequences encoding TRICH may be labeled by standard methods and added to a fluid or tissue sample from a patient under conditions suitable for the formation of hybridization complexes. After a suitable incubation period, the sample is washed and the signal is quantified and compared with a standard value. If the amount of signal in the patient sample is significantly altered in comparison to a control sample then the presence of altered levels of polynucleotides encoding TRICH in the sample indicates the presence of the associated disorder. Such assays may also be used to evaluate the efficacy of a particular therapeutic treatment regimen in animal studies, in clinical trials, or to monitor the treatment of an individual patient.

In order to provide a basis for the diagnosis of a disorder associated with expression of TRICH, a normal or standard profile for expression is established. This may be accomplished by combining body fluids or cell extracts taken from normal subjects, either animal or human, with a sequence, or a fragment thereof, encoding TRICH, under conditions suitable for hybridization or amplification. Standard hybridization may be quantified by comparing the values obtained from normal subjects with values from an experiment in which a known amount of a substantially purified polynucleotide is used. Standard values obtained in this manner may be compared with values obtained from samples from patients who are symptomatic for a disorder. Deviation from standard values is used to establish the presence of a disorder.

Once the presence of a disorder is established and a treatment protocol is initiated, hybridization assays may be repeated on a regular basis to determine if the level of expression in the

patient begins to approximate that which is observed in the normal subject. The results obtained from successive assays may be used to show the efficacy of treatment over a period ranging from several days to months.

With respect to cancer, the presence of an abnormal amount of transcript (either under- or overexpressed) in biopsied tissue from an individual may indicate a predisposition for the development of the disease, or may provide a means for detecting the disease prior to the appearance of actual clinical symptoms. A more definitive diagnosis of this type may allow health professionals to employ preventative measures or aggressive treatment earlier, thereby preventing the development or further progression of the cancer.

Additional diagnostic uses for oligonucleotides designed from the sequences encoding TRICH may involve the use of PCR. These oligomers may be chemically synthesized, generated enzymatically, or produced *in vitro*. Oligomers will preferably contain a fragment of a polynucleotide encoding TRICH, or a fragment of a polynucleotide complementary to the polynucleotide encoding TRICH, and will be employed under optimized conditions for identification of a specific gene or condition. Oligomers may also be employed under less stringent conditions for detection or quantification of closely related DNA or RNA sequences.

In a particular aspect, oligonucleotide primers derived from polynucleotides encoding TRICH may be used to detect single nucleotide polymorphisms (SNPs). SNPs are substitutions, insertions and deletions that are a frequent cause of inherited or acquired genetic disease in humans. Methods of SNP detection include, but are not limited to, single-stranded conformation polymorphism (SSCP) and fluorescent SSCP (fSSCP) methods. In SSCP, oligonucleotide primers derived from polynucleotides encoding TRICH are used to amplify DNA using the polymerase chain reaction (PCR). The DNA may be derived, for example, from diseased or normal tissue, biopsy samples, bodily fluids, and the like. SNPs in the DNA cause differences in the secondary and tertiary structures of PCR products in single-stranded form, and these differences are detectable using gel electrophoresis in non-denaturing gels. In fSSCP, the oligonucleotide primers are fluorescently labeled, which allows detection of the amplimers in high-throughput equipment such as DNA sequencing machines. Additionally, sequence database analysis methods, termed *in silico* SNP (isSNP), are capable of identifying polymorphisms by comparing the sequence of individual overlapping DNA fragments which assemble into a common consensus sequence. These computer-based methods filter out sequence variations due to laboratory preparation of DNA and sequencing errors using statistical models and automated analyses of DNA sequence chromatograms. In the alternative, SNPs may be detected and characterized by mass

spectrometry using, for example, the high throughput MASSARRAY system (Sequenom, Inc., San Diego CA).

SNPs may be used to study the genetic basis of human disease. For example, at least 16 common SNPs have been associated with non-insulin-dependent diabetes mellitus. SNPs are also
5 useful for examining differences in disease outcomes in monogenic disorders, such as cystic fibrosis, sickle cell anemia, or chronic granulomatous disease. For example, variants in the mannose-binding lectin, MBL2, have been shown to be correlated with deleterious pulmonary outcomes in cystic fibrosis. SNPs also have utility in pharmacogenomics, the identification of genetic variants that influence a patient's response to a drug, such as life-threatening toxicity. For example, a variation in
10 N-acetyl transferase is associated with a high incidence of peripheral neuropathy in response to the anti-tuberculosis drug isoniazid, while a variation in the core promoter of the ALOX5 gene results in diminished clinical response to treatment with an anti-asthma drug that targets the 5-lipoxygenase pathway. Analysis of the distribution of SNPs in different populations is useful for investigating genetic drift, mutation, recombination, and selection, as well as for tracing the origins of populations
15 and their migrations (Taylor, J.G. et al. (2001) Trends Mol. Med. 7:507-512; Kwok, P.-Y. and Z. Gu (1999) Mol. Med. Today 5:538-543; Nowotny, P. et al. (2001) Curr. Opin. Neurobiol. 11:637-641).

Methods which may also be used to quantify the expression of TRICH include radiolabeling or biotinylating nucleotides, coamplification of a control nucleic acid, and interpolating results from standard curves (Melby, P.C. et al. (1993) J. Immunol. Methods 159:235-244; Duplaa, C. et al. (1993)
20 Anal. Biochem. 212:229-236). The speed of quantitation of multiple samples may be accelerated by running the assay in a high-throughput format where the oligomer or polynucleotide of interest is presented in various dilutions and a spectrophotometric or colorimetric response gives rapid quantitation.

In further embodiments, oligonucleotides or longer fragments derived from any of the
25 polynucleotides described herein may be used as elements on a microarray. The microarray can be used in transcript imaging techniques which monitor the relative expression levels of large numbers of genes simultaneously as described below. The microarray may also be used to identify genetic variants, mutations, and polymorphisms. This information may be used to determine gene function, to understand the genetic basis of a disorder, to diagnose a disorder, to monitor progression/regression of
30 disease as a function of gene expression, and to develop and monitor the activities of therapeutic agents in the treatment of disease. In particular, this information may be used to develop a pharmacogenomic profile of a patient in order to select the most appropriate and effective treatment

regimen for that patient. For example, therapeutic agents which are highly effective and display the fewest side effects may be selected for a patient based on his/her pharmacogenomic profile.

In another embodiment, TRICH, fragments of TRICH, or antibodies specific for TRICH may be used as elements on a microarray. The microarray may be used to monitor or measure protein-
5 protein interactions, drug-target interactions, and gene expression profiles, as described above.

A particular embodiment relates to the use of the polynucleotides of the present invention to generate a transcript image of a tissue or cell type. A transcript image represents the global pattern of gene expression by a particular tissue or cell type. Global gene expression patterns are analyzed by quantifying the number of expressed genes and their relative abundance under given conditions and at
10 a given time (Seilhamer et al., "Comparative Gene Transcript Analysis," U.S. Patent No. 5,840,484; hereby expressly incorporated by reference herein). Thus a transcript image may be generated by hybridizing the polynucleotides of the present invention or their complements to the totality of transcripts or reverse transcripts of a particular tissue or cell type. In one embodiment, the hybridization takes place in high-throughput format, wherein the polynucleotides of the present
15 invention or their complements comprise a subset of a plurality of elements on a microarray. The resultant transcript image would provide a profile of gene activity.

Transcript images may be generated using transcripts isolated from tissues, cell lines, biopsies, or other biological samples. The transcript image may thus reflect gene expression *in vivo*, as in the case of a tissue or biopsy sample, or *in vitro*, as in the case of a cell line.

20 Transcript images which profile the expression of the polynucleotides of the present invention may also be used in conjunction with *in vitro* model systems and preclinical evaluation of pharmaceuticals, as well as toxicological testing of industrial and naturally-occurring environmental compounds. All compounds induce characteristic gene expression patterns, frequently termed molecular fingerprints or toxicant signatures, which are indicative of mechanisms of action and toxicity
25 (Nuwaysir, E.F. et al. (1999) Mol. Carcinog. 24:153-159; Steiner, S. and N.L. Anderson (2000) Toxicol. Lett. 112-113:467-471). If a test compound has a signature similar to that of a compound with known toxicity, it is likely to share those toxic properties. These fingerprints or signatures are most useful and refined when they contain expression information from a large number of genes and gene families. Ideally, a genome-wide measurement of expression provides the highest quality
30 signature. Even genes whose expression is not altered by any tested compounds are important as well, as the levels of expression of these genes are used to normalize the rest of the expression data. The normalization procedure is useful for comparison of expression data after treatment with different

compounds. While the assignment of gene function to elements of a toxicant signature aids in interpretation of toxicity mechanisms, knowledge of gene function is not necessary for the statistical matching of signatures which leads to prediction of toxicity (see, for example, Press Release 00-02 from the National Institute of Environmental Health Sciences, released February 29, 2000, available at <http://www.niehs.nih.gov/oc/news/toxchip.htm>). Therefore, it is important and desirable in toxicological screening using toxicant signatures to include all expressed gene sequences.

In an embodiment, the toxicity of a test compound can be assessed by treating a biological sample containing nucleic acids with the test compound. Nucleic acids that are expressed in the treated biological sample are hybridized with one or more probes specific to the polynucleotides of the present invention, so that transcript levels corresponding to the polynucleotides of the present invention may be quantified. The transcript levels in the treated biological sample are compared with levels in an untreated biological sample. Differences in the transcript levels between the two samples are indicative of a toxic response caused by the test compound in the treated sample.

Another embodiment relates to the use of the polypeptides disclosed herein to analyze the proteome of a tissue or cell type. The term proteome refers to the global pattern of protein expression in a particular tissue or cell type. Each protein component of a proteome can be subjected individually to further analysis. Proteome expression patterns, or profiles, are analyzed by quantifying the number of expressed proteins and their relative abundance under given conditions and at a given time. A profile of a cell's proteome may thus be generated by separating and analyzing the polypeptides of a particular tissue or cell type. In one embodiment, the separation is achieved using two-dimensional gel electrophoresis, in which proteins from a sample are separated by isoelectric focusing in the first dimension, and then according to molecular weight by sodium dodecyl sulfate slab gel electrophoresis in the second dimension (Steiner and Anderson, *supra*). The proteins are visualized in the gel as discrete and uniquely positioned spots, typically by staining the gel with an agent such as Coomassie Blue or silver or fluorescent stains. The optical density of each protein spot is generally proportional to the level of the protein in the sample. The optical densities of equivalently positioned protein spots from different samples, for example, from biological samples either treated or untreated with a test compound or therapeutic agent, are compared to identify any changes in protein spot density related to the treatment. The proteins in the spots are partially sequenced using, for example, standard methods employing chemical or enzymatic cleavage followed by mass spectrometry. The identity of the protein in a spot may be determined by comparing its partial sequence, preferably of at least 5 contiguous

amino acid residues, to the polypeptide sequences of interest. In some cases, further sequence data may be obtained for definitive protein identification.

A proteomic profile may also be generated using antibodies specific for TRICH to quantify the levels of TRICH expression. In one embodiment, the antibodies are used as elements on a
5 microarray, and protein expression levels are quantified by exposing the microarray to the sample and detecting the levels of protein bound to each array element (Lueking, A. et al. (1999) *Anal. Biochem.* 270:103-111; Mendoz, L.G. et al. (1999) *Biotechniques* 27:778-788). Detection may be performed by a variety of methods known in the art, for example, by reacting the proteins in the sample with a thiol- or amino-reactive fluorescent compound and detecting the amount of fluorescence bound at each
10 array element.

Toxicant signatures at the proteome level are also useful for toxicological screening, and should be analyzed in parallel with toxicant signatures at the transcript level. There is a poor correlation between transcript and protein abundances for some proteins in some tissues (Anderson, N.L. and J. Seilhamer (1997) *Electrophoresis* 18:533-537), so proteome toxicant signatures may be
15 useful in the analysis of compounds which do not significantly affect the transcript image, but which alter the proteomic profile. In addition, the analysis of transcripts in body fluids is difficult, due to rapid degradation of mRNA, so proteomic profiling may be more reliable and informative in such cases.

In another embodiment, the toxicity of a test compound is assessed by treating a biological sample containing proteins with the test compound. Proteins that are expressed in the treated
20 biological sample are separated so that the amount of each protein can be quantified. The amount of each protein is compared to the amount of the corresponding protein in an untreated biological sample. A difference in the amount of protein between the two samples is indicative of a toxic response to the test compound in the treated sample. Individual proteins are identified by sequencing the amino acid residues of the individual proteins and comparing these partial sequences to the polypeptides of the
25 present invention.

In another embodiment, the toxicity of a test compound is assessed by treating a biological sample containing proteins with the test compound. Proteins from the biological sample are incubated with antibodies specific to the polypeptides of the present invention. The amount of protein recognized by the antibodies is quantified. The amount of protein in the treated biological sample is compared
30 with the amount in an untreated biological sample. A difference in the amount of protein between the two samples is indicative of a toxic response to the test compound in the treated sample.

Microarrays may be prepared, used, and analyzed using methods known in the art (Brennan, T.M. et al. (1995) U.S. Patent No. 5,474,796; Schena, M. et al. (1996) Proc. Natl. Acad. Sci. USA 93:10614-10619; Baldeschweiler et al. (1995) PCT application WO95/25116; Shalon, D. et al. (1995) PCT application WO95/35505; Heller, R.A. et al. (1997) Proc. Natl. Acad. Sci. USA 94:2150-2155; 5 Heller, M.J. et al. (1997) U.S. Patent No. 5,605,662). Various types of microarrays are well known and thoroughly described in Schena, M., ed. (1999; DNA Microarrays: A Practical Approach, Oxford University Press, London).

In another embodiment of the invention, nucleic acid sequences encoding TRICH may be used to generate hybridization probes useful in mapping the naturally occurring genomic sequence. 10 Either coding or noncoding sequences may be used, and in some instances, noncoding sequences may be preferable over coding sequences. For example, conservation of a coding sequence among members of a multi-gene family may potentially cause undesired cross hybridization during chromosomal mapping. The sequences may be mapped to a particular chromosome, to a specific region of a chromosome, or to artificial chromosome constructions, e.g., human artificial chromosomes 15 (HACs), yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), bacterial P1 constructions, or single chromosome cDNA libraries (Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355; Price, C.M. (1993) Blood Rev. 7:127-134; Trask, B.J. (1991) Trends Genet. 7:149-154). Once mapped, the nucleic acid sequences may be used to develop genetic linkage maps, for example, which correlate the inheritance of a disease state with the inheritance of a particular chromosome region or 20 restriction fragment length polymorphism (RFLP) (Lander, E.S. and D. Botstein (1986) Proc. Natl. Acad. Sci. USA 83:7353-7357).

Fluorescent *in situ* hybridization (FISH) may be correlated with other physical and genetic map data (Heinz-Ulrich, et al. (1995) in Meyers, *supra*, pp. 965-968). Examples of genetic map data can be found in various scientific journals or at the Online Mendelian Inheritance in Man (OMIM) 25 World Wide Web site. Correlation between the location of the gene encoding TRICH on a physical map and a specific disorder, or a predisposition to a specific disorder, may help define the region of DNA associated with that disorder and thus may further positional cloning efforts.

In situ hybridization of chromosomal preparations and physical mapping techniques, such as linkage analysis using established chromosomal markers, may be used for extending genetic maps. 30 Often the placement of a gene on the chromosome of another mammalian species, such as mouse, may reveal associated markers even if the exact chromosomal locus is not known. This information is valuable to investigators searching for disease genes using positional cloning or other gene discovery

techniques. Once the gene or genes responsible for a disease or syndrome have been crudely localized by genetic linkage to a particular genomic region, e.g., ataxia-telangiectasia to 11q22-23, any sequences mapping to that area may represent associated or regulatory genes for further investigation (Gatti, R.A. et al. (1988) Nature 336:577-580). The nucleotide sequence of the instant invention may
5 also be used to detect differences in the chromosomal location due to translocation, inversion, etc., among normal, carrier, or affected individuals.

In another embodiment of the invention, TRICH, its catalytic or immunogenic fragments, or oligopeptides thereof can be used for screening libraries of compounds in any of a variety of drug screening techniques. The fragment employed in such screening may be free in solution, affixed to a
10 solid support, borne on a cell surface, or located intracellularly. The formation of binding complexes between TRICH and the agent being tested may be measured.

Another technique for drug screening provides for high throughput screening of compounds having suitable binding affinity to the protein of interest (Geysen, et al. (1984) PCT application WO84/03564). In this method, large numbers of different small test compounds are synthesized on a
15 solid substrate. The test compounds are reacted with TRICH, or fragments thereof, and washed. Bound TRICH is then detected by methods well known in the art. Purified TRICH can also be coated directly onto plates for use in the aforementioned drug screening techniques. Alternatively, non-neutralizing antibodies can be used to capture the peptide and immobilize it on a solid support.

In another embodiment, one may use competitive drug screening assays in which neutralizing
20 antibodies capable of binding TRICH specifically compete with a test compound for binding TRICH. In this manner, antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with TRICH.

In additional embodiments, the nucleotide sequences which encode TRICH may be used in any molecular biology techniques that have yet to be developed, provided the new techniques rely on
25 properties of nucleotide sequences that are currently known, including, but not limited to, such properties as the triplet genetic code and specific base pair interactions.

Without further elaboration, it is believed that one skilled in the art can, using the preceding description, utilize the present invention to its fullest extent. The following preferred specific
30 embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever.

The disclosures of all patents, applications, and publications mentioned above and below, including U.S. Ser. No. 60/368,840, and U.S. Ser. No. 60/375,637, are hereby expressly incorporated by reference.

5

EXAMPLES

I. Construction of cDNA Libraries

Incyte cDNAs were derived from cDNA libraries described in the LIFESEQ GOLD database (Incyte Genomics, Palo Alto CA). Some tissues were homogenized and lysed in guanidinium isothiocyanate, while others were homogenized and lysed in phenol or in a suitable mixture of
 10 denaturants, such as TRIZOL (Invitrogen), a monophasic solution of phenol and guanidine isothiocyanate. The resulting lysates were centrifuged over CsCl cushions or extracted with chloroform. RNA was precipitated from the lysates with either isopropanol or sodium acetate and ethanol, or by other routine methods.

Phenol extraction and precipitation of RNA were repeated as necessary to increase RNA
 15 purity. In some cases, RNA was treated with DNase. For most libraries, poly(A)+ RNA was isolated using oligo d(T)-coupled paramagnetic particles (Promega), OLIGOTEX latex particles (QIAGEN, Chatsworth CA), or an OLIGOTEX mRNA purification kit (QIAGEN). Alternatively, RNA was isolated directly from tissue lysates using other RNA isolation kits, e.g., the POLY(A)PURE mRNA purification kit (Ambion, Austin TX).

20 In some cases, Stratagene was provided with RNA and constructed the corresponding cDNA libraries. Otherwise, cDNA was synthesized and cDNA libraries were constructed with the UNIZAP vector system (Stratagene) or SUPERScript plasmid system (Invitrogen), using the recommended procedures or similar methods known in the art (Ausubel et al., *supra*, ch. 5). Reverse transcription was initiated using oligo d(T) or random primers. Synthetic oligonucleotide adapters were
 25 ligated to double stranded cDNA, and the cDNA was digested with the appropriate restriction enzyme or enzymes. For most libraries, the cDNA was size-selected (300-1000 bp) using SEPHACRYL S1000, SEPHAROSE CL2B, or SEPHAROSE CL4B column chromatography (Amersham Biosciences) or preparative agarose gel electrophoresis. cDNAs were ligated into compatible restriction enzyme sites of the polylinker of a suitable plasmid, e.g., PBLUESCRIPT plasmid
 30 (Stratagene), PSPORT1 plasmid (Invitrogen, Carlsbad CA), PCDNA2.1 plasmid (Invitrogen), PBK-CMV plasmid (Stratagene), PCR2-TOPOTA plasmid (Invitrogen), PCMV-ICIS plasmid (Stratagene), pIGEN (Incyte Genomics, Palo Alto CA), pRARE (Incyte Genomics), or pINCY (Incyte Genomics),

or derivatives thereof. Recombinant plasmids were transformed into competent *E. coli* cells including XL1-Blue, XL1-BlueMRF, or SOLR from Stratagene or DH5 α , DH10B, or ElectroMAX DH10B from Invitrogen.

II. Isolation of cDNA Clones

5 Plasmids obtained as described in Example I were recovered from host cells by *in vivo* excision using the UNIZAP vector system (Stratagene) or by cell lysis. Plasmids were purified using at least one of the following: a Magic or WIZARD Minipreps DNA purification system (Promega); an AGTC Miniprep purification kit (Edge Biosystems, Gaithersburg MD); and QIAWELL 8 Plasmid, QIAWELL 8 Plus Plasmid, QIAWELL 8 Ultra Plasmid purification systems or the R.E.A.L. PREP
10 96 plasmid purification kit from QIAGEN. Following precipitation, plasmids were resuspended in 0.1 ml of distilled water and stored, with or without lyophilization, at 4°C.

Alternatively, plasmid DNA was amplified from host cell lysates using direct link PCR in a high-throughput format (Rao, V.B. (1994) Anal. Biochem. 216:1-14). Host cell lysis and thermal cycling steps were carried out in a single reaction mixture. Samples were processed and stored in
15 384-well plates, and the concentration of amplified plasmid DNA was quantified fluorometrically using PICOGREEN dye (Molecular Probes, Eugene OR) and a FLUOROSKAN II fluorescence scanner (Labsystems Oy, Helsinki, Finland).

III. Sequencing and Analysis

Incyte cDNA recovered in plasmids as described in Example II were sequenced as follows.
20 Sequencing reactions were processed using standard methods or high-throughput instrumentation such as the ABI CATALYST 800 (Applied Biosystems) thermal cycler or the PTC-200 thermal cycler (MJ Research) in conjunction with the HYDRA microdispenser (Robbins Scientific) or the MICROLAB 2200 (Hamilton) liquid transfer system. cDNA sequencing reactions were prepared using reagents provided by Amersham Biosciences or supplied in ABI sequencing kits such as the
25 ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Applied Biosystems). Electrophoretic separation of cDNA sequencing reactions and detection of labeled polynucleotides were carried out using the MEGABACE 1000 DNA sequencing system (Amersham Biosciences); the ABI PRISM 373 or 377 sequencing system (Applied Biosystems) in conjunction with standard ABI protocols and base calling software; or other sequence analysis systems known in the art.
30 Reading frames within the cDNA sequences were identified using standard methods (Ausubel et al., *supra*, ch. 7). Some of the cDNA sequences were selected for extension using the techniques disclosed in Example VIII.

The polynucleotide sequences derived from Incyte cDNAs were validated by removing vector, linker, and poly(A) sequences and by masking ambiguous bases, using algorithms and programs based on BLAST, dynamic programming, and dinucleotide nearest neighbor analysis. The Incyte cDNA sequences or translations thereof were then queried against a selection of public

5 databases such as the GenBank primate, rodent, mammalian, vertebrate, and eukaryote databases, and BLOCKS, PRINTS, DOMO, PRODOM; PROTEOME databases with sequences from *Homo sapiens*, *Rattus norvegicus*, *Mus musculus*, *Caenorhabditis elegans*, *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, and *Candida albicans* (Incyte Genomics, Palo Alto CA); hidden Markov model (HMM)-based protein family databases such as PFAM, INCY, and TIGRFAM (Haft, D.H. et al. (2001) Nucleic Acids Res. 29:41-43); and HMM-based protein domain databases such as SMART (Schultz, J. et al. (1998) Proc. Natl. Acad. Sci. USA 95:5857-5864; Letunic, I. et al. (2002) Nucleic Acids Res. 30:242-244). (HMM is a probabilistic approach which analyzes consensus primary structures of gene families; see, for example, Eddy, S.R. (1996) Curr. Opin. Struct. Biol. 6:361-365.) The queries were performed using programs based on BLAST, FASTA, BLIMPS, and

15 HMMER. The Incyte cDNA sequences were assembled to produce full length polynucleotide sequences. Alternatively, GenBank cDNAs, GenBank ESTs, stitched sequences, stretched sequences, or Genscan-predicted coding sequences (see Examples IV and V) were used to extend Incyte cDNA assemblages to full length. Assembly was performed using programs based on Phred, Phrap, and Consed, and cDNA assemblages were screened for open reading frames using programs

20 based on GeneMark, BLAST, and FASTA. The full length polynucleotide sequences were translated to derive the corresponding full length polypeptide sequences. Alternatively, a polypeptide may begin at any of the methionine residues of the full length translated polypeptide. Full length polypeptide sequences were subsequently analyzed by querying against databases such as the GenBank protein databases (genpept), SwissProt, the PROTEOME databases, BLOCKS, PRINTS, DOMO, PRODOM, Prosite, hidden Markov model (HMM)-based protein family databases such as PFAM, INCY, and TIGRFAM; and HMM-based protein domain databases such as SMART. Full length polynucleotide sequences are also analyzed using MACDNASIS PRO software (MiraiBio, Alameda CA) and LASERGENE software (DNASTAR). Polynucleotide and polypeptide sequence alignments are generated using default parameters specified by the CLUSTAL algorithm as incorporated into the

30 MEGALIGN multisequence alignment program (DNASTAR), which also calculates the percent identity between aligned sequences.

Table 7 summarizes the tools, programs, and algorithms used for the analysis and assembly of Incyte cDNA and full length sequences and provides applicable descriptions, references, and threshold parameters. The first column of Table 7 shows the tools, programs, and algorithms used, the second column provides brief descriptions thereof, the third column presents appropriate references, all of which are incorporated by reference herein in their entirety, and the fourth column presents, where applicable, the scores, probability values, and other parameters used to evaluate the strength of a match between two sequences (the higher the score or the lower the probability value, the greater the identity between two sequences).

The programs described above for the assembly and analysis of full length polynucleotide and polypeptide sequences were also used to identify polynucleotide sequence fragments from SEQ ID NO:60-118. Fragments from about 20 to about 4000 nucleotides which are useful in hybridization and amplification technologies are described in Table 4, column 2.

IV. Identification and Editing of Coding Sequences from Genomic DNA

Putative transporters and ion channels were initially identified by running the Genscan gene identification program against public genomic sequence databases (e.g., gbpri and gbhtg). Genscan is a general-purpose gene identification program which analyzes genomic DNA sequences from a variety of organisms (Burge, C. and S. Karlin (1997) *J. Mol. Biol.* 268:78-94; Burge, C. and S. Karlin (1998) *Curr. Opin. Struct. Biol.* 8:346-354). The program concatenates predicted exons to form an assembled cDNA sequence extending from a methionine to a stop codon. The output of Genscan is a FASTA database of polynucleotide and polypeptide sequences. The maximum range of sequence for Genscan to analyze at once was set to 30 kb. To determine which of these Genscan predicted cDNA sequences encode transporters and ion channels, the encoded polypeptides were analyzed by querying against PFAM models for transporters and ion channels. Potential transporters and ion channels were also identified by homology to Incyte cDNA sequences that had been annotated as transporters and ion channels. These selected Genscan-predicted sequences were then compared by BLAST analysis to the genpept and gbpri public databases. Where necessary, the Genscan-predicted sequences were then edited by comparison to the top BLAST hit from genpept to correct errors in the sequence predicted by Genscan, such as extra or omitted exons. BLAST analysis was also used to find any Incyte cDNA or public cDNA coverage of the Genscan-predicted sequences, thus providing evidence for transcription. When Incyte cDNA coverage was available, this information was used to correct or confirm the Genscan predicted sequence. Full length polynucleotide sequences were obtained by assembling Genscan-predicted coding sequences with Incyte cDNA sequences and/or public cDNA

sequences using the assembly process described in Example III. Alternatively, full length polynucleotide sequences were derived entirely from edited or unedited Genscan-predicted coding sequences.

V. Assembly of Genomic Sequence Data with cDNA Sequence Data

5 "Stitched" Sequences

Partial cDNA sequences were extended with exons predicted by the Genscan gene identification program described in Example IV. Partial cDNAs assembled as described in Example III were mapped to genomic DNA and parsed into clusters containing related cDNAs and Genscan exon predictions from one or more genomic sequences. Each cluster was analyzed using an algorithm
10 based on graph theory and dynamic programming to integrate cDNA and genomic information, generating possible splice variants that were subsequently confirmed, edited, or extended to create a full length sequence. Sequence intervals in which the entire length of the interval was present on more than one sequence in the cluster were identified, and intervals thus identified were considered to be equivalent by transitivity. For example, if an interval was present on a cDNA and two genomic
15 sequences, then all three intervals were considered to be equivalent. This process allows unrelated but consecutive genomic sequences to be brought together, bridged by cDNA sequence. Intervals thus identified were then "stitched" together by the stitching algorithm in the order that they appear along their parent sequences to generate the longest possible sequence, as well as sequence variants. Linkages between intervals which proceed along one type of parent sequence (cDNA to cDNA or
20 genomic sequence to genomic sequence) were given preference over linkages which change parent type (cDNA to genomic sequence). The resultant stitched sequences were translated and compared by BLAST analysis to the genpept and gbpr public databases. Incorrect exons predicted by Genscan were corrected by comparison to the top BLAST hit from genpept. Sequences were further extended with additional cDNA sequences, or by inspection of genomic DNA, when necessary.

25 "Stretched" Sequences

Partial DNA sequences were extended to full length with an algorithm based on BLAST analysis. First, partial cDNAs assembled as described in Example III were queried against public databases such as the GenBank primate, rodent, mammalian, vertebrate, and eukaryote databases using the BLAST program. The nearest GenBank protein homolog was then compared by BLAST
30 analysis to either Incyte cDNA sequences or GenScan exon predicted sequences described in Example IV. A chimeric protein was generated by using the resultant high-scoring segment pairs (HSPs) to map the translated sequences onto the GenBank protein homolog. Insertions or deletions

may occur in the chimeric protein with respect to the original GenBank protein homolog. The GenBank protein homolog, the chimeric protein, or both were used as probes to search for homologous genomic sequences from the public human genome databases. Partial DNA sequences were therefore "stretched" or extended by the addition of homologous genomic sequences. The resultant stretched sequences were examined to determine whether it contained a complete gene.

VI. Chromosomal Mapping of TRICH Encoding Polynucleotides

The sequences which were used to assemble SEQ ID NO:60-118 were compared with sequences from the Incyte LIFESEQ database and public domain databases using BLAST and other implementations of the Smith-Waterman algorithm. Sequences from these databases that matched SEQ ID NO:60-118 were assembled into clusters of contiguous and overlapping sequences using assembly algorithms such as Phrap (Table 7). Radiation hybrid and genetic mapping data available from public resources such as the Stanford Human Genome Center (SHGC), Whitehead Institute for Genome Research (WIGR), and Généthon were used to determine if any of the clustered sequences had been previously mapped. Inclusion of a mapped sequence in a cluster resulted in the assignment of all sequences of that cluster, including its particular SEQ ID NO., to that map location.

Map locations are represented by ranges, or intervals, of human chromosomes. The map position of an interval, in centiMorgans, is measured relative to the terminus of the chromosome's p-arm. (The centiMorgan (cM) is a unit of measurement based on recombination frequencies between chromosomal markers. On average, 1 cM is roughly equivalent to 1 megabase (Mb) of DNA in humans, although this can vary widely due to hot and cold spots of recombination.) The cM distances are based on genetic markers mapped by Généthon which provide boundaries for radiation hybrid markers whose sequences were included in each of the clusters. Human genome maps and other resources available to the public, such as the NCBI "GeneMap'99" World Wide Web site (<http://www.ncbi.nlm.nih.gov/genemap/>), can be employed to determine if previously identified disease genes map within or in proximity to the intervals indicated above.

VII. Analysis of Polynucleotide Expression

Northern analysis is a laboratory technique used to detect the presence of a transcript of a gene and involves the hybridization of a labeled nucleotide sequence to a membrane on which RNAs from a particular cell type or tissue have been bound (Sambrook and Russell, *supra*, ch. 7; Ausubel et al., *supra*, ch. 4).

Analogous computer techniques applying BLAST were used to search for identical or related molecules in databases such as GenBank or LIFESEQ (Incyte Genomics). This analysis is much

faster than multiple membrane-based hybridizations. In addition, the sensitivity of the computer search can be modified to determine whether any particular match is categorized as exact or similar. The basis of the search is the product score, which is defined as:

5

$$\frac{\text{BLAST Score} \times \text{Percent Identity}}{5 \times \text{minimum \{length(Seq. 1), length(Seq. 2)\}}}$$

The product score takes into account both the degree of similarity between two sequences and the length of the sequence match. The product score is a normalized value between 0 and 100, and is calculated as follows: the BLAST score is multiplied by the percent nucleotide identity and the product is divided by (5 times the length of the shorter of the two sequences). The BLAST score is calculated by assigning a score of +5 for every base that matches in a high-scoring segment pair (HSP), and -4 for every mismatch. Two sequences may share more than one HSP (separated by gaps). If there is more than one HSP, then the pair with the highest BLAST score is used to calculate the product score. The product score represents a balance between fractional overlap and quality in a BLAST alignment. For example, a product score of 100 is produced only for 100% identity over the entire length of the shorter of the two sequences being compared. A product score of 70 is produced either by 100% identity and 70% overlap at one end, or by 88% identity and 100% overlap at the other. A product score of 50 is produced either by 100% identity and 50% overlap at one end, or 79% identity and 100% overlap.

Alternatively, polynucleotides encoding TRICH are analyzed with respect to the tissue sources from which they were derived. For example, some full length sequences are assembled, at least in part, with overlapping Incyte cDNA sequences (see Example III). Each cDNA sequence is derived from a cDNA library constructed from a human tissue. Each human tissue is classified into one of the following organ/tissue categories: cardiovascular system; connective tissue; digestive system; embryonic structures; endocrine system; exocrine glands; genitalia, female; genitalia, male; germ cells; hemic and immune system; liver; musculoskeletal system; nervous system; pancreas; respiratory system; sense organs; skin; stomatognathic system; unclassified/mixed; or urinary tract. The number of libraries in each category is counted and divided by the total number of libraries across all categories. Similarly, each human tissue is classified into one of the following disease/condition categories: cancer, cell line, developmental, inflammation, neurological, trauma, cardiovascular, pooled, and other, and the number of libraries in each category is counted and divided by the total number of libraries across all categories. The resulting percentages reflect the tissue- and disease-specific

expression of cDNA encoding TRICH. cDNA sequences and cDNA library/tissue information are found in the LIFESEQ GOLD database (Incyte Genomics, Palo Alto CA).

VIII. Extension of TRICH Encoding Polynucleotides

Full length polynucleotides are produced by extension of an appropriate fragment of the full length molecule using oligonucleotide primers designed from this fragment. One primer was synthesized to initiate 5' extension of the known fragment, and the other primer was synthesized to initiate 3' extension of the known fragment. The initial primers were designed using OLIGO 4.06 software (National Biosciences), or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the target sequence at temperatures of about 68°C to about 72°C. Any stretch of nucleotides which would result in hairpin structures and primer-primer dimerizations was avoided.

Selected human cDNA libraries were used to extend the sequence. If more than one extension was necessary or desired, additional or nested sets of primers were designed.

High fidelity amplification was obtained by PCR using methods well known in the art. PCR was performed in 96-well plates using the PTC-200 thermal cycler (MJ Research, Inc.). The reaction mix contained DNA template, 200 nmol of each primer, reaction buffer containing Mg^{2+} , $(NH_4)_2SO_4$, and 2-mercaptoethanol, Taq DNA polymerase (Amersham Biosciences), ELONGASE enzyme (Invitrogen), and Pfu DNA polymerase (Stratagene), with the following parameters for primer pair PCI A and PCI B: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C. In the alternative, the parameters for primer pair T7 and SK+ were as follows: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 57°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C.

The concentration of DNA in each well was determined by dispensing 100 μ l PICOGREEN quantitation reagent (0.25% (v/v) PICOGREEN; Molecular Probes, Eugene OR) dissolved in 1X TE and 0.5 μ l of undiluted PCR product into each well of an opaque fluorimeter plate (Corning Costar, Acton MA), allowing the DNA to bind to the reagent. The plate was scanned in a Fluoroskan II (Labsystems Oy, Helsinki, Finland) to measure the fluorescence of the sample and to quantify the concentration of DNA. A 5 μ l to 10 μ l aliquot of the reaction mixture was analyzed by electrophoresis on a 1 % agarose gel to determine which reactions were successful in extending the sequence.

The extended nucleotides were desalted and concentrated, transferred to 384-well plates, digested with CviJI cholera virus endonuclease (Molecular Biology Research, Madison WI), and sonicated or sheared prior to religation into pUC 18 vector (Amersham Biosciences). For shotgun sequencing, the digested nucleotides were separated on low concentration (0.6 to 0.8%) agarose gels, fragments were excised, and agar digested with Agar ACE (Promega). Extended clones were religated using T4 ligase (New England Biolabs, Beverly MA) into pUC 18 vector (Amersham Biosciences), treated with Pfu DNA polymerase (Stratagene) to fill-in restriction site overhangs, and transfected into competent *E. coli* cells. Transformed cells were selected on antibiotic-containing media, and individual colonies were picked and cultured overnight at 37°C in 384-well plates in LB/2x carb liquid media.

The cells were lysed, and DNA was amplified by PCR using Taq DNA polymerase (Amersham Biosciences) and Pfu DNA polymerase (Stratagene) with the following parameters: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 72°C, 2 min; Step 5: steps 2, 3, and 4 repeated 29 times; Step 6: 72°C, 5 min; Step 7: storage at 4°C. DNA was quantified by PICOGREEN reagent (Molecular Probes) as described above. Samples with low DNA recoveries were reamplified using the same conditions as described above. Samples were diluted with 20% dimethylsulfoxide (1:2, v/v), and sequenced using DYENAMIC energy transfer sequencing primers and the DYENAMIC DIRECT kit (Amersham Biosciences) or the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Applied Biosystems).

In like manner, full length polynucleotides are verified using the above procedure or are used to obtain 5' regulatory sequences using the above procedure along with oligonucleotides designed for such extension, and an appropriate genomic library.

IX. Identification of Single Nucleotide Polymorphisms in TRICH Encoding Polynucleotides

Common DNA sequence variants known as single nucleotide polymorphisms (SNPs) were identified in SEQ ID NO:60-118 using the LIFESEQ database (Incyte Genomics). Sequences from the same gene were clustered together and assembled as described in Example III, allowing the identification of all sequence variants in the gene. An algorithm consisting of a series of filters was used to distinguish SNPs from other sequence variants. Preliminary filters removed the majority of basecall errors by requiring a minimum Phred quality score of 15, and removed sequence alignment errors and errors resulting from improper trimming of vector sequences, chimeras, and splice variants. An automated procedure of advanced chromosome analysis analysed the original chromatogram files

in the vicinity of the putative SNP. Clone error filters used statistically generated algorithms to identify errors introduced during laboratory processing, such as those caused by reverse transcriptase, polymerase, or somatic mutation. Clustering error filters used statistically generated algorithms to identify errors resulting from clustering of close homologs or pseudogenes, or due to contamination by non-human sequences. A final set of filters removed duplicates and SNPs found in immunoglobulins or T-cell receptors.

Certain SNPs were selected for further characterization by mass spectrometry using the high throughput MASSARRAY system (Sequenom, Inc.) to analyze allele frequencies at the SNP sites in four different human populations. The Caucasian population comprised 92 individuals (46 male, 46 female), including 83 from Utah, four French, three Venezuelan, and two Amish individuals. The African population comprised 194 individuals (97 male, 97 female), all African Americans. The Hispanic population comprised 324 individuals (162 male, 162 female), all Mexican Hispanic. The Asian population comprised 126 individuals (64 male, 62 female) with a reported parental breakdown of 43% Chinese, 31% Japanese, 13% Korean, 5% Vietnamese, and 8% other Asian. Allele frequencies were first analyzed in the Caucasian population; in some cases those SNPs which showed no allelic variance in this population were not further tested in the other three populations.

X. Labeling and Use of Individual Hybridization Probes

Hybridization probes derived from SEQ ID NO:60-118 are employed to screen cDNAs, genomic DNAs, or mRNAs. Although the labeling of oligonucleotides, consisting of about 20 base pairs, is specifically described, essentially the same procedure is used with larger nucleotide fragments. Oligonucleotides are designed using state-of-the-art software such as OLIGO 4.06 software (National Biosciences) and labeled by combining 50 pmol of each oligomer, 250 μ Ci of [γ - 32 P] adenosine triphosphate (Amersham Biosciences), and T4 polynucleotide kinase (DuPont NEN, Boston MA). The labeled oligonucleotides are substantially purified using a SEPHADEX G-25 superfine size exclusion dextran bead column (Amersham Biosciences). An aliquot containing 10^7 counts per minute of the labeled probe is used in a typical membrane-based hybridization analysis of human genomic DNA digested with one of the following endonucleases: Ase I, Bgl II, Eco RI, Pst I, Xba I, or Pvu II (DuPont NEN).

The DNA from each digest is fractionated on a 0.7% agarose gel and transferred to nylon membranes (Nytran Plus, Schleicher & Schuell, Durham NH). Hybridization is carried out for 16 hours at 40°C. To remove nonspecific signals, blots are sequentially washed at room temperature under conditions of up to, for example, 0.1 x saline sodium citrate and 0.5% sodium dodecyl sulfate.

Hybridization patterns are visualized using autoradiography or an alternative imaging means and compared.

XI. Microarrays

The linkage or synthesis of array elements upon a microarray can be achieved utilizing photolithography, piezoelectric printing (ink-jet printing; see, e.g., Baldeschweiler et al., *supra*), mechanical microspotting technologies, and derivatives thereof. The substrate in each of the aforementioned technologies should be uniform and solid with a non-porous surface (Schena, M., ed. (1999) DNA Microarrays: A Practical Approach, Oxford University Press, London). Suggested substrates include silicon, silica, glass slides, glass chips, and silicon wafers. Alternatively, a procedure analogous to a dot or slot blot may also be used to arrange and link elements to the surface of a substrate using thermal, UV, chemical, or mechanical bonding procedures. A typical array may be produced using available methods and machines well known to those of ordinary skill in the art and may contain any appropriate number of elements (Schena, M. et al. (1995) *Science* 270:467-470; Shalon, D. et al. (1996) *Genome Res.* 6:639-645; Marshall, A. and J. Hodgson (1998) *Nat. Biotechnol.* 16:27-31).

Full length cDNAs, Expressed Sequence Tags (ESTs), or fragments or oligomers thereof may comprise the elements of the microarray. Fragments or oligomers suitable for hybridization can be selected using software well known in the art such as LASERGENE software (DNASTAR). The array elements are hybridized with polynucleotides in a biological sample. The polynucleotides in the biological sample are conjugated to a fluorescent label or other molecular tag for ease of detection. After hybridization, nonhybridized nucleotides from the biological sample are removed, and a fluorescence scanner is used to detect hybridization at each array element. Alternatively, laser desorption and mass spectrometry may be used for detection of hybridization. The degree of complementarity and the relative abundance of each polynucleotide which hybridizes to an element on the microarray may be assessed. In one embodiment, microarray preparation and usage is described in detail below.

Tissue or Cell Sample Preparation

Total RNA is isolated from tissue samples using the guanidinium thiocyanate method and poly(A)⁺ RNA is purified using the oligo-(dT) cellulose method. Each poly(A)⁺ RNA sample is reverse transcribed using MMLV reverse-transcriptase, 0.05 pg/ μ l oligo-(dT) primer (21mer), 1X first strand buffer, 0.03 units/ μ l RNase inhibitor, 500 μ M dATP, 500 μ M dGTP, 500 μ M dTTP, 40 μ M dCTP, 40 μ M dCTP-Cy3 (BDS) or dCTP-Cy5 (Amersham Biosciences). The reverse transcription

reaction is performed in a 25 ml volume containing 200 ng poly(A)⁺ RNA with GEMBRIGHT kits (Incyte Genomics). Specific control poly(A)⁺ RNAs are synthesized by *in vitro* transcription from non-coding yeast genomic DNA. After incubation at 37°C for 2 hr, each reaction sample (one with Cy3 and another with Cy5 labeling) is treated with 2.5 ml of 0.5M sodium hydroxide and incubated for
5 20 minutes at 85°C to stop the reaction and degrade the RNA. Samples are purified using two successive CHROMA SPIN 30 gel filtration spin columns (Clontech, Palo Alto CA) and after combining, both reaction samples are ethanol precipitated using 1 ml of glycogen (1 mg/ml), 60 ml sodium acetate, and 300 ml of 100% ethanol. The sample is then dried to completion using a SpeedVAC (Savant Instruments Inc., Holbrook NY) and resuspended in 14 μ l 5X SSC/0.2% SDS.

10 Microarray Preparation

Sequences of the present invention are used to generate array elements. Each array element is amplified from bacterial cells containing vectors with cloned cDNA inserts. PCR amplification uses primers complementary to the vector sequences flanking the cDNA insert. Array elements are amplified in thirty cycles of PCR from an initial quantity of 1-2 ng to a final quantity greater than 5 μ g.
15 Amplified array elements are then purified using SEPHACRYL-400 (Amersham Biosciences).

Purified array elements are immobilized on polymer-coated glass slides. Glass microscope slides (Corning) are cleaned by ultrasound in 0.1% SDS and acetone, with extensive distilled water washes between and after treatments. Glass slides are etched in 4% hydrofluoric acid (VWR Scientific Products Corporation (VWR), West Chester PA), washed extensively in distilled water, and
20 coated with 0.05% aminopropyl silane (Sigma-Aldrich, St. Louis MO) in 95% ethanol. Coated slides are cured in a 110°C oven.

Array elements are applied to the coated glass substrate using a procedure described in U.S. Patent No. 5,807,522, incorporated herein by reference. 1 μ l of the array element DNA, at an average concentration of 100 ng/ μ l, is loaded into the open capillary printing element by a high-speed robotic
25 apparatus. The apparatus then deposits about 5 nl of array element sample per slide.

Microarrays are UV-crosslinked using a STRATALINKER UV-crosslinker (Stratagene). Microarrays are washed at room temperature once in 0.2% SDS and three times in distilled water. Non-specific binding sites are blocked by incubation of microarrays in 0.2% casein in phosphate buffered saline (PBS) (Tropix, Inc., Bedford MA) for 30 minutes at 60°C followed by washes in 0.2%
30 SDS and distilled water as before.

Hybridization

Hybridization reactions contain 9 μ l of sample mixture consisting of 0.2 μ g each of Cy3 and Cy5 labeled cDNA synthesis products in 5X SSC, 0.2% SDS hybridization buffer. The sample mixture is heated to 65°C for 5 minutes and is aliquoted onto the microarray surface and covered with an 1.8 cm² coverslip. The arrays are transferred to a waterproof chamber having a cavity just slightly larger than a microscope slide. The chamber is kept at 100% humidity internally by the addition of 140 μ l of 5X SSC in a corner of the chamber. The chamber containing the arrays is incubated for about 6.5 hours at 60°C. The arrays are washed for 10 min at 45°C in a first wash buffer (1X SSC, 0.1% SDS), three times for 10 minutes each at 45°C in a second wash buffer (0.1X SSC), and dried.

Detection

Reporter-labeled hybridization complexes are detected with a microscope equipped with an Innova 70 mixed gas 10 W laser (Coherent, Inc., Santa Clara CA) capable of generating spectral lines at 488 nm for excitation of Cy3 and at 632 nm for excitation of Cy5. The excitation laser light is focused on the array using a 20X microscope objective (Nikon, Inc., Melville NY). The slide containing the array is placed on a computer-controlled X-Y stage on the microscope and raster-scanned past the objective. The 1.8 cm x 1.8 cm array used in the present example is scanned with a resolution of 20 micrometers.

In two separate scans, a mixed gas multiline laser excites the two fluorophores sequentially. Emitted light is split, based on wavelength, into two photomultiplier tube detectors (PMT R1477, Hamamatsu Photonics Systems, Bridgewater NJ) corresponding to the two fluorophores. Appropriate filters positioned between the array and the photomultiplier tubes are used to filter the signals. The emission maxima of the fluorophores used are 565 nm for Cy3 and 650 nm for Cy5. Each array is typically scanned twice, one scan per fluorophore using the appropriate filters at the laser source, although the apparatus is capable of recording the spectra from both fluorophores simultaneously.

The sensitivity of the scans is typically calibrated using the signal intensity generated by a cDNA control species added to the sample mixture at a known concentration. A specific location on the array contains a complementary DNA sequence, allowing the intensity of the signal at that location to be correlated with a weight ratio of hybridizing species of 1:100,000. When two samples from different sources (e.g., representing test and control cells), each labeled with a different fluorophore, are hybridized to a single array for the purpose of identifying genes that are differentially expressed, the calibration is done by labeling samples of the calibrating cDNA with the two fluorophores and adding identical amounts of each to the hybridization mixture.

The output of the photomultiplier tube is digitized using a 12-bit RTI-835H analog-to-digital (A/D) conversion board (Analog Devices, Inc., Norwood MA) installed in an IBM-compatible PC computer. The digitized data are displayed as an image where the signal intensity is mapped using a linear 20-color transformation to a pseudocolor scale ranging from blue (low signal) to red (high signal). The data is also analyzed quantitatively. Where two different fluorophores are excited and measured simultaneously, the data are first corrected for optical crosstalk (due to overlapping emission spectra) between the fluorophores using each fluorophore's emission spectrum.

A grid is superimposed over the fluorescence signal image such that the signal from each spot is centered in each element of the grid. The fluorescence signal within each element is then integrated to obtain a numerical value corresponding to the average intensity of the signal. The software used for signal analysis is the GEMTOOLS gene expression analysis program (Incyte Genomics). Array elements that exhibit at least about a two-fold change in expression, a signal-to-background ratio of at least about 2.5, and an element spot size of at least about 40%, are considered to be differentially expressed.

Expression

Breast cancer

For example, SEQ ID NO:85 showed decreased expression in nonmalignant breast adenocarcinoma cells treated with serum tumor necrosis factor alpha (TNF- α) versus untreated nonmalignant breast adenocarcinoma cells as determined by microarray analysis. MCF7 is a nonmalignant breast adenocarcinoma cell line isolated from the pleural effusion of a 69-year-old female. MCF7 has retained characteristics of the mammary epithelium such as the ability to process estradiol via cytoplasmic estrogen receptors and the capacity to form domes in culture. MCF7 cells were treated with TNF- α for 1, 4, 8, 12, 24, 36, 48, and 72 hours. Treated cells were compared to untreated cells kept in culture for the same amount of time. The expression of SEQ ID NO:85 was reduced by at least two-fold at later time points. In addition, SEQ ID NO:85 showed decreased expression in breast carcinoma cells treated with interferon gamma (IFN γ) versus untreated breast carcinoma cells. T-47D is a breast carcinoma cell line isolated from a pleural effusion obtained from a 54-year-old female with an infiltrating ductal carcinoma of the breast. T-47D cells were treated with 200 ng/ml IFN γ for 1, 4, 8, 24, 48 hours and 3 days. These treated cells were compared to untreated cells. The expression of SEQ ID NO:85 was reduced by at least two-fold at later time points.

In a further example, SEQ ID NO:88 showed differential expression in breast cell carcinoma cells versus nonmalignant mammary epithelial cells as determined by microarray analysis. Gene expression profiles of nonmalignant mammary epithelial cells were compared to the gene expression profile of a breast carcinoma line. The cells were grown in defined serum-free H14 medium to 70-80% confluence prior to RNA harvest. Cell lines compared include T-47D, a breast carcinoma cell line isolated from a pleural effusion obtained from a 54-year-old female with an infiltrating ductal carcinoma of the breast versus MCF-10A, a breast mammary gland cell line isolated from a 36-year-old woman with fibrocystic breast disease, and HMEC, a primary breast epithelial cell line isolated from a normal donor. The expression of SEQ ID NO:88 was increased by at least two-fold in T-47D cells as compared to either HMEC or MCF-10A cells.

In a further example, SEQ ID NO:112 showed differential expression in breast tumor tissue as compared to normal breast tissue from the same donor as determined by microarray analysis. Tumor from the right breast was compared to grossly uninvolved breast tissue from the same donor, a 43-year-old female diagnosed with invasive lobular carcinoma *in situ*. The expression of SEQ ID NO:112 was decreased by at least two-fold in the tumor tissue as compared to the matched non-tumor tissue.

In a further example, SEQ ID NO:113 showed differential expression in breast cancer cell lines as compared to non-cancerous breast epithelial cell lines as determined by microarray analysis. Cell lines compared included: a) BT-20, a breast carcinoma cell line derived *in vitro* from the cells emigrating out of thin slices of tumor mass isolated from a 74-year-old female, b) BT-474, a breast ductal carcinoma cell line that was isolated from a solid, invasive ductal carcinoma of the breast obtained from a 60-year-old woman, c) BT-483, a breast ductal carcinoma cell line that was isolated from a papillary invasive ductal tumor obtained from a 23-year-old normal, menstruating, parous female with a family history of breast cancer, d) Hs 578T, a breast ductal carcinoma cell line isolated from a 74-year-old female with breast carcinoma, e) MCF7, a nonmalignant breast adenocarcinoma cell line isolated from the pleural effusion of a 69-year-old female, f) MCF-10A, a breast mammary gland (luminal ductal characteristics) cell line isolated from a 36-year-old woman with fibrocystic breast disease, g) MDA-MB-468, a breast adenocarcinoma cell line isolated from the pleural effusion of a 51-year-old female with metastatic adenocarcinoma of the breast, and h) HMEC, a primary breast epithelial cell line isolated from a normal donor. Expression of SEQ ID NO: 113 was decreased by at least two-fold in the BT-474 and BT-483 breast cancer cell lines as compared to the

non-malignant HMEC cells. Therefore, SEQ ID NO: 113 is useful in monitoring treatment of, and diagnostic assays for, breast cancer.

Therefore, in various embodiments, SEQ ID NO:85, SEQ ID NO:88, and SEQ ID NO: 112-113 can each be used for one or more of the following: i) monitoring treatment of breast
5 adenocarcinoma and other cell proliferative disorders, ii) diagnostic assays for breast adenocarcinoma and other cell proliferative disorders, and iii) developing therapeutics and/or other treatments for breast adenocarcinoma and other cell proliferative disorders.

Lung cancer

In another example, SEQ ID NO:85 showed increased expression in lung tumor tissue versus
10 normal lung tissue. Normal lung tissue from a 68 year-old female was compared to lung tumor from the same donor (Roy Castle International Centre for Lung Cancer Research, Liverpool, UK).

In a further example, SEQ ID NO:92, SEQ ID NO:93, and SEQ ID NO:94 showed differential expression in lung tumor tissues compared to normal lung tissue from the same donor as determined by microarray analysis. Samples of normal lung were compared to lung tumor from the
15 same donor (Roy Castle International Centre for Lung Cancer Research, Liverpool, UK). The expression of SEQ ID NO:92, SEQ ID NO:93, and SEQ ID NO:94 was decreased by at least two-fold in tumor tissue as compared to the matched normal lung for seven different donors in the case of SEQ ID NO:92, and for one donor in the case of SEQ ID NO:93 and SEQ ID NO:94.

Therefore, in various embodiments, SEQ ID NO:85, and SEQ ID NO:92, SEQ ID NO:93, and
20 SEQ ID NO:94 can each be used for one or more of the following: i) monitoring treatment of lung cancer and other cell proliferative disorders, ii) diagnostic assays for lung cancer and other cell proliferative disorders, and iii) developing therapeutics and/or other treatments for lung cancer and other cell proliferative disorders.

Colon cancer

25 In a further example, SEQ ID NO:85 showed decreased expression in sigmoid colon tumor tissue versus normal sigmoid colon tissue. Gene expression profiles were obtained by comparing normal sigmoid colon tissue from a 48-year-old female to a sigmoid colon tumor originating from a metastatic gastric sarcoma (stromal tumor) from the same donor (Huntsman Cancer Institute, Salt Lake City, UT).

30 In a further example, SEQ ID NO:91, SEQ ID NO:93, and SEQ ID NO:94 showed differential expression in colon tumor tissues compared to normal colon tissue from the same donor as determined by microarray analysis. Samples of normal colon were compared to colon tumor from the

same donor (Huntsman Cancer Institute, Salt Lake City, UT). The expression of SEQ ID NO:91, was decreased, and that of SEQ ID NO:93, and SEQ ID NO:94 increased, by at least two-fold in tumor tissue as compared to matched normal colon tissue.

Therefore, in various embodiments, SEQ ID NO:85, SEQ ID NO:91, SEQ ID NO:93, and
5 SEQ ID NO:94 can each be used for one or more of the following: i) monitoring treatment of colon cancer and other cell proliferative disorders, ii) diagnostic assays for colon cancer and other cell proliferative disorders, and iii) developing therapeutics and/or other treatments for colon cancer and other cell proliferative disorders.

Ovarian cancer

10 In another example, SEQ ID NO:88 showed differential expression associated with ovarian cancer, as determined by microarray analysis. A normal ovary from a 79 year-old female donor was compared to an ovarian tumor from the same donor (Huntsman Cancer Institute, Salt Lake City, UT). SEQ ID NO:88 expression was increased at least two-fold in the tumor tissue as compared to the normal tissue.

15 In a further example, SEQ ID NO:92, SEQ ID NO:109, and SEQ ID NO:112 showed differential expression in ovary tumor versus normal ovary tissue as determined by microarray analysis. A normal ovary from a 79-year-old female donor was compared to an ovarian tumor from the same donor (Huntsman Cancer Institute, Salt Lake City, UT). The expression of SEQ ID NO:92 and SEQ ID NO:109 was increased, and the expression of SEQ ID NO:112 decreased, by at least
20 two-fold in the ovarian tumor tissue as compared to the matched normal tissue.

Therefore, in various embodiments, SEQ ID NO:88, SEQ ID NO:92, SEQ ID NO:109, and SEQ ID NO:112 can each be used for one or more of the following: i) monitoring treatment of ovarian cancer and other cell proliferative disorders, ii) diagnostic assays for ovarian cancer and other cell proliferative disorders, and iii) developing therapeutics and/or other treatments for ovarian cancer and
25 other cell proliferative disorders.

Osteosarcoma

In a further example, SEQ ID NO:103, SEQ ID NO:109, and SEQ ID NO:118 showed differential expression in osteosarcoma associated tissues as compared to normal osteoblasts as determined by microarray analysis. Messenger RNA from normal human osteoblasts was compared with mRNA from biopsy specimens, osteosarcoma tissues, or primary cultures or metastasized tissues. A normal osteoblast primary culture, NHOst 5488, was chosen as the reference in the initial experiments. One basic set of experiments is defined as the comparison of mRNA from biopsy specimen with that of definitive surgical specimen from the same patient. Extended study of this basic set includes mRNA from primary cell cultures of the definitive surgical specimen, muscle, or cartilage tissue from the same patient. Biopsy specimens, definitive surgical specimens, or lung metastatic tissues from different individuals were also included to reveal individual variability. Expression of SEQ ID NO:103 was increased, and expression of SEQ ID NO:109 and SEQ ID NO:118 decreased, by at least two-fold in osteosarcoma associated tissues as compared to the normal osteoblasts.

Therefore, in various embodiments, SEQ ID NO:103, SEQ ID NO:109, and SEQ ID NO:118 can be used for one or more of the following: i) monitoring treatment of osteosarcoma and other cell proliferative disorders, ii) diagnostic assays for osteosarcoma and other cell proliferative disorders, and iii) developing therapeutics and/or other treatments for osteosarcoma and other cell proliferative disorders.

Autoimmune and inflammatory disorders

In a further example, PBMCs from 3 healthy volunteer donors were stimulated *in vitro* with TNF- α for 2 hours. Treated cells were compared to untreated cells from the same donors. In a separate experiment, PBMCs from 5 healthy volunteers were incubated in the presence of pro-inflammatory cytokines (IL-1 β , IL-2, IL-6, IL-8, IL-12, IL-18, IFN- γ , and TNF- α) for 2 and 4 hours. Cytokine-treated PBMCs were compared to untreated PBMCs from the same donors. In both cases, the expression of SEQ ID NO:93 and SEQ ID NO:94 was increased at least two-fold in the treated cells as compared to the untreated cells. Therefore, SEQ ID NO:93 and SEQ ID NO:94 are useful in monitoring treatment of, and diagnostic assays for, autoimmune and inflammatory disorders.

XII. Complementary Polynucleotides

Sequences complementary to the TRICH-encoding sequences, or any parts thereof, are used to detect, decrease, or inhibit expression of naturally occurring TRICH. Although use of oligonucleotides comprising from about 15 to 30 base pairs is described, essentially the same procedure is used with smaller or with larger sequence fragments. Appropriate oligonucleotides are

designed using OLIGO 4.06 software (National Biosciences) and the coding sequence of TRICH. To inhibit transcription, a complementary oligonucleotide is designed from the most unique 5' sequence and used to prevent promoter binding to the coding sequence. To inhibit translation, a complementary oligonucleotide is designed to prevent ribosomal binding to the TRICH-encoding transcript.

5 **XIII. Expression of TRICH**

Expression and purification of TRICH is achieved using bacterial or virus-based expression systems. For expression of TRICH in bacteria, cDNA is subcloned into an appropriate vector containing an antibiotic resistance gene and an inducible promoter that directs high levels of cDNA transcription. Examples of such promoters include, but are not limited to, the *trp-lac (tac)* hybrid
10 promoter and the T5 or T7 bacteriophage promoter in conjunction with the *lac* operator regulatory element. Recombinant vectors are transformed into suitable bacterial hosts, e.g., BL21(DE3). Antibiotic resistant bacteria express TRICH upon induction with isopropyl beta-D-thiogalactopyranoside (IPTG). Expression of TRICH in eukaryotic cells is achieved by infecting
insect or mammalian cell lines with recombinant *Autographica californica* nuclear polyhedrosis virus
15 (AcMNPV); commonly known as baculovirus. The nonessential polyhedrin gene of baculovirus is replaced with cDNA encoding TRICH by either homologous recombination or bacterial-mediated transposition involving transfer plasmid intermediates. Viral infectivity is maintained and the strong polyhedrin promoter drives high levels of cDNA transcription. Recombinant baculovirus is used to infect *Spodoptera frugiperda* (Sf9) insect cells in most cases, or human hepatocytes, in some cases.
20 Infection of the latter requires additional genetic modifications to baculovirus (Engelhard, E.K. et al. (1994) Proc. Natl. Acad. Sci. USA 91:3224-3227; Sandig, V. et al. (1996) Hum. Gene Ther. 7:1937-1945).

In most expression systems, TRICH is synthesized as a fusion protein with, e.g., glutathione S-transferase (GST) or a peptide epitope tag, such as FLAG or 6-His, permitting rapid, single-step,
25 affinity-based purification of recombinant fusion protein from crude cell lysates. GST, a 26-kilodalton enzyme from *Schistosoma japonicum*, enables the purification of fusion proteins on immobilized glutathione under conditions that maintain protein activity and antigenicity (Amersham Biosciences). Following purification, the GST moiety can be proteolytically cleaved from TRICH at specifically engineered sites. FLAG, an 8-amino acid peptide, enables immunoaffinity purification using
30 commercially available monoclonal and polyclonal anti-FLAG antibodies (Eastman Kodak). 6-His, a stretch of six consecutive histidine residues, enables purification on metal-chelate resins (QIAGEN). Methods for protein expression and purification are discussed in Ausubel et al. (*supra*, ch. 10 and 16).

Purified TRICH obtained by these methods can be used directly in the assays shown in Examples XVII, XVIII, and XIX, where applicable.

XIV. Functional Assays

TRICH function is assessed by expressing the sequences encoding TRICH at physiologically elevated levels in mammalian cell culture systems. cDNA is subcloned into a mammalian expression vector containing a strong promoter that drives high levels of cDNA expression. Vectors of choice include PCMV SPORT plasmid (Invitrogen, Carlsbad CA) and PCR3.1 plasmid (Invitrogen), both of which contain the cytomegalovirus promoter. 5-10 μ g of recombinant vector are transiently transfected into a human cell line, for example, an endothelial or hematopoietic cell line, using either liposome formulations or electroporation. 1-2 μ g of an additional plasmid containing sequences encoding a marker protein are co-transfected. Expression of a marker protein provides a means to distinguish transfected cells from nontransfected cells and is a reliable predictor of cDNA expression from the recombinant vector. Marker proteins of choice include, e.g., Green Fluorescent Protein (GFP; Clontech), CD64, or a CD64-GFP fusion protein. Flow cytometry (FCM), an automated, laser optics-based technique, is used to identify transfected cells expressing GFP or CD64-GFP and to evaluate the apoptotic state of the cells and other cellular properties. FCM detects and quantifies the uptake of fluorescent molecules that diagnose events preceding or coincident with cell death. These events include changes in nuclear DNA content as measured by staining of DNA with propidium iodide; changes in cell size and granularity as measured by forward light scatter and 90 degree side light scatter; down-regulation of DNA synthesis as measured by decrease in bromodeoxyuridine uptake; alterations in expression of cell surface and intracellular proteins as measured by reactivity with specific antibodies; and alterations in plasma membrane composition as measured by the binding of fluorescein-conjugated Annexin V protein to the cell surface. Methods in flow cytometry are discussed in Ormerod, M.G. (1994; Flow Cytometry, Oxford, New York NY).

The influence of TRICH on gene expression can be assessed using highly purified populations of cells transfected with sequences encoding TRICH and either CD64 or CD64-GFP. CD64 and CD64-GFP are expressed on the surface of transfected cells and bind to conserved regions of human immunoglobulin G (IgG). Transfected cells are efficiently separated from nontransfected cells using magnetic beads coated with either human IgG or antibody against CD64 (DYNAL, Lake Success NY). mRNA can be purified from the cells using methods well known by those of skill in the art. Expression of mRNA encoding TRICH and other genes of interest can be analyzed by northern analysis or microarray techniques.

XV. Production of TRICH Specific Antibodies

TRICH substantially purified using polyacrylamide gel electrophoresis (PAGE; see, e.g., Harrington, M.G. (1990) *Methods Enzymol.* 182:488-495), or other purification techniques, is used to immunize animals (e.g., rabbits, mice, etc.) and to produce antibodies using standard protocols.

5 Alternatively, the TRICH amino acid sequence is analyzed using LASERGENE software (DNASTAR) to determine regions of high immunogenicity, and a corresponding oligopeptide is synthesized and used to raise antibodies by means known to those of skill in the art. Methods for selection of appropriate epitopes, such as those near the C-terminus or in hydrophilic regions are well described in the art (Ausubel et al., *supra*, ch. 11).

10 Typically, oligopeptides of about 15 residues in length are synthesized using an ABI 431A peptide synthesizer (Applied Biosystems) using Fmoc chemistry and coupled to KLH (Sigma-Aldrich, St. Louis MO) by reaction with N-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS) to increase immunogenicity (Ausubel et al., *supra*). Rabbits are immunized with the oligopeptide-KLH complex in complete Freund's adjuvant. Resulting antisera are tested for antipeptide and anti-TRICH
15 activity by, for example, binding the peptide or TRICH to a substrate, blocking with 1% BSA, reacting with rabbit antisera, washing, and reacting with radio-iodinated goat anti-rabbit IgG.

XVI. Purification of Naturally Occurring TRICH Using Specific Antibodies

Naturally occurring or recombinant TRICH is substantially purified by immunoaffinity chromatography using antibodies specific for TRICH. An immunoaffinity column is constructed by
20 covalently coupling anti-TRICH antibody to an activated chromatographic resin, such as CNBr-activated SEPHAROSE (Amersham Biosciences). After the coupling, the resin is blocked and washed according to the manufacturer's instructions.

Media containing TRICH are passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of TRICH (e.g., high ionic strength
25 buffers in the presence of detergent). The column is eluted under conditions that disrupt antibody/TRICH binding (e.g., a buffer of pH 2 to pH 3, or a high concentration of a chaotrope, such as urea or thiocyanate ion), and TRICH is collected.

XVII. Identification of Molecules Which Interact with TRICH

Molecules which interact with TRICH may include transporter substrates, agonists or
30 antagonists, modulatory proteins such as G $\beta\gamma$ proteins (Reimann, *supra*) or proteins involved in TRICH localization or clustering such as MAGUKs (Craven, *supra*). TRICH, or biologically active fragments thereof, are labeled with ¹²⁵I Bolton-Hunter reagent. (See, e.g., Bolton A.E. and W.M.

Hunter (1973) Biochem. J. 133:529-539.) Candidate molecules previously arrayed in the wells of a multi-well plate are incubated with the labeled TRICH, washed, and any wells with labeled TRICH complex are assayed. Data obtained using different concentrations of TRICH are used to calculate values for the number, affinity, and association of TRICH with the candidate molecules.

5 Alternatively, proteins that interact with TRICH are isolated using the yeast 2-hybrid system (Fields, S. and O. Song (1989) Nature 340:245-246). TRICH, or fragments thereof, are expressed as fusion proteins with the DNA binding domain of Gal4 or lexA, and potential interacting proteins are expressed as fusion proteins with an activation domain. Interactions between the TRICH fusion protein and the TRICH interacting proteins (fusion proteins with an activation domain) reconstitute a
10 transactivation function that is observed by expression of a reporter gene. Yeast 2-hybrid systems are commercially available, and methods for use of the yeast 2-hybrid system with ion channel proteins are discussed in Niethammer, M. and M. Sheng (1998, Meth. Enzymol. 293:104-122).

 TRICH may also be used in the PATHCALLING process (CuraGen Corp., New Haven CT) which employs the yeast two-hybrid system in a high-throughput manner to determine all interactions
15 between the proteins encoded by two large libraries of genes (Nandabalan, K. et al. (2000) U.S. Patent No. 6,057,101).

 Potential TRICH agonists or antagonists may be tested for activation or inhibition of TRICH ion channel activity using the assays described in section XVIII.

XVIII. Demonstration of TRICH Activity

20 Ion channel activity of TRICH is demonstrated using an electrophysiological assay for ion conductance. TRICH can be expressed by transforming a mammalian cell line such as COS7, HeLa or CHO with a eukaryotic expression vector encoding TRICH. Eukaryotic expression vectors are commercially available, and the techniques to introduce them into cells are well known to those skilled in the art. A second plasmid which expresses any one of a number of marker genes, such as β -
25 galactosidase, is co-transformed into the cells to allow rapid identification of those cells which have taken up and expressed the foreign DNA. The cells are incubated for 48-72 hours after transformation under conditions appropriate for the cell line to allow expression and accumulation of TRICH and β -galactosidase.

 Transformed cells expressing β -galactosidase are stained blue when a suitable colorimetric
30 substrate is added to the culture media under conditions that are well known in the art. Stained cells are tested for differences in membrane conductance by electrophysiological techniques that are well known in the art. Untransformed cells, and/or cells transformed with either vector sequences alone or

β -galactosidase sequences alone, are used as controls and tested in parallel. Cells expressing TRICH will have higher anion or cation conductance relative to control cells. The contribution of TRICH to conductance can be confirmed by incubating the cells using antibodies specific for TRICH. The antibodies will bind to the extracellular side of TRICH, thereby blocking the pore in the ion channel, and the associated conductance.

Alternatively, ion channel activity of TRICH is measured as current flow across a TRICH-containing *Xenopus laevis* oocyte membrane using the two-electrode voltage-clamp technique (Ishi et al., *supra*; Jegla, T. and L. Salkoff (1997) J. Neurosci. 17:32-44). TRICH is subcloned into an appropriate *Xenopus* oocyte expression vector, such as pBF, and 0.5-5 ng of mRNA is injected into mature stage IV oocytes. Injected oocytes are incubated at 18°C for 1-5 days. Inside-out macropatches are excised into an intracellular solution containing 116 mM K-gluconate, 4 mM KCl, and 10 mM Hepes (pH 7.2). The intracellular solution is supplemented with varying concentrations of the TRICH mediator, such as cAMP, cGMP, or Ca^{+2} (in the form of CaCl_2), where appropriate. Electrode resistance is set at 2-5 M Ω and electrodes are filled with the intracellular solution lacking mediator. Experiments are performed at room temperature from a holding potential of 0 mV. Voltage ramps (2.5 s) from -100 to 100 mV are acquired at a sampling frequency of 500 Hz. Current measured is proportional to the activity of TRICH in the assay.

Transport activity of TRICH is assayed by measuring uptake of labeled substrates into *Xenopus laevis* oocytes. Oocytes at stages V and VI are injected with TRICH mRNA (10 ng per oocyte) and incubated for 3 days at 18°C in OR2 medium (82.5mM NaCl, 2.5 mM KCl, 1mM CaCl_2 , 1mM MgCl_2 , 1mM Na_2HPO_4 , 5 mM Hepes, 3.8 mM NaOH, 50 $\mu\text{g/ml}$ gentamycin, pH 7.8) to allow expression of TRICH. Oocytes are then transferred to standard uptake medium (100mM NaCl, 2 mM KCl, 1mM CaCl_2 , 1mM MgCl_2 , 10 mM Hepes/Tris pH 7.5). Uptake of various substrates (e.g., amino acids, sugars, drugs, ions, and neurotransmitters) is initiated by adding labeled substrate (e.g., radiolabeled with ^3H , fluorescently labeled with rhodamine, etc.) to the oocytes. After incubating for 30 minutes, uptake is terminated by washing the oocytes three times in Na^+ -free medium, measuring the incorporated label, and comparing with controls. TRICH activity is proportional to the level of internalized labeled substrate.

ATPase activity associated with TRICH can be measured by hydrolysis of radiolabeled ATP- $[\gamma\text{-}^{32}\text{P}]$, separation of the hydrolysis products by chromatographic methods, and quantitation of the recovered ^{32}P using a scintillation counter. The reaction mixture contains ATP- $[\gamma\text{-}^{32}\text{P}]$ and varying amounts of TRICH in a suitable buffer incubated at 37°C for a suitable period of time. The reaction

is terminated by acid precipitation with trichloroacetic acid and then neutralized with base, and an aliquot of the reaction mixture is subjected to membrane or filter paper-based chromatography to separate the reaction products. The amount of ^{32}P liberated is counted in a scintillation counter. The amount of radioactivity recovered is proportional to the ATPase activity of TRICH in the assay.

5 Lipocalin activity of TRICH is measured by ligand fluorescence enhancement spectrofluorometry (Lin et al. (1997) *Molecular Vision* 3:17). Examples of ligands include retinol (Sigma, St. Louis MO) and 16-anthyroxy-palmitic acid (16-AP) (Molecular Probes Inc., Eugene OR). Ligand is dissolved in 100% ethanol and its concentration is estimated using known extinction coefficients (retinol: 46,000 A/M/cm at 325 nm; 16-AP: 8,200 A/M/cm at 361 nm). A 700 μl aliquot of
10 1 μM TRICH in 10 mM Tris (pH 7.5), 2 mM EDTA, and 500 mM NaCl is placed in a 1 cm path length quartz cuvette and 1 μl aliquots of ligand solution are added. Fluorescence is measured 100 seconds after each addition until readings are stable. Change in fluorescence per unit change in ligand concentration is proportional to TRICH activity.

XIX. Identification of TRICH Agonists and Antagonists

15 TRICH is expressed in a eukaryotic cell line such as CHO (Chinese Hamster Ovary) or HEK (Human Embryonic Kidney) 293. Ion channel activity of the transformed cells is measured in the presence and absence of candidate agonists or antagonists. Ion channel activity is assayed using patch clamp methods well known in the art or as described in Example XVIII. Alternatively, ion channel activity is assayed using fluorescent techniques that measure ion flux across the cell
20 membrane (Velicelebi, G. et al. (1999) *Meth. Enzymol.* 294:20-47; West, M.R. and C.R. Molloy (1996) *Anal. Biochem.* 241:51-58). These assays may be adapted for high-throughput screening using microplates. Changes in internal ion concentration are measured using fluorescent dyes such as the Ca^{2+} indicator Fluo-4 AM, sodium-sensitive dyes such as SBFI and sodium green, or the Cl^- indicator MQAE (all available from Molecular Probes) in combination with the FLIPR fluorimetric plate reading
25 system (Molecular Devices). In a more generic version of this assay, changes in membrane potential caused by ionic flux across the plasma membrane are measured using oxonyl dyes such as DiBAC₄ (Molecular Probes). DiBAC₄ equilibrates between the extracellular solution and cellular sites according to the cellular membrane potential. The dye's fluorescence intensity is 20-fold greater when bound to hydrophobic intracellular sites, allowing detection of DiBAC₄ entry into the cell
30 (Gonzalez, J.E. and P.A. Negulescu (1998) *Curr. Opin. Biotechnol.* 9:624-631). Candidate agonists or antagonists may be selected from known ion channel agonists or antagonists, peptide libraries, or combinatorial chemical libraries.

Various modifications and variations of the described compositions, methods, and systems of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. It will be appreciated that the invention provides novel and useful proteins, and their encoding polynucleotides, which can be used in the drug discovery process, as well as methods for using these compositions for the detection, diagnosis, and treatment of diseases and conditions. Although the invention has been described in connection with certain embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Nor should the description of such embodiments be considered exhaustive or limit the invention to the precise forms disclosed. Furthermore, elements from one embodiment can be readily recombined with elements from one or more other embodiments. Such combinations can form a number of embodiments within the scope of the invention. It is intended that the scope of the invention be defined by the following claims and their equivalents.

Table 1

Incyte Project ID	Polypeptide SEQ ID NO:	Incyte Polypeptide ID	Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Incyte Full Length Clones
7509332	1	7509332CD1	60	7509332CB1	90124688CA2
7509102	2	7509102CD1	61	7509102CB1	90134847CA2
7509132	3	7509132CD1	62	7509132CB1	90134560CA2
7509136	4	7509136CD1	63	7509136CB1	90138017CA2
7509178	5	7509178CD1	64	7509178CB1	90138906CA2
7509214	6	7509214CD1	65	7509214CB1	90138823CA2
7509244	7	7509244CD1	66	7509244CB1	90137849CA2
7509256	8	7509256CD1	67	7509256CB1	2444801CA2, 4936749CA2, 90028858CA2, 90028990CA2, 90138157CA2, 90138181CA2, 90161926CA2, 90223995CA2
7509395	9	7509395CD1	68	7509395CB1	90139077CA2
7503287	10	7503287CD1	69	7503287CB1	
7503320	11	7503320CD1	70	7503320CB1	90036682CA2, 90036790CA2, 90036818CA2
7503335	12	7503335CD1	71	7503335CB1	
7503952	13	7503952CD1	72	7503952CB1	90103638CA2
7504530	14	7504530CD1	73	7504530CB1	90017261CA2, 90219736CA2, 90219792CA2, 90219860CA2, 90220851CA2, 90220883CA2
7509303	15	7509303CD1	74	7509303CB1	

Table 1

IncYTE Project ID	Polypeptide SEQ ID NO:	IncYTE Polypeptide ID	Polynucleotide SEQ ID NO:	IncYTE Polynucleotide ID	IncYTE Full Length Clones
7509910	16	7509910CD1	75	7509910CB1	7049239CA2
7509982	17	7509982CD1	76	7509982CB1	
7510082	18	7510082CD1	77	7510082CB1	
7510367	19	7510367CD1	78	7510367CB1	90023684CA2
7510413	20	7510413CD1	79	7510413CB1	
1721303	21	1721303CD1	80	1721303CB1	2905327CA2, 5765782CA2
7502007	22	7502007CD1	81	7502007CB1	90055806CA2, 90055838CA2, 90055846CA2
7506439	23	7506439CD1	82	7506439CB1	90117352CA2, 90117412CA2
7509243	24	7509243CD1	83	7509243CB1	7616162CA2
7509404	25	7509404CD1	84	7509404CB1	90138209CA2, 90224278CA2
7509439	26	7509439CD1	85	7509439CB1	8241250CA2
7510202	27	7510202CD1	86	7510202CB1	
7510203	28	7510203CD1	87	7510203CB1	
7510208	29	7510208CD1	88	7510208CB1	
7510446	30	7510446CD1	89	7510446CB1	90048796CA2, 90048896CA2
7505294	31	7505294CD1	90	7505294CB1	
7505631	32	7505631CD1	91	7505631CB1	
7506561	33	7506561CD1	92	7506561CB1	6156076CA2
7510733	34	7510733CD1	93	7510733CB1	
7510734	35	7510734CD1	94	7510734CB1	90057371CA2, 95157512CA2, 95157544CA2, 95157552CA2

Table 1

Incyte Project ID	Polypeptide SEQ ID NO:	Incyte Polypeptide ID	Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Incyte Full Length Clones
7503977	36	7503977CD1	95	7503977CB1	
7505084	37	7505084CD1	96	7505084CB1	
7506950	38	7506950CD1	97	7506950CB1	
7506951	39	7506951CD1	98	7506951CB1	90119019CA2
7506954	40	7506954CD1	99	7506954CB1	90119183CA2
7506956	41	7506956CD1	100	7506956CB1	90119035CA2, 90119259CA2
7506959	42	7506959CD1	101	7506959CB1	
7506960	43	7506960CD1	102	7506960CB1	90118991CA2, 90119051CA2, 90119110CA2, 90119118CA2, 90119127CA2, 90119174CA2, 90119218CA2, 90119251CA2, 90119258CA2, 90119266CA2, 90120004CA2
7510540	44	7510540CD1	103	7510540CB1	90059701CA2, 90059717CA2
7510545	45	7510545CD1	104	7510545CB1	90049442CA2
7510654	46	7510654CD1	105	7510654CB1	
7510660	47	7510660CD1	106	7510660CB1	
7510661	48	7510661CD1	107	7510661CB1	
7510680	49	7510680CD1	108	7510680CB1	90112131CA2
7505145	50	7505145CD1	109	7505145CB1	
7505162	51	7505162CD1	110	7505162CB1	95223082CA2
7505469	52	7505469CD1	111	7505469CB1	

Table 1

Incyte Project ID	Polypeptide SEQ ID NO:	Incyte Polypeptide ID	Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Incyte Full Length Clones
7505475	53	7505475CD1	112	7505475CB1	
7505568	54	7505568CD1	113	7505568CB1	90002693CA2, 90011331CA2, 90011519CA2
7506953	55	7506953CD1	114	7506953CB1	90119067CA2
7510176	56	7510176CD1	115	7510176CB1	4730495CA2
7510541	57	7510541CD1	116	7510541CB1	
7510923	58	7510923CD1	117	7510923CB1	
7510984	59	7510984CD1	118	7510984CB1	

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
1	7509332CD1	g182418	8.1E-77	[Homo sapiens] folate-binding protein precursor Elwood, P. C. Molecular cloning and characterization of the human folate-binding protein cDNA from placenta and malignant tissue culture (KB) cells J. Biol. Chem. 264, 14893-14901 (1989)
		606110[FOLR1	6.8E-78	[Homo sapiens] [Receptor (signalling); Small molecule-binding protein] [Unspecified membrane; Plasma membrane] Folate receptor 1 (folate receptor alpha), binds and transports folate and may play a role in neural tube morphogenesis; mutations in the corresponding gene may contribute to neural tube defects
				Campbell, I. G. et al. Folate-binding protein is a marker for ovarian cancer. Cancer Res 51, 5329-38 (1991).
		582905[Folr2	6.1E-77	[Mus musculus] [Small molecule-binding protein] Folate-binding protein, high affinity, low capacity Piedrahita, J. A. et al. Mice lacking the folic acid-binding protein Folbp1 are defective in early embryonic development. Nat Genet 23, 228-32 (1999).
2	7509102CD1	g1458110	9.7E-69	[Homo sapiens] nicotinic acetylcholine receptor alpha2 subunit precursor Elliott, K. J. et al. Comparative structure of human neuronal alpha 2-alpha 7 and beta 2-beta 4 nicotinic acetylcholine receptor subunits and functional expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and beta 4 subunits J. Mol. Neurosci. 7, 217-228 (1996)

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
		334652 CHRNA2	8.2E-70	[Homo sapiens] [Channel (passive transporter); Receptor (signalling); Transporter] [Plasma membrane] Cholinergic receptor nicotinic alpha polypeptide 2, a nicotinic acetylcholine-activated cation-selective channel that may play a role in signal transduction and synaptic transmission
				Sato, K. Z. et al.
				Diversity of mRNA expression for muscarinic acetylcholine receptor subtypes and neuronal nicotinic acetylcholine receptor subunits in human mononuclear leukocytes and leukemic cell lines.
				Neurosci Lett 266, 17-20 (1999).
		329298 Rn.9713	9.7E-41	[Rattus norvegicus] [Channel (passive transporter); Transporter; Receptor (signalling)] [Plasma membrane] Cholinergic receptor nicotinic alpha polypeptide 2, a nicotinic acetylcholine-activated cation-selective channel that may play a role in signal transduction and synaptic transmission
				Francis, M. M. et al.
				Subtype-selective inhibition of neuronal nicotinic acetylcholine receptors by cocaine is determined by the alpha4 and beta4 subunits
				Mol Pharmacol 58, 109-19 (2000).
3	7509132CD1	g183296	9.3E-167	[Homo sapiens] glucose transporter
				Buse, J. B. et al.
				Expression and regulation of the human GLUT4/muscle-fat facilitative glucose transporter gene in transgenic mice
				J. Biol. Chem. 267, 11673-11676 (1992)

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
		338070 SLC2A4	7.8E-168	[Homo sapiens] [Active transporter, secondary; Major Facilitator Superfamily; Transporter] [Unspecified membrane; Plasma membrane] Glucose transporter 4, a glucose transporter that translocates to the plasma membrane in response to insulin and plays a role in carbohydrate metabolism; targeted disruption of the gene for mouse Slc2a4 results in insulin resistance and diabetes
				Oshel, K. M. et al.
				Identification of a 30-base pair regulatory element and novel DNA binding protein that regulates the human GLUT4 promoter in transgenic mice.
		430572 Slc2a4	1.6E-160	J Biol Chem 275, 23666-73 (2000). [Rattus norvegicus] [Active transporter, secondary; Major Facilitator Superfamily; Transporter] [Endosome/Endosomal vesicles; Nuclear; Endoplasmic reticulum; Cytoplasmic; Unspecified membrane; Plasma membrane] Glucose transporter 4, a glucose transporter that translocates to the plasma membrane in response to insulin and plays a role in carbohydrate metabolism; targeted disruption of the gene for mouse Slc2a4 results in insulin resistance and diabetes
				Kanzaki, M. et al.
				The trimeric GTP-binding protein (G(q)/G(11)) alpha subunit is required for insulin-stimulated GLUT4 translocation in 3T3L1 adipocytes.
				J Biol Chem 275, 7167-75 (2000).
4	7509136CD1	g15030222	1.2E-109	[Homo sapiens] Similar to cholinergic receptor, nicotinic, beta polypeptide 1 (muscle)

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
		339230 CHRNA1	5.6E-110	[Homo sapiens] [Channel (passive transporter); Transporter; Receptor (signalling)] [Plasma membrane] Cholinergic receptor (nicotinic) beta 1 subunit, may play an important role in neuromuscular synaptic transmission; mutations in the corresponding gene are associated with slow-channel congenital myasthenic syndromes
				Quiram, P. A. et al.
				Mutation causing congenital myasthenia reveals acetylcholine receptor beta/delta subunit interaction essential for assembly.
				J Clin Invest 104, 1403-10. (1999).
		568818 CHRNA1	1.3E-74	[Homo sapiens] [Channel (passive transporter); Transporter; Receptor (signalling)] [Plasma membrane] Gamma subunit of the muscle nicotinic acetylcholine receptor, a fetal-type subunit that is replaced after birth by the epsilon subunit (CHRNA1), contains antigenic epitopes that may contribute to the development of myasthenia gravis
				Vernet-der Garabedian, B. et al.
				Association of neonatal myasthenia gravis with antibodies against the fetal acetylcholine receptor.
				J Clin Invest 94, 555-9 (1994).
5	7509178CD1	g669153	1.9E-159	[Homo sapiens] acetylcholine receptor
				Noda, M. et al.
				Cloning and sequence analysis of calf cDNA and human genomic DNA encoding alpha-subunit precursor of muscle acetylcholine receptor
				Nature 305, 818-823 (1983)

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
		339228 CHRNA1	1.6E-160	[Homo sapiens] [Channel (passive transporter); Transporter; Receptor (signalling)] [Plasma membrane] Alpha subunit of the muscle nicotinic acetylcholine receptor, contains the major binding site for acetylcholine and the immunogenic site associated with autoantibodies in myasthenia gravis; mutations are associated with slow-channel myasthenic syndrome
				Sine, S. M. et al.
				Mutation of the acetylcholine receptor alpha subunit causes a slow-channel myasthenic syndrome by enhancing agonist binding affinity.
				Neuron 15, 229-39 (1995).
		580847 Chrna1	3.7E-154	[Mus musculus] [Channel (passive transporter); Transporter; Receptor (signalling)] [Plasma membrane] Alpha subunit of the muscle nicotinic acetylcholine receptor, contains major binding site for acetylcholine and epitope for autoantibodies in experimental myasthenia gravis; mutations in human CHRNA1 are associated with slow-channel myasthenic syndrome
				Merlie, J. P. et al.
				Myogenin and acetylcholine receptor alpha gene promoters mediate transcriptional regulation in response to motor innervation.
				J Biol Chem 269, 2461-7 (1994).
6	7509214CD1	g488420	2.2E-55	[Homo sapiens] peripheral benzodiazepine receptor related protein
				Lin, D. et al.
				The human peripheral benzodiazepine receptor gene: cloning and characterization of alternative splicing in normal tissues and in a patient with congenital lipoid adrenal hyperplasia
				Genomics 18, 643-650 (1993)

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
		568290 BZRP	1.8E-56	[Homo sapiens] [Channel (passive transporter); Receptor (protein translocation); Transporter; Receptor (signalling)] [Cytoplasmic; Mitochondrial outer membrane; Mitochondrial] Benzodiazepine receptor (peripheral), involved in steroid biosynthesis, cell proliferation, and may contribute to mitochondrial biogenesis and inhibit oxygen radical induced apoptosis; expression, nuclear location may correlate to breast tumor progression
				Hardwick, M. et al.
				Peripheral-type benzodiazepine receptor (PBR) in human breast cancer: correlation of breast cancer cell aggressive phenotype with PBR expression, nuclear localization, and PBR-mediated cell proliferation and nuclear transport of cholesterol.
7	7509244CD1	g560155	1.9E-199	Cancer Res 59, 831-42 (1999).
				[Homo sapiens] acetylcholine receptor beta-subunit preprotein
				Beeson, D. et al.
				Nucleotide sequence of human muscle acetylcholine receptor beta-subunit
				Nucleic Acids Res. 17, 4391 (1989)
		339230 CHRN1	1.6E-200	[Homo sapiens] [Channel (passive transporter); Transporter; Receptor (signalling)] [Plasma membrane] Cholinergic receptor (nicotinic) beta 1 subunit, may play an important role in neuromuscular synaptic transmission; mutations in the corresponding gene are associated with slow-channel congenital myasthenic syndromes
				Quiram, P. A. et al. (supra)

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
		430536 Chrb1	1E-185	[Rattus norvegicus] [Channel (passive transporter); Receptor (signalling); Transporter] [Plasma membrane] Cholinergic receptor (nicotinic) beta 1 subunit, expression is differentially regulated during myogenesis; mutations of the corresponding human CHRNA1 gene are associated with slow-channel congenital myasthenic syndromes
				Witzemann, V. et al.
				Primary structure and functional expression of the alpha-, beta-, gamma-, delta- and epsilon-subunits of the acetylcholine receptor from rat muscle.
				Eur J Biochem 194, 437-48 (1990).
8	7509256CD1	g992687	7.7E-163	[Homo sapiens] glycine receptor beta subunit
				Handford, C. A. et al.
				The human glycine receptor beta subunit: primary structure, functional characterisation and chromosomal localisation of the human and murine genes
				Brain Res. Mol. Brain Res. 35, 211-219 (1996)
		335538 GLRB	6.5E-164	[Homo sapiens] [Channel (passive transporter); Transporter; Receptor (signalling)] [Plasma membrane] Glycine receptor beta, a subunit of the chloride channel important for inhibitory neurotransmission
				Milani, N. et al.
				The human glycine receptor beta subunit gene (GLRB): structure, refined chromosomal localization, and population polymorphism.
				Genomics 50, 341-5 (1998).
		760128 Glr1	1.7E-156	[Mus musculus] [Channel (passive transporter); Receptor (signalling); Transporter] [Plasma membrane] Glycine receptor beta, a subunit of the chloride channel important for inhibitory neurotransmission; implicated in congenital myoclonus
				Tintrup, H. et al.

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
				Exonic Sp1 sites are required for neural-specific expression of the glycine receptor beta subunit gene.
				Biochem J 355, 179-87. (2001).
9	7509395CD1	g669153	6.6E-195	[Homo sapiens] acetylcholine receptor
				Noda, M. et al. (supra)
		339228[CHRNA1	5.5E-196	[Homo sapiens] [Channel (passive transporter); Transporter; Receptor (signalling)] [Plasma membrane] Alpha subunit of the muscle nicotinic acetylcholine receptor, contains the major binding site for acetylcholine and the immunogenic site associated with autoantibodies in myasthenia gravis; mutations are associated with slow-channel myasthenic syndrome
				Sine, S. M. et al. (supra)
		580847[Chrna1	1.2E-182	[Mus musculus] [Channel (passive transporter); Transporter; Receptor (signalling)] [Plasma membrane] Alpha subunit of the muscle nicotinic acetylcholine receptor, contains major binding site for acetylcholine and epitope for autoantibodies in experimental myasthenia gravis; mutations in human CHRNA1 are associated with slow-channel myasthenic syndrome
				Boulter, J. et al.
				Isolation of a clone coding for the alpha-subunit of a mouse acetylcholine receptor.
				J Neurosci 5, 2545-52 (1985)
10	7503287CD1	g1871170	7.8E-133	[Homo sapiens] sodium channel 2
				Garcia-Anoveros, J. et al.
				BNAC1 and BNAC2 constitute a new family of human neuronal sodium channels related to degenerins and epithelial sodium channels
				Proc. Natl. Acad. Sci. U.S.A. 94, 1459-1464 (1997)

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
		610724 ACCN2	6.3E-134	[Homo sapiens] [Channel (passive transporter); Transporter] [Plasma membrane] Amiloride-sensitive cation channel 2 (acid-sensing ion channel), a member of the DEG/ENaC superfamily of sodium channels
				Sayegh, R. et al.
				Glucocorticoid induction of epithelial sodium channel expression in lung and renal epithelia occurs via trans-activation of a hormone response element in the 5'-flanking region of the human epithelial sodium channel alpha subunit gene.
				J Biol Chem 274, 12431-7 (1999).
		685845 Acct2	3.1E-132	[Rattus norvegicus] [Channel (passive transporter); Transporter] [Plasma membrane] Proton-gated cation channel (acid-sensing ion channel 1), amiloride-sensitive sodium channel that is a member of the DEG/ENaC superfamily, putatively mediates sensory perception and may define sensitivity to tarantula toxin
				Voilley, N. et al.
				Nonsteroid anti-inflammatory drugs inhibit both the activity and the inflammation-induced expression of acid-sensing ion channels in nociceptors.
				J Neurosci 21, 8026-33. (2001).
11	7503320CD1	g2808624	1.7E-34	[Homo sapiens] nicotinic acetylcholine receptor alpha7 subunit precursor
				Groot Kormelink, P. J. et al.
				Cloning and sequence of full-length cDNAs encoding the human neuronal nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and expression of seven nAChR subunits in the human neuroblastoma cell line SH-SY5Y and/or IMR-32
				FEBS Lett. 400, 309-314 (1997)

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
		334660 CHRNA7	1.4E-35	[Homo sapiens] [Channel (passive transporter); Transporter; Receptor (signalling)] [Plasma membrane] Alpha 7 subunit of the neuronal nicotinic acetylcholine receptor, binds alpha bungarotoxin, highly permeable to calcium, may be involved in Alzheimer's disease and schizophrenia
				Leonard, S. et al.
				Smoking and schizophrenia: abnormal nicotinic receptor expression.
				Eur J Pharmacol 393, 237-42 (2000).
		589947 Chrna7	1.3E-31	[Rattus norvegicus] [Channel (passive transporter); Transporter; Receptor (signalling)] [Plasma membrane] Alpha 7 subunit of the neuronal nicotinic acetylcholine receptor, binds alpha bungarotoxin; human CHRNA7 may be involved in Alzheimer's disease and schizophrenia
				Dominguez del Toro, E. et al.
				Expression of alpha 7 neuronal nicotinic receptors during postnatal development of the rat cerebellum.
				Brain Res Dev Brain Res 98, 125-33 (1997).
12	7503335CD1	g1854512	0.0	[Homo sapiens] ATP receptor
				Rassendren, F. et al.
				The permeabilizing ATP receptor (P2X7): Cloning and expression of human cDNA
				J Biol Chem 272, 5482-6 (1997).
		336736 P2RX7	0.0	[Homo sapiens] [Channel (passive transporter); Receptor (signalling); Transporter] [Plasma membrane] Purinergic receptor P2X (channel-7), ATP-gated cation channel capable of forming macropores permeable to large molecules, mediates macrophage lysis, IL-1beta (IL1B) release and cell fusion
				Humphreys, B. D. et al.

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID -	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
				Stress-activated protein kinase/JNK activation and apoptotic induction by the macrophage P2X7 nucleotide receptor.
				J Biol Chem 275, 26792-8 (2000).
		609795 P2rx7	2.1E-251	[Rattus norvegicus] [Channel (passive transporter); Receptor (signalling); Transporter] [Plasma membrane] Purnergic receptor P2X (channel-7), ATP-gated cation channel capable of forming macropores permeable to large molecules, mediates macrophage lysis and may play a role in fast synaptic transmission
				Boue-Grabot, E. et al.
				A protein kinase C site highly conserved in P2X subunits controls the desensitization kinetics of P2X(2) ATP-gated channels.
				J Biol Chem 275, 10190-5 (2000).
13	7503952CD1	g4218949	2.1E-123	[Homo sapiens] 5-hydroxytryptamine 3 receptor B subunit precursor
				Davies, P. A. et al.
				The 5-HT3B subunit is a major determinant of serotonin-receptor function
				Nature 397, 359-363 (1999)
13	7503952CD1	343014 HTR3B	1.7E-124	[Homo sapiens] [Channel (passive transporter); Receptor (signalling); Transporter] [Plasma membrane] 5-hydroxytryptamine 3B (serotonin) receptor subunit, ligand-gated cation channel subunit that is coexpressed in brain with 5-HT 3A receptor subunit (HTR3A), forms heteromers with HTR3A that exhibit serotonin-induced single-channel conductance
				Dang, H. et al.
				Probing the role of a conserved M1 proline residue in 5-hydroxytryptamine(3) receptor gating.
				Mol Pharmacol 57, 1114-22 (2000).

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
13	7503952CD1	611280 Htr3b	1.1E-97	[Mus musculus] [Channel (passive transporter); Receptor (signalling); Transporter] [Plasma membrane] 5-hydroxytryptamine 3B (serotonin) receptor subunit, putative ligand-gated cation channel subunit that is coexpressed with the 5-HT 3A receptor subunit (Htr3a) in several cell lines; predicted to form serotonin-responsive heteromers with Htr3a in neurons
				Hanna, M. C. et al.
				Evidence for expression of heteromeric serotonin 5-HT(3) receptors in rodents
14	7504530CD1	g2317274	3.4E-132	J Neurochem 75, 240-7 (2000).
				[Homo sapiens] aquaporin adipose
				Kuriyama, H. et al.
				Molecular cloning and expression of a novel human aquaporin from adipose tissue with glycerol permeability
				Biochem. Biophys. Res. Commun. 241, 53-58 (1997)
		339834 AQP7	2.7E-133	[Homo sapiens] [Channel (passive transporter); Transporter] [Plasma membrane] Aquaporin 7, a member of the aquaporin family of water channels, facilitates transport of water and glycerol, may regulate energy balance by facilitating adipocyte glycerol release, plays a likely role in cell volume control and pinocytosis
				Kishida, K. et al.
				Aquaporin adipose, a putative glycerol channel in adipocytes.
				J Biol Chem 275, 20896-902 (2000).
		583605 Aqp7	2.2E-101	[Mus musculus] [Channel (passive transporter); Transporter] [Cytoplasmic; Plasma membrane] Aquaporin 7, a member of the aquaporin family of water channels, facilitates transport of water and glycerol, may regulate glucose homeostasis by facilitating adipocyte glycerol release, may play a role in renal water resorption

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
				Nejsum, L. N. et al.
				Localization of aquaporin-7 in rat and mouse kidney using RT-PCR, immunoblotting, and immunocytochemistry
				Biochem Biophys Res Commun 277, 164-70 (2000).
15	7509303CD1	g4731109	1.1E-124	[Homo sapiens] epithelial sodium channel alpha-subunit
				Chow, Y. H. et al.
				Hormonal regulation and genomic organization of the human amiloride-sensitive epithelial sodium channel alpha-subunit gene
				Pediatr. Res. 46, 208-214 (1999)
		337892 SCNN1A	9.2E-126	[Homo sapiens] [Channel (passive transporter); Transporter] [Plasma membrane; Unspecified membrane] Sodium channel (nonvoltage-gated) channel 1 alpha subunit, a component of an amiloride-sensitive channel, may function in fluid and ion homeostasis; mutations in the corresponding gene are linked to pseudohypoaldosteronism type 1 and salt malabsorption
				Harvey, K. F. et al.
				The Nedd4-like Protein KIAA0439 Is a Potential Regulator of the Epithelial Sodium Channel.
				J Biol Chem 276, 8597-8601. (2001).
		711406 Scnn1a	5. E-102	[Rattus norvegicus] [Channel (passive transporter); Transporter] [Plasma membrane; Unspecified membrane] Sodium channel (nonvoltage-gated) 1 alpha subunit, a component of an amiloride-sensitive channel, functions in electrolyte homeostasis; mutations in human SCNN1A are linked to pseudohypoaldosteronism type 1 characterized by salt malabsorption
				Li, X. J. et al.
				Alternatively spliced forms of the alpha subunit of the epithelial sodium channel: distinct sites for amiloride binding and channel pore.
				Mol Pharmacol 47, 1133-40 (1995).

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
16	7509910CD1	g2597927	4.4E-194	[Homo sapiens] P2X7 receptor Buell, G. N. et al. Gene structure and chromosomal localization of the human P2X7 receptor Receptors Channels 5, 347-54 (1998).
		336736[P2RX7]	1.2E-194	[Homo sapiens] [Channel (passive transporter); Receptor (signalling); Transporter] [Plasma membrane] Purinergic receptor P2X (channel-7), ATP-gated cation channel capable of forming macropores permeable to large molecules, mediates macrophage lysis, IL-1beta (IL1B) release and cell fusion Rassendren, F. et al. (supra) The permeabilizing ATP receptor, P2X7. Cloning and expression of a human cDNA. J Biol Chem 272, 5482-6 (1997).
		609795[P2rx7]	7.5E-163	[Rattus norvegicus] [Channel (passive transporter); Receptor (signalling); Transporter] [Plasma membrane] Purinergic receptor P2X (channel-7), ATP-gated cation channel capable of forming macropores permeable to large molecules, mediates macrophage lysis and may play a role in fast synaptic transmission Boue-Grabot, E. et al. (supra)
17	7509982CD1	g17223622	0.0	[Homo sapiens] ATP-binding cassette A6
		568162[ABCA8]	0.0	[Homo sapiens] [ATP-binding cassette; Active transporter, primary; Hydrolase; Transporter; ATPase] [Unspecified membrane; Plasma membrane] ATP-binding cassette subfamily A member 8, a putative transporter Kaminski, W. E. et al. ABCA6, a novel a subclass ABC transporter. Biochem Biophys Res Commun 285, 1295-301. (2001).

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
		333996 ABCA3	6.1E-126	[Homo sapiens] [ATP-binding cassette; Active transporter, primary; Hydrolase; Transporter; ATPase] [Unspecified membrane] ATP-binding cassette subfamily A member 3 (ATP-binding cassette transporter C), a putative transporter that is a member of the ATP-binding cassette superfamily and may have a role in development of resistance to xenobiotics
				Klucken, J. et al.
				ABCG1 (ABC8), the human homolog of the Drosophila white gene, is a regulator of macrophage cholesterol and phospholipid transport.
				Proc Natl Acad Sci U S A 97, 817-22 (2000).
18	7510082CD1	g7415511	0.0	[Homo sapiens] peptide transporter 3
		662681 Ci1	1.8E-248	[Mus musculus] Protein induced by 8-bromo-cyclicAMP in RAW264 macrophages
				Takahashi, Y. et al.
				Identification of cAMP analogue inducible genes in RAW264 macrophages.
				Biochim Biophys Acta 1492, 385-94 (2000).
		331098 Rn.10770	3.3E-144	[Rattus norvegicus] [Active transporter, secondary; Transporter] [Unspecified membrane] Peptide-histidine transporter 1, a proton-dependent high-affinity histidine transporter that also transports peptides, may also be involved in the uptake of nutritional peptides, neuromodulators, and degraded neuropeptides
				Yamashita, T. et al.
				Cloning and functional expression of a brain peptide/histidine transporter.
				J Biol Chem 272, 10205-11 (1997).
19	7510367CD1	g11545417	1.1E-21	[Homo sapiens] folate transporter/carrier
				Titus, S. A. et al.

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
				Retrovirally mediated complementation of the glyB phenotype. Cloning of a human gene encoding the carrier for entry of folates into mitochondria
				J. Biol. Chem. 275, 36811-36817 (2000)
		700836 LOC81034	9.2E-23	[Homo sapiens] Mitochondrial folate transporter
20	7510413CD1	g473236	2.4E-106	[Homo sapiens] folate receptor FRGAMMA
				Shen, F. et al.
				Identification of a novel folate receptor, a truncated receptor, and receptor type beta in hematopoietic cells: cDNA cloning, expression, immunoreactivity, and tissue specificity
				Biochemistry 33, 1209-1215 (1994)
		335364 FOLR3	2.0E-107	[Homo sapiens] [Receptor (signalling); Small molecule-binding protein] [Unspecified membrane] Folate receptor 3 (gamma), one of a family of folate receptors that includes FOLR1 and FOLR2, binds folic acid, primarily a secreted protein due to lack of an efficient signal for glycosylphosphatidylinositol anchor modification
				Shen, F. et al.
				Structure and regulation of a polymorphic gene encoding folate receptor type gamma/gamma'
				Nucleic Acids Res 26, 2132-42 (1998).
		335362 FOLR2	5.9E-83	[Homo sapiens] [Small molecule-binding protein] [Unspecified membrane] Placental folate-binding protein (folate receptor beta)
				Ross, J. F. et al.
				Folate receptor type beta is a neutrophilic lineage marker and is differentially expressed in myeloid leukemia.
				Cancer 85, 348-57. (1999).
21	1721303CD1	g3335128	1.7E-20	[Homo sapiens] F1Fo-ATPase synthase f subunit
				Mao, M. et al.

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
				Identification of genes expressed in human CD34(+) hematopoietic stem/progenitor cells by expressed sequence tags and efficient full-length cDNA cloning
				Proc. Natl. Acad. Sci. U.S.A. 95, 8175-8180 (1998)
22	7502007CD1	g2317274	1.4E-128	[Homo sapiens] aquaporin adipose
				Kuriyama, H. et al. (supra)
23	7506439CD1	g681914	3.1E-74	[Homo sapiens] serotonin 5-HT3 receptor
				Miyake, A. et al.
				Molecular cloning of human 5-hydroxytryptamine3 receptor: heterogeneity in distribution and function among species
				Mol. Pharmacol. 48, 407-416 (1995)
		335904 HTR3A	2.5E-75	[Homo sapiens] [Channel (passive transporter); Receptor (signalling); Transporter] [Plasma membrane] 5-hydroxytryptamine receptor 3A, a serotonin receptor that is a ligand-gated ion channel, mediates a variety of physiological effects in the central and peripheral nervous system
				Bedford, F. K. et al.
				Neuronal expression of the 5HT3 serotonin receptor gene requires nuclear factor 1 complexes.
				J Neurosci 18, 6186-94 (1998).
		587085 Htr3a	1.9E-61	[Mus musculus] [Channel (passive transporter); Transporter; Receptor (signalling)] [Golgi; Endoplasmic reticulum; Cytoplasmic; Plasma membrane] 5-hydroxytryptamine receptor 3A, a serotonin receptor that is a ligand-gated ion channel, mediates a variety of physiological effects in the central and peripheral nervous system
				Miquel, M. C. et al.
				Developmental changes in the differential expression of two serotonin 5-HT3 receptor splice variants in the rat.
				J Neurochem 65, 475-83 (1995).

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
24	7509243CD1	g13926108	4.6E-57	[Homo sapiens] 2P domain potassium channel Talk-1
				Girard, C. et al.
				Genomic and functional characteristics of novel human pancreatic 2P domain K ⁺ channels
				Biochem Biophys Res Commun 282, 249-56. (2001).
		716701 KCNK16	3.7E-58	[Homo sapiens] Potassium channel subfamily K member 16 (Twik-related alkaline pH activated K ⁺ channel 1), a subunit of a pancreatic 2P domain background potassium channel that is open at all membrane potentials and is activated at alkaline pH
		743114 KCNK2	9.3E-18	[Homo sapiens] [Channel (passive transporter); Transporter] [Plasma membrane] Potassium channel subfamily K member 2, outwardly rectifying K ⁺ channel, activated by volatile anesthetics, inhibited by activated protein kinases A and C
				Medhurst, A. D. et al.
				Distribution analysis of human two pore domain potassium channels in tissues of the central nervous system and periphery.
				Brain Res Mol Brain Res 86, 101-114. (2001).
25	7509404CD1	g992687	4.2E-16	[Homo sapiens] glycine receptor beta subunit
				Handford, C. A. et al. (supra)
		335538 GLRB	3.4E-17	[Homo sapiens] [Channel (passive transporter); Transporter; Receptor (signalling)] [Plasma membrane] Glycine receptor beta, a subunit of the chloride channel important for inhibitory neurotransmission
				Handford, C. A. et al. (supra)
				Milani, N. et al. (supra)
26	7509439CD1	g12654223	3.8E-69	[Homo sapiens] ATP synthase, H ⁺ transporting, mitochondrial F1 complex, gamma polypeptide 1
27	7510202CD1	g17223624	0.0	[Homo sapiens] ATP-binding cassette A9

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
		568162 ABCA8	0.0	[Homo sapiens] [ATP-binding cassette; Active transporter, primary; Hydrolase; Transporter; ATPase] [Unspecified membrane; Plasma membrane] ATP-binding cassette subfamily A member 8, a putative transporter
				Kaminski, W. E. et al. (supra)
		333996 ABCA3	5.1E-95	[Homo sapiens] [ATP-binding cassette; Active transporter, primary; Hydrolase; Transporter; ATPase] [Unspecified membrane] ATP-binding cassette subfamily A member 3 (ATP-binding cassette transporter C), a putative transporter that is a member of the ATP-binding cassette superfamily and may have a role in development of resistance to xenobiotics
				Klucken, J. et al. (supra)
28	7510203CD1	g15130910	8E-42	[Canis familiaris] multidrug resistance protein 2
				Conrad, S. et al.
				Sequencing and tissue distribution of the canine MRP2 gene compared with MRP1 and MDR1
				Toxicology. 156, 81-91 (2001)
		626794 LOC64052	4.9E-43	[Rattus norvegicus] [ATP-binding cassette; Active transporter, primary; Hydrolase; Transporter; ATPase] [Plasma membrane] Multidrug resistance protein, an ATP-binding cassette transporter that acts as a multidrug efflux pump
				Saito, T. et al.
				Expression of multidrug resistance protein 1 (MRP1) in the rat cochlea with special reference to the blood-inner ear barrier.
				Brain Res 895, 253-7. (2001).

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
		1103 YCF1	6.9E-42	[Saccharomyces cerevisiae] [ATP-binding cassette; Active transporter, primary; Hydrolase; Transporter; ATPase] [Lysosome/vacuole; Unspecified membrane] Vacuolar glutathione S-conjugate transporter, member of the ATP-binding cassette (ABC) superfamily
				Balzi, E. et al.
				Yeast multidrug resistance: the PDR network.
				J Bioenerg Biomembr 27, 71-6 (1995).
29	7510208CD1	g9957467	0.0	[Homo sapiens] ATP-binding cassette sub-family A member 2
				Vulevic, B. et al.
				Cloning and characterization of human adenosine 5'-triphosphate-binding cassette, sub-family A, transporter 2 (ABCA2)
				Cancer Res. 61, 3339-3347 (2001)
30	7510446CD1	g398161	2.2E-53	[Homo sapiens] human ClC-1 muscle chloride channel
				Steinmeyer, K. et al.
				Multimeric structure of ClC-1 chloride channel revealed by mutations in dominant myotonia congenita (Thomsen)
				EMBO J. 13, 737-743 (1994)
		334688 CLCN1	1.8E-54	[Homo sapiens] [Channel (passive transporter); Transporter] [Plasma membrane] Chloride channel 1 (skeletal muscle), transports chloride which affects muscle contraction; mutations in human CLCN1 and mouse Clcn1 genes are associated with Becker disease and Thomsen disease, both characterized by muscle membrane hyperexcitability
				Zhang, J. et al.
				Mechanism of inverted activation of ClC-1 channels caused by a novel myotonia congenita mutation.
				J Biol Chem 275, 2999-3005. (2000).

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
		589953 Clcn1	4.7E-45	[Rattus norvegicus] [Channel (passive transporter); Transporter] [Plasma membrane] Chloride channel 1 (skeletal muscle), transports chloride which affects muscle contraction; mutations in human CLCN1 and mouse Clcn1 genes are associated with Becker disease and Thomsen disease, both characterized by muscle membrane hyperexcitability
				Enz, R. et al.
				Expression of the voltage-gated chloride channel ClC-2 in rod bipolar cells of the rat retina.
				J Neurosci 19, 9841-7 (1999).
31	7505294CD1	g7576452	2.0E-148	[Homo sapiens] potent brain type organic ion transporter
		476069 LOC51310	1.7E-149	[Homo sapiens][Transporter][Plasma membrane; Unspecified membrane]
				Member of the sugar transporter family, has low similarity to rat 1-Oct, which is an organic cation transporter with broad specificity, and which is likely involved in drug elimination in kidney and liver
		430266 Slc22a3	1.6E-22	[Mus musculus][Active transporter, secondary, Major Facilitator Superfamily; Transporter][Unspecified membrane, Plasma membrane] Solute carrier family 22 member 3 (extraneuronal monoamine transporter), regulates monoamine transport in the heart and placenta
				Kekuda, R. et al.
				Cloning and functional characterization of a potential-sensitive, polyspecific organic cation transporter (OCT3) most abundantly expressed in placenta.
				J Biol Chem 273, 15971-9 (1998).
				Impaired activity of the extraneuronal monoamine transporter system known as uptake-2 in Orct3/Slc22a3-deficient mice.
				Mol Cell Biol 21, 4188-96. (2001).
32	7505631CD1	598972 FLJ11274	6.7E-132	[Homo sapiens] Protein with weak similarity to S. cerevisiae Atx2p, which is a manganese-trafficking protein

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
33	7506561CD1	g473236	1.1E-46	[Homo sapiens] folate receptor FRGAMMA Shen, F. et al. Identification of a novel folate receptor: a truncated receptor, and receptor type beta in hematopoietic cells: cDNA cloning, expression, immunoreactivity, and tissue specificity Biochemistry 33, 1209-1215 (1994)
		335364[FOLR3	9.3E-48	[Homo sapiens][Receptor (signaling); Small molecule-binding protein][Unspecified membrane] Folate receptor 3 (gamma), one of a family of folate receptors that includes FOLR1 and FOLR2, binds folic acid, primarily a secreted protein (unlike FOLR1 and FOLR2) and may be a potential drug target in CML and AML leukemias Shen, F. et al. (supra) Wang, H. et al. Structure and regulation of a polymorphic gene encoding folate receptor type gamma/gamma'.
		335362[FOLR2	1.6E-34	Nucleic Acids Res 26, 2132-42 (1998). [Homo sapiens][Small molecule-binding protein][Unspecified membrane] Placental folate-binding protein (folate receptor beta) Ross, J. F. et al. Folate receptor type beta is a neutrophilic lineage marker and is differentially expressed in myeloid leukemia. Cancer 85, 348-57. (1999).
34	7510733CD1	g2887407	2.6E-126	[Homo sapiens] aquaporin 9 Ishibashi, K. et al. Cloning and functional expression of a new aquaporin (AQP9) abundantly expressed in the peripheral leukocytes permeable to water and urea, but not to glycerol Biochem. Biophys. Res. Commun. 244, 268-274 (1998)

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
		613389 AQP9	2.2E-127	[Homo sapiens][Channel (passive transporter); Transporter][Plasma membrane] Aquaporin 9, member of the aquaporin channel family, mediates the transport of water and urea, expressed predominantly in leukocytes where it may play a role in immunological function
				Ishibashi, K. et al. (supra)
		662851 Aqp9	1.1E-95	[Rattus norvegicus][Channel (passive transporter); Transporter][Plasma membrane] Neutral solute channel aquaporin 9, member of the aquaporin channel family, functions as a neutral solute channel with broad selectivity, mediates the transport of water and many non-charged solutes including carbamides, polyols, purines, and pyrimidines
				Elkjaer, M. et al.
				Immunolocalization of AQP9 in liver, epididymis, testis, spleen, and brain
				Biochem Biophys Res Commun 276, 1118-28 (2000).
				Pastor-Soler, N. et al.
				Aquaporin 9 expression along the male reproductive tract.
				Biol Reprod 65, 384-93. (2001).
35	7510734CD1	g2887407	1.4E-83	[Homo sapiens] aquaporin 9
				Ishibashi, K. et al. (supra)
		613389 AQP9	1.2E-84	[Homo sapiens][Channel (passive transporter); Transporter][Plasma membrane] Aquaporin 9, member of the aquaporin channel family, mediates the transport of water and urea, expressed predominantly in leukocytes where it may play a role in immunological function
				Ishibashi, K. et al. (supra)
		662851 Aqp9	3.0E-65	[Rattus norvegicus][Channel (passive transporter); Transporter][Plasma membrane] Neutral solute channel aquaporin 9, member of the aquaporin channel family, functions as a neutral solute channel with broad selectivity, mediates the transport of water and many non-charged solutes including carbamides, polyols, purines, and pyrimidines

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
				Elkjaer, M. et al. (supra)
				Pastor-Soler, N. et al. (supra)
36	7503977CD1	g15617229	6.8E-109	[Homo sapiens] TRP-related cation influx channel
				Xu, X. Z. S. et al.
				Regulation of melastatin, a TRP-related protein, through interaction with a cytoplasmic isoform
				Proc. Natl. Acad. Sci. U.S.A. 98, 10692-10697 (2001)
37	7505084CD1	g17223724	2.2E-197	[Homo sapiens] sodium/glucose cotransporter KST1
				Roll, P. et al.
				New human sodium/glucose cotransporter gene (KST1): identification, characterization, and mutation analysis in ICCA (infantile convulsions and choreoathetosis) and BFIC (benign familial infantile convulsions) families
				Gene 285, 141-148 (2002)
		762539 RKST1	1.9E-198	[Homo sapiens] Protein with high similarity to sodium-glucose cotransporter 1 (human SLC5A1), which is a high affinity glucose transporter associated with glucose-galactose malabsorption syndrome, member of the sodium:solute symporter family of membrane transporters
		590623 Slc5a1	8.1E-120	[Rattus norvegicus] [Active transporter, secondary; Transporter] [Unspecified membrane; Plasma membrane] Sodium-glucose cotransporter 1, a high affinity glucose transporter that is inhibited by phlorizin; mutation in human SLC5A1 is associated with glucose-galactose malabsorption syndrome
				You, G. et al.
				Molecular characteristics of Na(+)-coupled glucose transporters in adult and embryonic rat kidney.
				J Biol Chem 270, 29365-71 (1995).
				Corpe, C. et al.

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
				Effects of type-2 diabetes and troglitazone on the expression patterns of small intestinal sugar transporters and ppar-gamma in the Zucker diabetic fatty rat.
				Digestion 63, 116-23. (2001).
38	7506950CD1	g386422	1.7E-82	[Homo sapiens] gamma-aminobutyric acidA receptor alpha 2 subunit; GABAA receptor alpha 2
				Hadingham, K. L. et al.
				Cloning of cDNA sequences encoding human alpha 2 and alpha 3 gamma-aminobutyric acidA receptor subunits and characterization of the benzodiazepine pharmacology of recombinant alpha 1-, alpha 2-, alpha 3-, and alpha 5-containing human gamma-aminobutyric acidA receptors
				Mol. Pharmacol. 43, 970-975 (1993)
		339368[GABRA2]	1.4E-83	[Homo sapiens][Channel (passive transporter); Receptor (signaling); Transporter][Plasma membrane] Alpha 2 subunit of the gamma-aminobutyric acid type A (GABA-A) receptor, a chloride channel that is the major inhibitory neurotransmitter receptor in the brain
				Hadingham, K. L. et al. (supra)
				Loup, F. et al.
				Selective alterations in GABAA receptor subtypes in human temporal lobe epilepsy
				J Neurosci 20, 5401-19 (2000).
		582959[Gabra2]	1.3E-78	[Mus musculus][Channel (passive transporter); Transporter; Receptor (signaling)][Plasma membrane] Alpha 2 subunit of the gamma-aminobutyric acid type A (GABA-A) receptor, a putative chloride channel that is the major inhibitory neurotransmitter receptor in the brain
				Sibille, E. et al.

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
				Genetic inactivation of the Serotonin(1A) receptor in mice results in downregulation of major GABA(A) receptor alpha subunits, reduction of GABA(A) receptor binding, and benzodiazepine-resistant anxiety.
				J Neurosci 20, 2758-65 (2000).
				Bouillere, V. et al.
				Early loss of interneurons and delayed subunit-specific changes in GABA(A)-receptor expression in a mouse model of mesial temporal lobe epilepsy
				Hippocampus 10, 305-24 (2000).
39	7506951CD1	g386422	3.4E-153	[Homo sapiens] gamma-aminobutyric acidA receptor alpha 2 subunit; GABAA receptor alpha 2
				Haddingham, K. L. et al. (supra)
		339368 GABRA2	2.9E-154	[Homo sapiens][Channel (passive transporter); Receptor (signaling); Transporter][Plasma membrane] Alpha 2 subunit of the gamma-aminobutyric acid type A (GABA-A) receptor, a chloride channel that is the major inhibitory neurotransmitter receptor in the brain
				Haddingham, K. L. et al. (supra)
				Loup, F. et al. (supra)
		582959 Gabra2	2.8E-149	[Mus musculus][Channel (passive transporter); Transporter; Receptor (signaling)][Plasma membrane] Alpha 2 subunit of the gamma-aminobutyric acid type A (GABA-A) receptor, a putative chloride channel that is the major inhibitory neurotransmitter receptor in the brain
				Sibille, E. et al. (supra)
				Bouillere, V. et al. (supra)
40	7506954CD1	g386422	7.9E-28	[Homo sapiens] gamma-aminobutyric acidA receptor alpha 2 subunit; GABAA receptor alpha 2
				Haddingham, K. L. et al. (supra)

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
		339368 GABRA2	6.7E-29	[Homo sapiens][Channel (passive transporter); Receptor (signaling); Transporter][Plasma membrane] Alpha 2 subunit of the gamma-aminobutyric acid type A (GABA-A) receptor, a chloride channel that is the major inhibitory neurotransmitter receptor in the brain
				Hadingham, K. L. et al. (supra)
				Loup, F. et al. (supra)
		582959 Gabra2	1.7E-23	[Mus musculus][Channel (passive transporter); Transporter; Receptor (signaling)][Plasma membrane] Alpha 2 subunit of the gamma-aminobutyric acid type A (GABA-A) receptor, a putative chloride channel that is the major inhibitory neurotransmitter receptor in the brain
				Sibille, E. et al. (supra)
				Bouilleret, V. et al. (supra)
41	7506956CD1	g386422	5.4E-215	[Homo sapiens] gamma-aminobutyric acidA receptor alpha 2 subunit; GABAA receptor alpha 2
				Hadingham, K. L. et al. (supra)
		339368 GABRA2	4.6E-216	[Homo sapiens][Channel (passive transporter); Receptor (signaling); Transporter][Plasma membrane] Alpha 2 subunit of the gamma-aminobutyric acid type A (GABA-A) receptor, a chloride channel that is the major inhibitory neurotransmitter receptor in the brain
				Hadingham, K. L. et al. (supra)
				Loup, F. et al. (supra)
		582959 Gabra2	4.3E-211	[Mus musculus][Channel (passive transporter); Transporter; Receptor (signaling)][Plasma membrane] Alpha 2 subunit of the gamma-aminobutyric acid type A (GABA-A) receptor, a putative chloride channel that is the major inhibitory neurotransmitter receptor in the brain
				Sibille, E. et al. (supra)
				Bouilleret, V. et al. (supra)
42	7506959CD1	g369	6.1E-214	[Bos taurus] GABA-A receptor alpha-2 precursor

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
				Schofield, P. R. et al.
				Structural and functional basis for GABAA receptor heterogeneity
				Nature 335, 76-79 (1988)
		339368[GABRA2]	1.7E-216	[Homo sapiens][Channel (passive transporter); Receptor (signaling); Transporter][Plasma membrane] Alpha 2 subunit of the gamma-aminobutyric acid type A (GABA-A) receptor, a chloride channel that is the major inhibitory neurotransmitter receptor in the brain
				Hadingham, K. L. et al. (supra)
				Loup, F. et al. (supra)
		582959[Gabra2]	1.6E-211	[Mus musculus][Channel (passive transporter); Transporter; Receptor (signaling)][Plasma membrane] Alpha 2 subunit of the gamma-aminobutyric acid type A (GABA-A) receptor, a putative chloride channel that is the major inhibitory neurotransmitter receptor in the brain
				Sibille, E. et al. (supra)
				Bouilleret, V. et al. (supra)
43	7506960CD1	g386422	1.3E-27	[Homo sapiens] gamma-aminobutyric acidA receptor alpha 2 subunit; GABAA receptor alpha 2
				Hadingham, K. L. et al. (supra)
		339368[GABRA2]	1.1E-28	[Homo sapiens][Channel (passive transporter); Receptor (signaling); Transporter][Plasma membrane] Alpha 2 subunit of the gamma-aminobutyric acid type A (GABA-A) receptor, a chloride channel that is the major inhibitory neurotransmitter receptor in the brain
				Hadingham, K. L. et al. (supra)
				Loup, F. et al. (supra)
		582959[Gabra2]	2.8E-23	[Mus musculus][Channel (passive transporter); Transporter; Receptor (signaling)][Plasma membrane] Alpha 2 subunit of the gamma-aminobutyric acid type A (GABA-A) receptor, a putative chloride channel that is the major inhibitory neurotransmitter receptor in the brain

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
				Sibille, E. et al. (supra)
				Bouilleret, V. et al. (supra)
44	7510540CD1	g307125	6.3E-13	[Homo sapiens] glucose transporter-like protein
				Fukumoto, H. et al.
				Sequence, tissue distribution, and chromosomal localization of mRNA encoding a human glucose transporter-like protein
				Proc. Natl. Acad. Sci. U.S.A. 85, 5434-5438 (1988)
		339590 SLC2A2	5.4E-14	[Homo sapiens][Active transporter, secondary; Major Facilitator Superfamily; Transporter][Unspecified membrane; Plasma membrane] Facilitative glucose transporter 2, a low-affinity, high-capacity glucose transporter; mutations in the gene may cause Fanconi-Bickel syndrome and may be associated with pathogenesis of non-insulin-dependent diabetes
				Santer, R. et al.
				Mutations in GLUT2, the gene for the liver-type glucose transporter, in patients with Fanconi-Bickel syndrome
				[published erratum appears in Nat Genet 1998 Mar;18(3):298]
		704295 Slc2a2	2.1E-12	[Mus musculus][Active transporter, secondary; Major Facilitator Superfamily; Transporter][Plasma membrane] Facilitative glucose transporter 2, a putative low-affinity, high-capacity glucose transporter, may act as a glucose sensor; mutations in human SLC2A2 may cause Fanconi-Bickel syndrome and may be associated with non-insulin-dependent diabetes
				Thorens, B. et al.
				Transgenic reexpression of GLUT1 or GLUT2 in pancreatic beta cells rescues GLUT2-null mice from early death and restores normal glucose-stimulated insulin secretion.
				J Biol Chem 275, 23751-8 (2000).

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
45	7510545CD1	g306850	8.9E-42	[Homo sapiens] HK1
				Lytton, J. et al.
				Molecular cloning of cDNAs from human kidney coding for two alternatively spliced products of the cardiac Ca ²⁺ -ATPase gene
				J. Biol. Chem. 263, 15024-15031 (1988)
		334260 ATP2A2	6.4E-43	[Homo sapiens][Active transporter, primary; Hydrolase; Transporter; ATPase][Endoplasmic reticulum; Microsomal fraction; Cytoplasmic; Unspecified membrane; Plasma membrane] Sarcoplasmic reticulum Ca(2+)-ATPase 2, slow twitch muscle, cardiac and nonmuscle form, pumps calcium from cytoplasm into ER; reduced activity in the heart is implicated in dilated cardiomyopathy and gene mutations are associated with Darier Disease
				Sakuntabhai, A. et al.
				Mutations in ATP2A2, encoding a Ca ²⁺ pump, cause Darier disease
				Nat Genet 21, 271-7 (1999).
		586225 Atp2a2	1.3E-42	[Mus musculus][Active transporter, primary; Hydrolase; Transporter; ATPase][Unspecified membrane] Sarcoplasmic reticulum Ca(2+)-ATPase 2, slow twitch muscle, cardiac and nonmuscle form, pumps calcium from cytoplasm into ER; associated with dilated cardiomyopathy and gene mutations in human ATP2A2 are associated with Darier Disease
				Reed, T. D. et al.
				The expression of SR calcium transport ATPase and the Na(+)/Ca(2+)Exchanger are antithetically regulated during mouse cardiac development and in Hypo/hyperthyroidism.
				J Mol Cell Cardiol 32, 453-64 (2000).
46	7510654CD1	g7018306	8.8E-171	[Homo sapiens] glucose transporter
				Ibberson, M. et al.

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
				GLUTX1, a novel mammalian glucose transporter expressed in the central nervous system and insulin-sensitive tissues
				J. Biol. Chem. 275, 4607-4612 (2000)
		569540 SLC2A8	7.6E-172	[Homo sapiens][Active transporter, secondary; Major Facilitator Superfamily; Transporter][Plasma membrane] Solute carrier family 2 member 8 (glucose transporter X1), glucose transporter that may play a role in glucose sensing
				Ibberson, M. et al. (supra)
				Proc Natl Acad Sci U S A 97, 7313-8 (2000).
		757694 Slc2a8	1.9E-150	[Rattus norvegicus][Transporter] Solute carrier family 2 member 8 (glucose transporter X1), glucose transporter associated with streptozotocin diabetes upon upregulation of mRNA but not protein
				Reagan, L. P. et al.
				Localization and regulation of GLUTx1 glucose transporter in the hippocampus of streptozotocin diabetic rats.
				Proc Natl Acad Sci U S A 98, 2820-5. (2001).
47	7510660CD1	g12248394	0.0	[Mus musculus] cation-transporting apase
		610956 CGI-152	0.0	[Homo sapiens][Active transporter, primary; Hydrolase; Transporter; ATPase] Member of the E1-E2 ATPase family of cation transporters, has a region of weak similarity to a region of rat Atp1a2, which is the catalytic subunit of the sodium- and potassium-transporting ATPase
		239097 C10C6.6	0.0	[Caenorhabditis elegans][Active transporter, primary; Hydrolase; Transporter; ATPase][Unspecified membrane] Member of the P-type ATPase, Ca ²⁺ -type subfamily protein family
48	7510661CD1	g12248394	0.0	[Mus musculus] cation-transporting apase

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
		610956 CGI-152	5.7E-254	[Homo sapiens][Active transporter, primary; Hydrolase; Transporter; ATPase] Member of the E1-E2 ATPase family of cation transporters, has a region of weak similarity to a region of rat Atp1a2, which is the catalytic subunit of the sodium- and potassium-transporting ATPase
		239097 C10C6.6	6.7E-164	[Caenorhabditis elegans][Active transporter, primary; Hydrolase; Transporter; ATPase][Unspecified membrane] Member of the P-type ATPase, Ca ²⁺ -type subfamily protein family
49	7510680CD1	g3901268	4.4E-82	[Rattus norvegicus] SV2 related protein
				Janz, R. et al.
				SVOP, an evolutionarily conserved synaptic vesicle protein, suggests novel transport functions of synaptic vesicles
				J. Neurosci. 18, 9269-9281 (1998)
		332780 Rn.30057	3.8E-83	[Rattus norvegicus][Vesicle coat protein; Transporter][Cytoplasmic; Unspecified membrane] Synaptic vesicle protein containing twelve transmembrane domains
				Janz, R. et al. (supra)
		757012 Slc22a7	3.5E-29	[Rattus norvegicus][Active transporter, secondary; Major Facilitator Superfamily; Transporter][Plasma membrane] Organic cation transporter 2 (solute carrier family 22 member 7), a multispecific sodium-independent organic anion transporter expressed predominantly in the liver, mediates the uptake of salicylate, indomethacin, and nucleoside derivatives
				Sekine, T. et al.
				Identification of multispecific organic anion transporter 2 expressed predominantly in the liver.
				FEBS Lett 429, 179-82 (1998).
				Morita, N. et al.
				Functional characterization of rat organic anion transporter 2 in LLC-PK1 cells.

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
50	7505145CD1	g15929042	2.7E-160	J Pharmacol Exp Ther 298, 1179-84. (2001).
		343916 TETTRAN	2.3E-161	[Homo sapiens] tetracycline transporter-like protein
				[Homo sapiens][Active transporter, secondary; Major Facilitator Superfamily; Transporter][Unspecified membrane] Tetracycline transporter-like protein, member of a superfamily of transporter proteins, may be involved in tetracycline transport
				Duyao, M. P. et al.
				A gene from chromosome 4p16.3 with similarity to a superfamily of transporter proteins.
				Hum Mol Genet 2, 673-6 (1993).
51	7505162CD1	g2765461	2.9E-140	[Homo sapiens] glucose 6-phosphate translocase
				Gerin, I. et al.
				Sequence of a putative glucose 6-phosphate translocase, mutated in glycogen storage disease type Ib
				FEBS Lett. 419, 235-238 (1997)
		335420 G6PT1	2.5E-141	[Homo sapiens][Active transporter, secondary; Transporter][Endoplasmic reticulum; Cytoplasmic; Microsomal fraction; Unspecified membrane] Glucose-6-phosphate translocase, component of glucose-6-phosphatase enzyme complex, involved in glycogen metabolism, inhibited by chlorogenic acid and its synthetic derivatives; deficiency is a cause of glycogen storage disease type Ib, Ic, and Id
				Kure, S. et al.
				Molecular analysis of glycogen storage disease type Ib: identification of a prevalent mutation among Japanese patients and assignment of a putative glucose-6-phosphate translocase gene to chromosome 11.
				Biochem Biophys Res Commun 248, 426-31 (1998).
				Narisawa, K. et al.

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
				A new variant of glycogen storage disease type I probably due to a defect in the glucose-6-phosphate transport system.
				Biochem Biophys Res Commun 83, 1360-4 (1978).
				Gerin, I. et al.
				Sequence of a putative glucose 6-phosphate translocase, mutated in glycogen storage disease type Ib
				FEBS Lett 419, 235-8 (1997).
				Hou, D. C. et al.
				Glycogen storage disease type Ib: structural and mutational analysis of the microsomal glucose-6-phosphate transporter gene.
				Am J Med Genet 86, 253-7. (1999).
		711464 G6pt1	1.1E-133	[Rattus norvegicus][Active transporter, secondary; Transporter][Endoplasmic reticulum; Cytoplasmic; Unspecified membrane] Glucose-6-phosphate translocase, component of glucose-6-phosphatase enzyme complex, inhibited by chlorogenic acid and its synthetic derivatives, upregulated by insulin deficiency and hyperglycemia in streptozotocin-induced diabetes
				Lin, B. et al.
				Cloning and characterization of cDNAs encoding a candidate glycogen storage disease type Ib protein in rodents.
				J Biol Chem 273, 31656-60 (1998).
				Li, Y. et al.
				Diabetes affects similarly the catalytic subunit and putative glucose-6-phosphate translocase of glucose-6-phosphatase.
				J Biol Chem 274, 33866-8 (1999).
52	7505469CD1	g13111752	1.8E-76	[Homo sapiens] solute carrier family 7 (cationic amino acid transporter, y+ system), member 7

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
		742298 SLC7A6	6.3E-113	[Homo sapiens] Protein with high similarity to solute carrier family 7 member 7 (human SLC7A7), which is a cationic and dibasic amino acid transporter associated with lysinuric protein intolerance, member of the amino acid permease family of membrane transporters
		338114 SLC7A7	1.5E-77	[Homo sapiens][Active transporter, secondary; Transporter][Plasma membrane] Solute carrier family 7 (y+L amino acid transporter-1) member 7, a cationic and dibasic amino acid transporter that forms a heterodimer with the 4F2 heavy chain (SLC3A2); mutation in the corresponding gene causes lysinuric protein intolerance
				Mykkanen, J. et al.
				Functional analysis of novel mutations in y(+)-LAT-1 amino acid transporter gene causing lysinuric protein intolerance (LPI).
				Hum Mol Genet 9, 431-8. (2000).
53	7505475CD1	g17223622	0.0	[Homo sapiens] ATP-binding cassette A6
		762515 ABCA9	1.5E-189	[Homo sapiens] Member of the ABC transporter family, which are involved in translocation of a variety of compounds across biological membranes, has low similarity to ATP binding cassette subfamily A member 1 (human ABCA1), which is associated with Tangier disease
		568162 ABCA8	4.1E-180	[Homo sapiens][ATP-binding cassette; Active transporter, primary; Hydrolase; Transporter; ATPase][Unspecified membrane; Plasma membrane] ATP-binding cassette subfamily A member 8, a putative transporter
				Kaminski, W. E. et al.
				ABCA6, a novel subclass ABC transporter.
				Biochem Biophys Res Commun 285, 1295-301. (2001).
54	7505568CD1	g9230651	2.5E-40	[Homo sapiens] facilitative glucose transporter family member GLUT9
				Phay, J. E. et al.

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
				Cloning and expression analysis of a novel member of the facilitative glucose transporter family, SLC2A9 (GLUT9)
				Genomics 66, 217-220 (2000)
		606512 SLC2A9	2.1E-41	[Homo sapiens][Transporter][Plasma membrane; Unspecified membrane] Solute carrier family 2 (facilitated glucose transporter) member 9, member of the glucose transporter family, a putative plasma membrane protein that may be involved in the transport of carbohydrates, expressed in the kidney and liver
				Phay, J. E. et al.
				Cloning and expression analysis of a novel member of the facilitative glucose transporter family, SLC2A9 (GLUT9).
				Genomics 66, 217-20 (2000).
				Doege, H. et al.
				Activity and genomic organization of human glucose transporter 9 (GLUT9), a novel member of the family of sugar-transport facilitators predominantly expressed in brain and leucocytes.
				Biochem J 350, 771-776 (2000).
55	7506953CD1	g204204	3.2E-160	[Rattus rattus] GABA-A receptor alpha-2 subunit
				Wisden, W. et al.
				The distribution of 13 GABAA receptor subunit mRNAs in the rat brain. I.
				Telencephalon, diencephalon, mesencephalon
				J. Neurosci. 12, 1040-1062 (1992)
				Laurie, D. J. et al.
				The distribution of 13 GABAA receptor subunit mRNAs in the rat brain. II.
				Olfactory bulb and cerebellum
				J. Neurosci. 12, 1063-1076 (1992)

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
		339368[GABRA2]	9.3E-172	[Homo sapiens][Channel (passive transporter); Receptor (signaling); Transporter][Plasma membrane] Alpha 2 subunit of the gamma-aminobutyric acid type A (GABA-A) receptor, a chloride channel that is the major inhibitory neurotransmitter receptor in the brain
				Hadingham, K. L. et al. (supra)
				Loup, F. et al. (supra)
		582959[Gabra2]	8.6E-167	[Mus musculus][Channel (passive transporter); Transporter; Receptor (signaling)][Plasma membrane] Alpha 2 subunit of the gamma-aminobutyric acid type A (GABA-A) receptor, a putative chloride channel that is the major inhibitory neurotransmitter receptor in the brain
				Sibille, E. et al. (supra)
				Bouilleret, V. et al. (supra)
56	7510176CD1	g12620132	6.9E-11	[Homo sapiens] renal sodium/sulfate cotransporter
				Lee, A. et al.
				The Human Renal Sodium Sulfate Cotransporter (SLC13A1; hNaSi-1) cDNA and Gene: Organization, Chromosomal Localization, and Functional Characterization
				Genomics 70, 354-363 (2000)
		657791[SLC13A1]	5.9E-12	[Homo sapiens] Protein with strong similarity to sodium/sulfate cotransporter 2 (rat Slc13a1), which mediates sodium-dependent transport of sulfate in brush border cells of renal proximal tubules, member of the Sodium:sulfate symporter family of membrane transporters
				Lee A et al.
				The human renal sodium sulfate cotransporter (SLC13A1; hNaSi-1) cDNA and gene: organization, chromosomal localization, and functional characterization.
				Genomics 70, 354-63 (2000).
57	7510541CD1	g10242111	8.2E-49	[Homo sapiens] Na+ and H+ coupled amino acid transport system N

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
				Fei, Y. J. et al.
				Primary structure, genomic organization, and functional and electrogenic characteristics of human system N 1, a Na ⁺ - and H ⁺ -coupled glutamine transporter
				J. Biol. Chem. 275, 23707-23717 (2000)
		428246 SLC38A3	7.0E-50	[Homo sapiens][Transporter][Plasma membrane] Member of the transmembrane amino acid transporter (permease) family
				Gu, S. et al.
				Identification and characterization of an amino acid transporter expressed differentially in liver.
				Proc Natl Acad Sci U S A 97, 3230-5 (2000).
				Nakanishi, T. et al.
				Structure, function, and tissue expression pattern of human sn2, a subtype of the amino acid transport system n.
				Biochem Biophys Res Commun 281, 1343-8. (2001).
		749242 SLC38A5	6.2E-16	[Homo sapiens] Solute carrier family 38 member 5 (amino acid transport system N2), a system N amino acid transporter that mediates transport of neutral specific amino acids glutamine, asparagine, and histidine, as well as the transport of serine, alanine, and glycine
				Nakanishi, T. et al. (supra)
58	7510923CD1	g1840045	3.3E-148	[Homo sapiens] transporter protein
		428246 SLC38A3	2.8E-149	[Homo sapiens][Transporter][Plasma membrane] Member of the transmembrane amino acid transporter (permease) family
				Gu, S. et al. (supra)
				Nakanishi, T. et al. (supra)

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
		749242 SLC38A5	1.4E-67	[Homo sapiens] Solute carrier family 38 member 5 (amino acid transport system N2), a system N amino acid transporter that mediates transport of neutral specific amino acids glutamine, asparagine, and histidine, as well as the transport of serine, alanine, and glycine
				Nakanishi, T. et al. (supra)
59	7510984CD1	g3643190	0.0	[Homo sapiens] sulfonylurea receptor 1
		338358 ABCC8	0.0	[Homo sapiens][ATP-binding cassette; Hydrolase; Channel (passive transporter); Transporter; Receptor (signaling); ATPase][Plasma membrane] ATP-binding cassette subfamily C member 8, sulfonylurea receptor and subunit of a potassium channel, regulates insulin secretion and potassium transport; gene mutations are implicated in familial persistent hyperinsulinemic hypoglycemia in infancy
				Inagaki, N. et al.
				Reconstitution of IKATP: an inward rectifier subunit plus the sulfonylurea receptor
				Science 270, 1166-70 (1995).
				Thomas, P. M. et al.
				Mutations in the sulfonylurea receptor gene in familial persistent hyperinsulinemic hypoglycemia of infancy
				Science 268, 426-9 (1995).
		590671 Abcc8	0.0	[Rattus norvegicus][ATP-binding cassette; Hydrolase; Channel (passive transporter); Transporter; Receptor (signaling); ATPase][Plasma membrane] ATP-binding cassette subfamily C member 8, sulfonylurea receptor and subunit of a potassium channel, regulates potassium transport; mutations in human ABCC8 are linked to familial persistent hyperinsulinemic hypoglycemia in infancy
				Aguilar-Bryan, L. et al.

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
				Cloning of the beta cell high-affinity sulfonylurea receptor: a regulator of insulin secretion
				Science 268, 423-6 (1995).
				Thomas, P. M. et al. (supra)
				Malhi, H. et al.
				KATP channels regulate mitogenically induced proliferation in primary rat hepatocytes and human liver cell lines. Implications for liver growth control and potential therapeutic targeting.
				J Biol Chem 275, 26050-7 (2000).

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
1	7509332CD1	195	S26 S48 S126 S146 S156 T70 T78 T101	N111 N151	Signal_cleavage: M1-A22	SPSCAN
					Signal Peptide: M8-A22	HMMER
					Signal Peptide: M7-P24	HMMER
					Signal Peptide: M3-Q23	HMMER
					Signal Peptide: M1-A22	HMMER
					Signal Peptide: M3-A27	HMMER
					Signal Peptide: M3-A22	HMMER
					Signal Peptide: M3-A29	HMMER
					Folate receptor family: M7-S195	HMMER_PFAM
					PROTEIN FOLATE RECEPTOR GLYCOPROTEIN PRECURSOR SIGNAL FOLATEBINDING MEMBRANE GPIANCHOR MULTIGENE PD006906: E50-I192, P24-Y100	BLAST_PRODOR
					FOLATE-BINDING PROTEIN DM02165 P15328 22- 256: D87-P188, A22-C102	BLAST_DOMO
					FOLATE-BINDING PROTEIN DM02165 P02702 1- 221: D87-I192, P24-C102	BLAST_DOMO
					FOLATE-BINDING PROTEIN DM02165 P41439 2- 242: K41-S195, A4-Y100	BLAST_DOMO
					FOLATE-BINDING PROTEIN DM02165 P14207 2- 254: D87-G191, W5-G155	BLAST_DOMO
2	7509102CD1	138	S54 S81 S117 T56 T136	N79 N114 N134	Signal_cleavage: M1-G26	SPSCAN
					Signal Peptide: M1-T22	HMMER
					Signal Peptide: M1-A24	HMMER
					Signal Peptide: M1-A29	HMMER

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					Neurotransmitter-gated ion-channel ligand binding: E59-K135	HMMER_PFAM
					Neurotransmitter-gated ion-channels proteins BL00236: N71-N108, I125-N134	BLIMPS_BLOCKS
					Neurotransmitter-gated ion channel family signature PR00252: T91-W107, M124-K135	BLIMPS_PRINTS
					Nicotinic acetylcholine receptor signature PR00254: P78-V94, F112-W126, I130-R138	BLIMPS_PRINTS
					Luteovirus ORF6 protein signature PR00910: P40-G52	BLIMPS_PRINTS
					NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA2 CHAIN PRECURSOR POSTSYNAPTIC MEMBRANE IONIC CHANNEL GLYCOPROTEIN SIGNAL TRANSMEMBRANE MULTIGENE FAMILY PD108915: M1-T58	BLAST_PRODROM
					CHANNEL IONIC TRANSMEMBRANE GLYCOPROTEIN POSTSYNAPTIC MEMBRANE RECEPTOR PRECURSOR SIGNAL PROTEIN PD000153: E57-N134	BLAST_PRODROM
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00195 A40110 16-509: L16-A24, P46-N134	BLAST_DOMO
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00195 P09480 14-526: H55-N134	BLAST_DOMO
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00195 P4368 17-626: S54-N134	BLAST_DOMO
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00195 JC4021 17-627: S54-N134	BLAST_DOMO

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
3	7509132CD1	355	S2 S23 S24 S72 S89 S158 S334 T94 T129 T344 Y348	N273	Sugar (and other) transporter: C5-F329	HMMER_PFAM
					Cytosolic domains: P70-P133, E191-R196, I252-P263, R313-D355; Transmembrane domains: L47-C69, L134-F153, P168-V190, T197-L219, V229-F251, A264-Y286, A290-L312; Non-cytosolic domains: M1-S46, Y154-Q167, L220-Y228, V287-E289	TMHMMER
					Sugar transport proteins signatures: Y170-A225	PROFILES SCAN
					Sugar transporter signature PR00171: Q144-Y154, I231-I252, A254-M266	BLIMPS_PRINTS
					Glucose transporter signature PR00172: L134-Y155, A169-V190, L200-L220, I231-A254, A264-M282, Y294-V314	BLIMPS_PRINTS
					GLUCOSE TRANSPORTER TYPE INSULIN RESPONSIVE DUPLICATION TRANSMEMBRANE SUGAR TRANSPORT GLYCOPROTEIN MULTIGENE PD015687: G319-D355	BLAST_PRODROM
					GLUCOSE TRANSPORTER TYPE 3 CEFGT3 DUPLICATION TRANSMEMBRANE SUGAR TRANSPORT GLYCOPROTEIN MULTIGENE FAMILY PD073462: A288-E353	BLAST_PRODROM
					SUGAR TRANSPORT PROTEINS DM00135 P14672 122-474: Q34-T321	BLAST_DOMO
					SUGAR TRANSPORT PROTEINS DM00135 P19357 122-474: Q34-T321	BLAST_DOMO

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					SUGAR TRANSPORT PROTEINS DM00135[P14142]124-475: Q34-T321	BLAST_DOMO
					SUGAR TRANSPORT PROTEINS DM00135[P27674]126-458: Q34-T321	BLAST_DOMO
					Sugar transport proteins signature 1: S186-G202	MOTIFS
4	7509136CD1	380	S2 S28 S66 S291 T129	N92	Neurotransmitter-gated ion-channel ligand binding domain: M1-P173	HMMER_PFAM
					Neurotransmitter-gated ion-channel transmembrane region: V180-F366	HMMER_PFAM
					Cytosolic domain: P198-R348; Transmembrane domains: F175-L197, L349-Y371; Non-cytosolic domains: M1-L174, H372-P380	TMHMMER
					Neurotransmitter-gated ion-channels proteins BL00236: V36-N45, D64-Y102, R160-A201	BLIMPS_BLOCKS
					Neurotransmitter-gated ion-channels signature: V59-Q110	PROFILESCAN
					Neurotransmitter-gated ion channel family signature PR00252: S2-W18, S35-N46, C79-C93, L167-N179	BLIMPS_PRINTS
					Nicotinic acetylcholine receptor signature PR00254: H23-W37, V41-V53, V59-S77	BLIMPS_PRINTS
					CHANNEL IONIC TRANSMEMBRANE GLYCOPROTEIN POSTSYNAPTIC MEMBRANE RECEPTOR PRECURSOR SIGNAL PROTEIN PD000153: S2-A201, P302-F366, V178-D247	BLAST_PRODROM
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00195[P02712]7-486: M1-A201, I185-P374	BLAST_DOMO

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00195 P04758 7-498: M1-Q287, I185-P374	BLAST_DOMO
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00195 P04759 4-495: M1-D200, Q161-P374	BLAST_DOMO
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00195 P02718 4-501: M1-A201, L186-P374	BLAST_DOMO
					Leucine zipper pattern: L190-L211	MOTIFS
					Neurotransmitter-gated ion-channels signature: C79-C93	MOTIFS
5	7509178CD1	375	S21 S81 S271 S290 N79 S312 S326 T266 T323 Y319		Signal_cleavage: M1-G20	SPSCAN
					Signal Peptide: M1-A15, M1-G20, M1-H23	HMMER
					Neurotransmitter-gated ion-channel ligand binding domain: Q78-P149, E24-K77	HMMER_PFAM
					Neurotransmitter-gated ion-channel transmembrane region: V156-F364	HMMER_PFAM
					Cytosolic domains: P174-S184, N235-H346; Transmembrane domains: Y151-L173, I185-I202, I212-I234, I347-I369; Non-cytosolic domains: M1-L150, P203-L211, E370-G375	TMHMMER
					Neurotransmitter-gated ion-channels proteins BL00236: V51-Y89, Y136-S177	BLIMPS_BLOCKS
					Nicotinic acetylcholine receptor signature PR00254: I58-V74	BLIMPS_PRINTS

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					Metabotropic glutamate receptor signature PR00593: T182-L196	BLIMPS_PRINTS
					CHANNEL IONIC TRANSMEMBRANE GLYCOPROTEIN POSTSYNAPTIC MEMBRANE RECEPTOR PRECURSOR SIGNAL PROTEIN PD000153: K77-K338, S287-F364, E22-W87	BLAST_PRODOR
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00195 P25108 4-453: Q68-N372, L6-I116	BLAST_DOMO
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00195 P22456 4-453: Q78-N372, L6-R120	BLAST_DOMO
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00195 P02711 8-457: Q68-N372, L6-I116	BLAST_DOMO
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00195 S60589 5-492: Q78-S271, P308-F364, L7-S92	BLAST_DOMO
6	7509214CD1	153	S128 T138		Signal Peptide: M1-G18	HMMER
					PERIPHERAL BENZODIAZEPINE RECEPTOR RELATED PROTEIN PD068564: M52-S153	BLAST_PRODOR
7	7509244CD1	369	S2 S28 S66 T129 N92		Neurotransmitter-gated ion-channel ligand binding domain: M1-P173	HMMER_PFAM
					Neurotransmitter-gated ion-channel transmembrane region: V180-F355	HMMER_PFAM
					Cation transporter family protein: M1-A358	HMMER_TIGRFAM

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					Cytosolic domains: P198-M205, H261-R337; Transmembrane domains: F175-L197, G206-A223, K238-L260, L338-Y360; Non-cytosolic domains: M1-L174, D224-I237, H361-P369	TMHMMER
					Neurotransmitter-gated ion-channels proteins BL00236: V36-N45, D64-Y102, R160-A201	BLIMPS_BLOCKS
					Neurotransmitter-gated ion-channels signature: V59-Q110	PROFILES CAN
					Neurotransmitter-gated ion channel family signature PR00252: S2-W18, S35-N46, C79-C93, L167-N179	BLIMPS_PRINTS
					Gamma-aminobutyric acid (GABA) receptor signature PR00253: Y176-Y196, A201-L222, L231-I252	BLIMPS_PRINTS
					Nicotinic acetylcholine receptor signature PR00254: H23-W37, V41-V53, V59-S77	BLIMPS_PRINTS
					CHANNEL IONIC TRANSMEMBRANE GLYCOPROTEIN POSTSYNAPTIC MEMBRANE RECEPTOR PRECURSOR SIGNAL PROTEIN PD000153: S2-S309, P291-F355	BLAST_PRODROM
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00195 P04758 7-498: M1-E300, L297-P363	BLAST_DOMO
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00195 P02712 7-486: M1-L301, L297-P363	BLAST_DOMO

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00195 P09484 2-474; M1-K292, P291-Y360	BLAST_DOMO
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00195 P02713 5-498; M1-R313, P299-H361	BLAST_DOMO
					Neurotransmitter-gated ion-channels signature: C79-C93	MOTIFS
8	7509256CD1	303	S26 S27 S44 S93 S174 T97 T194 T207 T254 T261 Y206 Y240	N54 N242	Signal_cleavage: M1-S22	SPSCAN
					Signal Peptide: M1-L15	HMIMER
					Signal Peptide: M1-E19	HMIMER
					Signal Peptide: M1-A20	HMIMER
					Signal Peptide: M1-S22	HMIMER
					Signal Peptide: M1-W16	HMIMER
					Neurotransmitter-gated ion-channel ligand binding domain: T56-V266	HMIMER_PFAM
					Cation transporter family protein: L5-W303	HMIMER_TIGRFAM
					Cytosolic domain: I290-W303; Transmembrane domain: G267-W289; Non-cytosolic domain: M1-V266	TMHMIMER
					Neurotransmitter-gated ion-channels proteins BL00236: V82-P119, L138-N147, D168-Y206, Y253-A294	BLIMPS_BLOCKS
					Neurotransmitter-gated ion-channels signature: L163-S217	PROFILESCAN

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					Neurotransmitter-gated ion channel family signature PR00252: R102-L118, C137-E148, C183-C197, F260-G272	BLIMPS_PRINTS
					Gamma-aminobutyric acid (GABA) receptor signature PR00253: Y269-W289	BLIMPS_PRINTS
					CHANNEL IONIC TRANSMEMBRANE GLYCOPROTEIN POSTSYNAPTIC MEMBRANE RECEPTOR PRECURSOR SIGNAL PROTEIN PD000153: I59-G302	BLAST_PRODROM
					GLYCINE RECEPTOR BETA CHAIN PRECURSOR POSTSYNAPTIC MEMBRANE IONIC CHANNEL GLYCOPROTEIN PD022977: M1-N58	BLAST_PRODROM
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00560 P48167 I13-497: I13-G302	BLAST_DOMO
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00560 S18836 I18-453: E19-G302	BLAST_DOMO
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00560 B49970 I18-452: E19-D131, G30-G302	BLAST_DOMO
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00560 P23415 I12-449: L38-G302	BLAST_DOMO
					Neurotransmitter-gated ion-channels signature: C183-C197	MOTIFS
9	7509395CD1	370	S21 S76 S266 S285 S307 S321 T261 T318 Y314	N74	Signal_cleavage: M1-G20	SPSCAN
					Signal Peptide: M1-A15	HMMER
					Signal Peptide: M1-G20	HMMER

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					Signal Peptide: M1-H23	HMMER
					Neurotransmitter-gated ion-channel ligand binding domain: N74-P144, E24-N73	HMMER_PFAM
					Neurotransmitter-gated ion-channel transmembrane region: V151-F359	HMMER_PFAM
					Cytosolic domains: P169-S179, N230-H341; Transmembrane domains: Y146-L168, I180-I197, I207-I229, I342-I364; Non-cytosolic domains: M1-L145, P198-L206, E365-G370	TMHMMER
					Cation transporter family protein M1-V358	HMMER_TIGRFAM
					Neurotransmitter-gated ion-channels proteins BL00236: R46-Y84, Y131-S172	BLIMPS_BLOCKS
					Neurotransmitter-gated ion channel family signature PR00252: F138-N150	BLIMPS_PRINTS
					Nicotinic acetylcholine receptor signature PR00254: I58-N74	BLIMPS_PRINTS
					CHANNEL IONIC TRANSMEMBRANE GLYCOPROTEIN POSTSYNAPTIC MEMBRANE RECEPTOR PRECURSOR SIGNAL PROTEIN PD000153: N74-K333, S282-F359, E22-N73	BLAST_PRODOR
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00195 P25108 4-453: L6-N73, N74-N367	BLAST_DOMO
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00195 P02711 8-457: L6-N73, N74-N367	BLAST_DOMO

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00195 P22456 4-453: L6-N73, N74-N367	BLAST_DOMO
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00195 P18845 7-510: L6-G289, P303-I364	BLAST_DOMO
10	7503287CD1	283	S40 S104 S146 S180 S199 T62 T75 T209 T239	N276	Signal_cleavage: M1-C61	SPSCAN
					Amiloride-sensitive sodium channel: F21-N283	HMMER_PFAM
					ENaC: sodium channel transporter: S17-N283	HMMER_TIGRFAM
					Amiloride-sensitive sodium channels proteins BL01206: A20-L30, Y191-R204, G213-P231	BLIMPS_BLOCKS
					Amiloride-sensitive sodium channel alpha-subunit signature PR01078: R43-V60, S83-R99, L169-S180, E182-N198, G213-P231	BLIMPS_PRINTS
					CHANNEL IONIC TRANSMEMBRANE ION TRANSPORT SODIUM GLYCOPROTEIN AMILORIDESENSITIVE SUBUNIT NA+ PD001186: F21-PI51, R160-I249	BLAST_PRODROM
					CHANNEL IONIC TRANSMEMBRANE SODIUM ION TRANSPORT PROTON GATED CATION ASIC1 PD151848: N119-D159	BLAST_PRODROM
					SODIUM; SENSITIVE; AMILORIDE; CHANNEL; DM01114 P51169 10-589: F21-E123, G162-P231	BLAST_DOMO

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					SODIUM; SENSITIVE; AMILORIDE; CHANNEL; DM011114 P51167 1-556: F21-L108, G162-V232	BLAST_DOMO
					SODIUM; SENSITIVE; AMILORIDE; CHANNEL; DM011114 P51170 7-576: F21-Q134, H163-P231	BLAST_DOMO
					SODIUM; SENSITIVE; AMILORIDE; CHANNEL; DM011114 P51171 8-580: I18-I137, G162-P231	BLAST_DOMO
11	7503320CD1	90	S84	N46	Signal_cleavage: M1-Q22	SPSCAN
					Signal Peptide: M1-V19	HMMER
					Signal Peptide: M1-G23	HMMER
					Signal Peptide: M1-F25	HMMER
					Signal Peptide: M1-Q22	HMMER
					Nicotinic acetylcholine receptor signature PR00254: L60-T76	BLIMPS_PRINTS
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00195 P54131 3-491: G6-T74	BLAST_DOMO
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00195 JH0173 14-503: V8-T74	BLAST_DOMO
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00195 P48180 2-497: L10-L72	BLAST_DOMO
12	7503335CD1	549	S6 S47 S86 S131 S344 S356 S374 S444 T15 T28 T124 T149 T204 T351 T421 T462 T509	N187 N202 N213	ATP P2X receptor: F11-V358	HMMER_PFAM

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					P2X: cation transporter protein: M1-C328	HMMER_TIGRFAM
					Cytosolic domain: S47-Q286; Transmembrane domains: M24-V46, L287-I309; Non-cytosolic domains: M1-S23, D310-Y549	TMHMMER
					ATP P2X receptors proteins BL01212: F38-T90, C129-V153, T161-E171, R261-V288	BLIMPS_BLOCKS
					P2X PURINOCEPTOR ATP RECEPTOR P2X7 PURINERGIC P2Z IONIC CHANNEL	BLAST_PRODROM
					TRANSMEMBRANE PD041643: I309-Y549	
					RECEPTOR ATP IONIC CHANNEL	BLAST_PRODROM
					TRANSMEMBRANE ION TRANSPORT P2X PURINOCEPTOR PURINERGIC PD002383: F11-Q243, E335-K349, G211-I309	
					PORE-FORMING MOTIF DOMAIN	BLAST_DOMO
					DM02085[P51577]1-384: M1-Q243, W245-I309, C331-E347	
					PORE-FORMING MOTIF DOMAIN	BLAST_DOMO
					DM02085[P51579]1-378: Y13-I234, W245-I309	
					PORE-FORMING MOTIF DOMAIN	BLAST_DOMO
					DM02085[P51578]1-385: V10-Q243, W245-I309	
					PORE-FORMING MOTIF DOMAIN	BLAST_DOMO
					DM02085[P51575]1-380: V10-E237, G200-I309	
13	7503952CD1	246	S98 S190 S205 T172 T179 Y134	N52 N96 N138 N168 N203 N232	Signal_cleavage: M1-A21	SPSCAN
					Signal Peptide: M6-A21	HMMER
					Signal Peptide: M6-D23	HMMER
					Signal Peptide: M1-A21	HMMER
					Signal Peptide: M1-T24	HMMER

Table 3

SEQ ID NO:	Incye Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					Signal Peptide: M1-P27	HMMER
					Neurotransmitter-gated ion-channel ligand binding domain: L32-P237	HMMER_PFAM
					Neurotransmitter-gated ion-channels proteins BL00236: V59-N96, I113-E122, S140-H178	BLIMPS_BLOCKS
					Neurotransmitter-gated ion-channels signature: V135-R189	PROFILES SCAN
					Neurotransmitter-gated ion channel family signature PR00252: K79-W95, A112-F123, C155-C169	BLIMPS_PRINTS
					Nicotinic acetylcholine receptor signature PR00254: H66-V82, F100-W114, V135-S153	BLIMPS_PRINTS
					CHANNEL IONIC TRANSMEMBRANE GLYCOPROTEIN POSTSYNAPTIC MEMBRANE RECEPTOR PRECURSOR SIGNAL PROTEIN PD000153: L35-N232	BLAST_PROD OM
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00195[P46098]7-476: A31-F231	BLAST_DOMO
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00195[P1239]15-459: W10-S211	BLAST_DOMO
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00195[P54131]3-491: C12-V212	BLAST_DOMO
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00195[A40110]16-309: L9-S217	BLAST_DOMO
14	7504530CD1	273	S10 T11 T190		Major intrinsic protein: E27-H251	HMMER_PFAM
					MIP family channel proteins: A39-V273	HMMER_TIGRFAM

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					Cytosolic domains: M1-E36, H92-K111, L162-T167, N226-V273; Transmembrane domains: F37-V59, G69-A91, F112-F134, L139-Y161, L168-T190, A203-I225; Non-cytosolic domains: L60-L68, Y135-I138, D191-E202	TMHMMER
					MIP family proteins BL00221: A39-V49, I88-T98, E175-D191, T221-I235, T237-F247	BLIMPS_BLOCKS
					Major intrinsic protein family signature PR00783: R35-S54, F74-T98, K111-I130, N174-Q192, G207-R229	BLIMPS_PRINTS
					TRANSMEMBRANE TRANSPORT PROTEIN AQUAPORIN INTRINSIC CHANNEL MEMBRANE WATER TONOPLAST FAMILY PD000295: R35-H259	BLAST_PRODROM
					AQUAPORIN7 LIKE AQUAPORIN ADIPOSE AQPAP TRANSPORT TRANSMEMBRANE PD062309: M1-V34	BLAST_PRODROM
					MIP FAMILY DM00228 p47862 15-263: L29-V273	BLAST_DOMO
					MIP FAMILY DM00228 I59266 15-263: L29-V273	BLAST_DOMO
					MIP FAMILY DM00228 p43549 340-587: R31-G272	BLAST_DOMO
					MIP FAMILY DM00228 p11244 1-253: L38-G272	BLAST_DOMO
					Prenyl group binding site (CAAX box):	MOTIFS
					Amiloride-sensitive sodium channel: F62-L228	HMMER_PFAM
15	7509303CD1	245	S54 S122 S176 S209 T42 T157	N64 N65	Cytosolic domain: M1-T84; Transmembrane domain: A85-G107; Non-cytosolic domain: E108-Q245	TMHMMER

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					Amiloride-sensitive sodium channels proteins BL01206: F61-A71	BLIMPS_BLOCKS
					Amiloride-sensitive sodium channel alpha-subunit signature PR01078: T84-Q101, D123-R139	BLIMPS_PRINTS
					CHANNEL IONIC TRANSMEMBRANE ION TRANSPORT SODIUM GLYCOPROTEIN AMILORIDESENSITIVE SUBUNIT NA+ PD001186: F62-V217	BLAST_PRODOM
					AMILORIDESENSITIVE SODIUM CHANNEL ALPHASUBUNIT NA+ ALPHA SUBUNIT ENAC NONVOLTAGEGATED SCNEA PD040285: M1-F61	BLAST_PRODOM
					SODIUM; SENSITIVE; AMILORIDE; CHANNEL; DM01114 A49585 37-598: A37-L228	BLAST_DOMO
					SODIUM; SENSITIVE; AMILORIDE; CHANNEL; DM01114 P37088 37-598: A37-L228	BLAST_DOMO
					SODIUM; SENSITIVE; AMILORIDE; CHANNEL; DM01114 P55270 17-579: P38-L228	BLAST_DOMO
					SODIUM; SENSITIVE; AMILORIDE; CHANNEL; DM01114 P37089 63-626: A37-L228	BLAST_DOMO
16	7509910CD1	364	S6 S47 S86 S131 S274 T15 T28 T124 T149 T204	N187 N202 N213 N241 N284	Signal_cleavage: M1-A44	SPSCAN
					ATP P2X receptor: F11-V347	HMMER_PFAM
					Cation transporter protein: M1-W358	HMMER_TIGRFAM

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					Cytosolic domain: M1-M24; Transmembrane domain: N25-S47; Non-cytosolic domain: D48-D364	TMHMMER
					ATP P2X receptors proteins BL01212: F38-T90, C129-V153, T161-E171, A185-I208, P224-L278, P289-Y299, R307-V334	BLIMPS_BLOCKS
					RECEPTOR ATP IONIC CHANNEL TRANSMEMBRANE ION TRANSPORT P2X PURINOCEPTOR PURINERGIC PD002383: F11-L346	BLAST_PRODOM
					PORE-FORMING MOTIF DOMAIN DM02085 P51577 1-384: M1-L346	BLAST_DOMO
					PORE-FORMING MOTIF DOMAIN DM02085 P51575 1-380: V10-L346	BLAST_DOMO
					PORE-FORMING MOTIF DOMAIN DM02085 P49654 1-370: S6-V335	BLAST_DOMO
					PORE-FORMING MOTIF DOMAIN DM02085 P51578 1-385: V10-G345	BLAST_DOMO
					ATP P2X receptors signature: G249-F275	MOTIFS

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
17	7509982CD1	1623	S30 S50 S134 S249 S353 S491 S672 S761 S792 S815 S825 S921 S929 S960 S1041 S1133 S1199 S1275 S1301 S1335 S1494 T111 T206 T558 T572 T624 T643 T755 T772 T780 T858 T974 T1178 T1263 T1346 T1376 T1424 T1447 T1468 T1551 T1611 Y953	N71 N84 N91 N109 N130 N241 N436 N544 N576 N917 N946 N996 N1311	Signal peptide: M26-A45, M26-M51	HMMER
					ABC transporter: G507-G689, G1319-G1495	HMMER_PFAM
					ATPases associated with a variety of cellular activities: E1318-R1496, E506-R690	HMMER_INCY
					3a0106s01: sulfate transport system permease protein: I478-I717, C1299-Y1526	HMMER_TIGRFAM
					3a0501s02: Type II (General) Secretory Pathway (IUSP) Family protein: A477-L691	HMMER_TIGRFAM
					cbiO: cobalt transport protein ATP-bin: G492-A676	HMMER_TIGRFAM
					dmrA: daunorubicin resistance ABC transporter ATP-binding subunit: K1302-K1597, K485-G790	HMMER_TIGRFAM

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					nodI: nodulation ABC transporter NodI: G474-E795, S1286-K1590	HMMER_TIGRFAM
					nttCD: nitrate transport ATP-binding subunits C and D: A1309-F1537, L497-L710	HMMER_TIGRFAM
					thiQ: ABC transporter, ATP-binding protein, ThiQ subfamily: I478-S697	HMMER_TIGRFAM
					Cytosolic domains: M1-E29, K244-F263, S319-K324, D418-K859, D1044-A1062, S1123-S1133, R1183-D1202; Transmembrane domains: S30-S49, E221-T243, W264-I286, G296-L318, A325-F347, T395-F417, V860-Y882, F1024-S1043, Y1063-I1085, I1100-I1122, G1134-F1156, I1160-V1182, F1203-L1225; Non-cytosolic domains: S50-N220, T287-T295, Y348-Y394, A883-S1023, F1086-Q1099, D1157-S1159, K1226-P1623	TMHMMER
					ABC Transporters family signature: V595-D646	PROFILES CAN
					ABC TRANSPORTERS FAMILY	BLAST_DOMO
					DM00008 P41233 839-1045: I478-N688, K1306-M1492	
					ABC TRANSPORTERS FAMILY	BLAST_DOMO
					DM00008 P34358 611-816: I478-N688, A1308-M1492	
					ABC TRANSPORTERS FAMILY	BLAST_DOMO
					DM00008 P41233 1851-2058: K1302-S1494, I478-N688	
					ABC TRANSPORTERS FAMILY	BLAST_DOMO
					DM00008 P23703 41-246: L500-G689, E1291-G1495	

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					ATP/GTP-binding site motif A (P-loop): G514-S521, G1326-S1333	MOTIFS
18	7510082CD1	611	S174 S281 S302 S572 T195 T369 T594	N61 N66 N178 N223 N356 N439 N597	POT family: Y101-S259, R362-S503	HMMER_PFAM
					Cytosolic domains: M1-A37, D95-R100, N178-R197, T253-Q311, D391-K410, S485-M496, R562-C611; Transmembrane domains: V38-L60, A75-A94, Y101-F123, P155-S177, F198-I220, Y230-I252, V312-F331, Y368-K390, M411-L428, I462-Y484, G497-L519, D539-G561; Non-cytosolic domains: N61-R74, P124-S154, Q221-G229, Q332-S367, E429-Q461, P520-M538	TMHMMER
					PTR2 family proton/oligopeptide symporters proteins BL01022: E42-L60, A72-L117, G164-V187, F199-V211, E472-S507	BLIMPS_BLOCKS
					TRANSPORTER TRANSPORT TRANSMEMBRANE PEPTIDE OLIGOPEPTIDE PROTEIN SYMPORT ISOFORM H+/PEPTIDE COTRANSPORTER PD001550: Y101-S507 PEPTIDE/HISTIDINE TRANSPORTER PD127516: S503-R565	BLAST_PRODUM
					PTR2 FAMILY PROTON/OLIGOPEPTIDE SYMPORTERS DM01990 P46032 46-551: E42-S518	BLAST_DOMO
					PTR2 FAMILY PROTON/OLIGOPEPTIDE SYMPORTERS DM01990 Q05085 32-539: A33-N271, S367-H525, D306-V442	BLAST_DOMO

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					PTR2 FAMILY PROTON/OLIGOPEPTIDE SYMPORTERS DM01990[P4603]84-554: V38-I349, V381-L509	BLAST_DOMO
					PTR2 FAMILY PROTON/OLIGOPEPTIDE SYMPORTERS DM01990[P32901]81-545: V38-V261, A163-F350, I370-L513	BLAST_DOMO
19	7510367CD1	55			Mitochondrial energy transfer proteins signature: N25-T53	PROFILES SCAN
					Mitochondrial energy transfer proteins signature: P42-A51	MOTIFS
20	7510413CD1	287	S26 S48 S165 S218 S238 S248 T193	N163 N203 N243	Signal_cleavage: M1-A22	SPSCAN
					Signal Peptide: M8-A22	HMMER
					Signal Peptide: M7-P24	HMMER
					Signal Peptide: M3-Q23	HMMER
					Signal Peptide: M1-A22	HMMER
					Signal Peptide: M3-A27	HMMER
					Signal Peptide: M3-A22	HMMER
					Signal Peptide: M3-A29	HMMER
					Folate receptor family: M7-S287	HMMER PFAM
					PROTEIN FOLATE RECEPTOR GLYCOPROTEIN PRECURSOR SIGNAL FOLATE BINDING MEMBRANE GPIANCHOR MULTIGENE PD006906: P24-Q56, E150-I284	BLAST_PRODROM
					FOLATE-BINDING PROTEIN DM02165[P41439]2-242: A4-Q56, E150-S287	BLAST_DOMO
					FOLATE-BINDING PROTEIN DM02165[P14207]2-254: W5-Q56, T146-G283	BLAST_DOMO

Table 3

SEQ ID NO.	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					FOLATE-BINDING PROTEIN DM02165 P15328 22-256: A22-Q56, T146-P280	BLAST_DOMO
					FOLATE-BINDING PROTEIN DM02165 P02702 1-221: P24-Q56, T146-I284	BLAST_DOMO
21	1721303CD1	55	S3		F ATP SYNTHASE CHAIN MITOCHONDRIAL SYNTHESIS HYDROGEN ION TRANSPORT CF0 PD015221: V11-Y54	BLAST_PRODOM
22	7502007CD1	272	S9 T189		Major intrinsic protein: E26-H250	HMMER_PFAM
					MIP: MIP family channel proteins: A38-V272	HMMER_TIGRFAM
					Cytosolic domains: M1-E35, H91-K110, L161-T166, N225-V272; Transmembrane domains: F36-V58, G68-A90, F111-F133, L138-Y160, L167-T189, A202-I224; Non-cytosolic domains: L59-L67, Y134-I137, D190-E201	TMHMMER
					MIP family proteins BL00221: A38-V48, I87-T97, E174-D190, T220-I234, T236-F246	BLIMPS_BLOCKS
					Major intrinsic protein family signature PR00783: R34-S53, F73-T97, K110-I129, N173-Q191, G206-R228	BLIMPS_PRINTS
					TRANSMEMBRANE TRANSPORT PROTEIN AQUAPORIN INTRINSIC CHANNEL MEMBRANE WATER TONOPLAST FAMILY PD000295: R34-H258	BLAST_PRODOM
					MIP FAMILY DM00228 P47862 15-263: L28-V272	BLAST_DOMO
					MIP FAMILY DM00228 I59266 15-263: L28-V272	BLAST_DOMO
					MIP FAMILY DM00228 P43549 340-587: R30-G271	BLAST_DOMO
					MIP FAMILY DM00228 P11244 1-253: L37-G271	BLAST_DOMO

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
23	7506439CD1	188	T35 T65	N34 N110	Prenyl group binding site (CAAX box): Signal cleavage: M1-G27	MOTIFS
					Signal Peptide: M7-A25	SPSCAN
					Signal Peptide: M7-G27	HMMER
					Signal Peptide: M7-A29	HMMER
					Signal Peptide: M1-A29	HMMER
					Signal Peptide: M1-G27	HMMER
					Neurotransmitter-gated ion-channel ligand binding domain: L40-R146	HMMER_PFAM
					Neurotransmitter-gated ion-channels proteins BL00236: V67-N104, I121-E130	BLIMPS_BLOCKS
					Neurotransmitter-gated ion channel family signature PR00252: T87-W103, S120-F131	BLIMPS_PRINTS
					Nicotinic acetylcholine receptor signature PR00254: Y74-I90, F108-W122	BLIMPS_PRINTS
					CHANNEL IONIC TRANSMEMBRANE GLYCOPROTEIN POSTSYNAPTIC MEMBRANE RECEPTOR PRECURSOR SIGNAL PROTEIN PD000153: R42-D125	BLAST_PRODROM
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00195 P46098 7-476: Q13-Q148	BLAST_DOMO
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00195 P09480 14-526: R42-F151	BLAST_DOMO
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00195 P45963 9-466: L47-Y142, Y142-F168	BLAST_DOMO
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00195 P26152 13-440: R42-D133	BLAST_DOMO
					Leucine zipper pattern: L2-L23	MOTIFS

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
24	7509243CD1	111	S91 T59	N57 N86	Signal_cleavage: M1-A41 Cytosolic domain: Q33-H111; Transmembrane domain: W10-F32; Non-cytosolic domain: M1-C9	SPSCAN TMHMMER
					TWIK-1 K+ channel subunit signature PR01096: V22-A41, S43-Q63, W64-G80	BLIMPS_PRINTS
25	7509404CD1	46	S26 S27 S41		Signal_cleavage: M1-S22 Signal Peptide: M1-L15 Signal Peptide: M1-E19 Signal Peptide: M1-A20 Signal Peptide: M1-S22 Signal Peptide: M1-W16	SPSCAN HMMER HMMER HMMER HMMER HMMER
					GLYCINE RECEPTOR BETA CHAIN PRECURSOR POSTSYNAPTIC MEMBRANE IONIC CHANNEL GLYCOPROTEIN PD022977: M1-R43	BLAST_PRODUM
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00560P48167I13-497: I13-R43	BLAST_DOMO
26	7509439CD1	204	S37 S47 S98 S184 T27 T32	N158	ATP synthase: A26-L141 ATPsyn_F1gamma: ATP synthase F1.; M25- Y204 ATP synthase gamma subunit proteins BL00153: K29-A53, G104-S143 ATP synthase gamma subunit signature PR00126: K88-H107 GAMMA ATP SYNTHASE CHAIN HYDROLASE SYNTHESIS CF1 HYDROGEN ION TRANSPORT PD001150: A26-R138	HMMER_FFAM HMMER_TIGRFAM BLIMPS_BLOCKS BLIMPS_PRINTS BLAST_PRODUM

Table 3

SEQ ID NO:	Incye Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					ATP SYNTHASE GAMMA SUBUNIT DM00493 P05631 25-297: M25-Y142	BLAST_DOMO
					ATP SYNTHASE GAMMA SUBUNIT DM00493 P49377 17-288: A26-L141	BLAST_DOMO
					ATP SYNTHASE GAMMA SUBUNIT DM00493 P05436 1-285: M25-R138	BLAST_DOMO
					ATP SYNTHASE GAMMA SUBUNIT DM00493 P07227 1-298: M25-R138	BLAST_DOMO
27	7510202CD1	1400	S2 S7 S61 S70 S113 S197 S625 S755 S778 S788 S884 S892 S923 S1004 S1053 S1096 S1157 S1201 S1261 T30 T86 T458 T463 T575 T716 T743 T756 T792 T937 T966 T970 T1266 T1295 T1338 T1380 Y916	N72 N120 N195 N244 N456 N545 N556 N880 N909 N959 N1271 N1336	Signal peptides: M26-S49, M26-D56	HMMER
					ATPases associated with a variety of cellular activities: E509-K653, K1278-P1400	HMMER_SMART
					ABC transporter: G510-G652	HMMER_PFAM
					drfA: daunorubicin resistance ABC transport: K488-G753	HMMER_TIGRFAM

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					Cytosolic domains: M1-T30, N244-A265, K326-F329, H379-Y397, E846-N985, M1045-L1064, D1115-G1120, E1184-P1400; Transmembrane domains: L31-Q53, V221-V243, F266-I288, V303-I325, L330-T352, A356-I378, L398-F420, S823-Y845, T986-I1005, A1025-L1044, L1065-F1087, G1097-T1114, F1121-F1143, I1161-L1183; Non-cytosolic domains: V54-G220, V289-M302, H353-P355, D421-K822, G1006-S1024, I1088-S1096, S1144-E1160	TMHMMER
					ABC TRANSPORTERS FAMILY DM00008 P41233 839-1045: I481-P610, I1267-L1393, V597-N651	BLAST_DOMO
					ABC TRANSPORTERS FAMILY DM00008 P34358 611-816: I481-D602, A1268-V1389, E595-I649	BLAST_DOMO
					ABC TRANSPORTERS FAMILY DM00008 P36879 5-211: I481-E578	BLAST_DOMO
					DM06389 P41233 1047-1849: D682-D758, G652-L675, A994-R1090, I796-Y861	BLAST_DOMO
					ATP/GTP-binding site motif A (P-loop): G517-T524, G1286-S1293	MOTIFS
28	7510203CD1	438	S24 S194 S378 T127 T229 T312	N23 N65	ABC transporter transmembrane region: W10-L304	HMMER_Pfam
					Cytosolic domains: M1-F72, R133-D143, Q188-Q255, F311-G438; Transmembrane domains: Y73-F95, L110-N132, S144-L166, L170-V187, W256-V278, G288-S310; Non-cytosolic domains: A96-R109, G167-G169, Q279-P287	TMHMMER

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					RESISTANCE; MULTIDRUG; SAUROLEISHMANIA; C3F10.11C; DM01525 P39109 861-1270: G50-G357	BLAST_DOMO
					RESISTANCE; MULTIDRUG; SAUROLEISHMANIA; C3F10.11C; DM01525 P33527 868-1291: A7-E27, N65-T328	BLAST_DOMO
					RESISTANCE; MULTIDRUG; SAUROLEISHMANIA; C3F10.11C; DM01525 S64757 872-1300: A7-E27, N65-G357	BLAST_DOMO
					RESISTANCE; MULTIDRUG; SAUROLEISHMANIA; C3F10.11C; DM01525 Q10185 827-1237: F72-S359	BLAST_DOMO
					Leucine zipper pattern: L145-L166, L152-L173, L159-L180	MOTIFS
29	7510208CD1	871	S21 S50 S119 S140 S199 S256 S281 S467 S502 S533 S631 S823 T16 T48 T252 T353 T382 T440 T612 T633 T696 T799	N14 N90 N169 N174 N306 N369 N380 N421 N433 N477 N485 N495 N531 N545 N591 N601 N629	Signal_cleavage: M1-R43	SPSCAN
					Cytosolic domain: R43-E53; Transmembrane domains: R20-L42, V54-P76; Non-cytosolic domains: M1-R19, D77-A871	TMHMMER
					ATPBINDING TRANSPORTER CASSETTE ABC GLYCOPROTEIN TRANSMEMBRANE TRANSPORT RIM ABCR SIMILARITY PD006867: Y643-Q664, I663-S744	BLAST_PRODOM

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					Leucine zipper pattern: L509-L530, L516-L537, L534-L555	MOTIFS
					Cell attachment sequence: R863-D865	MOTIFS
					Eukaryotic molybdopter in oxidoreductases signature: A391-E425	MOTIFS
30	7510446CD1	104	S70 S86 S90		PROTEIN CHLORIDE CHANNEL SKELETAL MUSCLE CLC1 IONIC ION TRANSPORT VOLTAGEGATED PD035113: M1-H57	BLAST_PRODROM
31	7505294CD1	336	S25 S239 S291 T53 T183	N23 N32	signal_cleavage: M1-A48	SPSCAN
					Cytosolic domains: D123-R128, R176-R187, E238-P336	TMHMMER
					Transmembrane domains: V100-A122, G129-A148, G153-M175, V188-S210, F215-L237	
					Non-cytosolic domains: M1-Q99, G149-T152, K211-R214	
					Sugar transport proteins signature 1: L118-T134	MOTIFS
32	7505631CD1	271	S83 S132 S232 T259	N29 N241	signal_cleavage: M1-A52	SPSCAN
					Signal Peptide: M1-G22	HMMER
					ZIP Zinc transporter: R140-M271	HMMER_PFAM
					Cytosolic domains: M1-F4, H60-Q103, H199-H210, V260-M271	TMHMMER
					Transmembrane domains: I5-A27, L37-V59, L104-G126, L176-M198, L211-S230, V240-T259	
					Non-cytosolic domains: V28-K36, N127-Q175, K231-E239	
33	7506561CD1	107	S24 S46 S98 T68 T76		signal_cleavage: M1-A20	SPSCAN

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					Signal Peptide: M1-A20, M1-Q21, M1-P22, M1-A25, M1-A27, M5-P22, M6-A20	HMMER
					Folate receptor family: M5-L107	HMMER_PFAM
					PROTEIN FOLATE RECEPTOR GLYCOPROTEIN PRECURSOR SIGNAL FOLATEBINDING MEMBRANE GPIANCHOR MULTIGENE PD006906: P22-H97	BLAST_PRODOR
					FOLATE-BINDING PROTEIN DM02165[P41439]2-242: A2-H97	BLAST_DOMO
					FOLATE-BINDING PROTEIN DM02165[P14207]2-254: W3-H97	BLAST_DOMO
					FOLATE-BINDING PROTEIN DM02165[P02702]1-221: P22-H97	BLAST_DOMO
					FOLATE-BINDING PROTEIN DM02165[P15328]22-256: A20-H97	BLAST_DOMO
34	7510733CD1	249	S11 S176 T26	N96	signal_cleavage: M1-A45	SPSCAN
					Major intrinsic protein: R15-Y216	HMMER_PFAM
					MIP: MIP family channel proteins: S28-Y216	HMMER_TIGRFAM
					Cytosolic domains: S50-R53, D135-E146, I220-M249 Transmembrane domains: F30-L49, F54-G76, A115-F134, P147-M169, F197-V219 Non-cytosolic domains: M1-E29, G77-N114, N170-N196	TMHMMER
					MIP family proteins BL00221: S28-V38, Q119-D135, S165-L179, W198-G208	BLIMPS_BLOCKS
					Major intrinsic protein family signature PR00783: K24-C43, G151-R173, W199-V219	BLIMPS_PRINTS

Table 3

SEQ ID NO.	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					TRANSMEMBRANE TRANSPORT PROTEIN AQUAPORIN INTRINSIC CHANNEL MEMBRANE WATER TONOPLAST FAMILY PD000295: E95-Y216	BLAST_PRODOM
					AQUAPORIN 9 TRANSPORT TRANSMEMBRANE PD162891: V217-M249	BLAST_PRODOM
					MIP FAMILY DM00228[P47862][5-263: L16-S79, F64-V219]	BLAST_DOMO
					MIP FAMILY DM00228[59266][15-263: L16-S79, F64-V219]	BLAST_DOMO
					MIP FAMILY DM00228[P11244][1-253: S20-S79, A99-Y216]	BLAST_DOMO
					MIP FAMILY DM00228[P44826][1-251: L18-S79, A99-Y216]	BLAST_DOMO
35	7510734CD1	216	S11 S200 S201 T26	N142	signal_cleavage: M1-A45	SPSCAN
					Major intrinsic protein: R15-H197	HMMER_PFAM
					MIP: MIP family channel proteins: S28-H197	HMMER_TIGRFAM
					Cytosolic domains: M1-T26, H82-K101 Transmembrane domains: L27-L49, T59-G81, L102-Y124	TMHMMER
					Non-cytosolic domains: S50-I58, Y125-V216 MIP family proteins BL00221: S28-V38, V78-S88	BLIMPS_BLOCKS
					Major intrinsic protein family signature PR00783: K24-C43, F64-S88, K101-V120	BLIMPS_PRINTS

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					TRANSMEMBRANE TRANSPORT PROTEIN AQUAPORIN INTRINSIC CHANNEL MEMBRANE WATER TONOPLAST FAMILY PD000295: L18-S169	BLAST_PRODOM
					MIP FAMILY DM00228 P47862 15-263: L16-S169	BLAST_DOMO
					MIP FAMILY DM00228 S9266 15-263: L16-S169	BLAST_DOMO
					MIP FAMILY DM00228 P43549 340-587: K24-S169	BLAST_DOMO
					MIP FAMILY DM00228 P11244 1-253: S20-A163	BLAST_DOMO
					MIP family signature: H82-A90	MOTIFS
36	7503977CD1	223	S191 T93 T112 T140 T182	N54 N116	PROTEIN MELASTATIN CHROMOSOME TRANSMEMBRANE C05C12.3 T01H8.5 IF54D1.5 IV PD018035: K8-K209	BLAST_PRODOM
37	7505084CD1	394	S99 S242 S394 T47 T50 T54 T127	N243 N247 N301	signal_cleavage: M1-A41	SPSCAN
					Sodium: solute symporter family: Y58-G388	HMIMER_PFAM
					sss: SSS sodium solute transporter superfamily: Y58-S385	HMIMER_TIGRFAM
					Cytosolic domains: T47-M65, T126-G137, T203-T208, C287-K306 Transmembrane domains: I29-S46, V66-A88, L103-V125, G138-V160, A180-Y202, L209-G231, L269-W286, G307-V329 Non-cytosolic domains: M1-D28, G89-E102, D161-L179, L232-D268, S330-S394	TMHMMER
					Sodium: solute symporter family proteins BL00456: Y35-G89, M111-R140, L173-G227	BLIMPS_BLOCKS

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					Sodium: solute symporter family signatures: Q170-T217	PROFILES CAN
					TRANSMEMBRANE TRANSPORT PERMEASE PROTEIN SODIUM SYMPORTER PROLINE COTRANSPORTER SYMPORTER GLYCOPROTEIN PD000991: Y58-I383	BLAST_PROD OM
					SODIUM: SOLUTE SYMPORTER FAMILY DM00745 P13866 24-561:D28-P370	BLAST_DOMO
					SODIUM: SOLUTE SYMPORTER FAMILY DM00745 A53582 24-561:D28-P370	BLAST_DOMO
					SODIUM: SOLUTE SYMPORTER FAMILY DM00745 P53790 24-561:D28-P370	BLAST_DOMO
					SODIUM: SOLUTE SYMPORTER FAMILY DM00745 S48858 24-561:D28-P370	BLAST_DOMO
38	7506950CD1	202	S64 S81 T83 T157	N38 N138	signal_cleavage: M1-L25	SPSCAN
					Signal Peptide: M10-A28	HMIMER
					Neurotransmitter-gated ion-channel ligand binding domain: F42-V198	HMIMER_PFAM
					Neurotransmitter-gated ion-channels proteins BL00236: V68-K105, I121-N130	BLIMPS_BLOCKS
					Neurotransmitter-gated ion channel family signature PR00252: T88-F104, K120-G131	BLIMPS_PRINTS
					Gamma-aminobutyric-acid receptor alpha subunit signature PR01079: T40-D51, G60-F77, F104-L116	BLIMPS_PRINTS
					CHANNEL IONIC TRANSMEMBRANE GLYCOPROTEIN POSTSYNAPTIC MEMBRANE RECEPTOR PRECURSOR SIGNAL PROTEIN PD000153: R44-P164	BLAST_PROD OM

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					GAMMAAMINOBUTYRICACID RECEPTOR ALPHA2 SUBUNIT PRECURSOR GABAA POSTSYNAPTIC MEMBRANE IONIC CHANNEL PD151117: M1-T43	BLAST_PRODOM
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00560 P08219 14-456: E32-P164	BLAST_DOMO
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00560 P20237 20-556: F42-P164	BLAST_DOMO
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00560 P16305 4-443: L14-P164	BLAST_DOMO
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00560 P23574 26-465: T43-S177	BLAST_DOMO
39	750695 CD1	337	S64 S81 S233 S310 S315 T83 T157 T190 T229 T283 T328	N38 N138 N201	signal_cleavage: M1-L25	SPSCAN
					Signal Peptide: M10-A28	HMMER
					Neurotransmitter-gated ion-channel ligand binding domain: F42-I250	HMMER_PFAM
					LIC: Cation transporter family protein: F12-S337	HMMER_TIGRFAM
					Cytosolic domain: M1-K249	TMHMMER
					Transmembrane domain: I250-F272	
					Non-cytosolic domain: W273-S337	
					Neurotransmitter-gated ion-channels proteins BL00236: V68-K105, I121-N130, D151-Y189, Y237-S278	BLIMPS_BLOCKS
					Neurotransmitter-gated ion-channels signature: L146-T199	PROFILESCAN

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					Neurotransmitter-gated ion channel family signature PR00252: T88-F104, K120-G131, C166-C180, F244-Q256	BLIMPS_PRINTS
					Gamma-aminobutyric-acid receptor alpha subunit signature PR01079: T40-D51, G60-F77, F104-L116, Y196-V208, S213-G235	BLIMPS_PRINTS
					CHANNEL IONIC TRANSMEMBRANE GLYCOPROTEIN POSTSYNAPTIC MEMBRANE RECEPTOR PRECURSOR SIGNAL PROTEIN PD000153: R44-R282	BLAST_PRODOM
					GAMMAAMINOBUTYRICACID RECEPTOR ALPHA2 SUBUNIT PRECURSOR GABAA POSTSYNAPTIC MEMBRANE IONIC CHANNEL PD151117: M1-T43	BLAST_PRODOM
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00560[P08219]14-456: E32-F285	BLAST_DOMO
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00560[P20237]20-556: F42-F285	BLAST_DOMO
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00560[P16305]4-443: L14-F285	BLAST_DOMO
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00560[P23574]26-465: T43-T283	BLAST_DOMO
					Neurotransmitter-gated ion-channels signature: C166-C180	MOTIFS
40	7506954CD1	114	S87 S92 T105	N38	signal_cleavage: M1-L25	SPSCAN
					Signal Peptide: M10-A28	HMMER
					Gamma-aminobutyric-acid receptor alpha subunit signature PR01079: T40-D51	BLIMPS_PRINTS

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					GAMMAAMINOBUTYRICACID RECEPTOR ALPHA2 SUBUNIT PRECURSOR GABAA POSTSYNAPTIC MEMBRANE IONIC CHANNEL PD151117: M1-T43	BLAST_PRODOM
41	7506956CD1	400	S64 S81 S248 S364 T83 T157 T190 T229 T260 T287 T341	N38 N138 N201 N326	signal_cleavage: M1-L25	SPSCAN
					Signal Peptide: M10-A28	HMMER
					Neurotransmitter-gated ion-channel ligand binding domain: F42-N251	HMMER_PFAM
					Neurotransmitter-gated ion-channel transmembrane domain: T229-W386	HMMER_PFAM
					LIC: Cation transporter family protein: F12-Y389	HMMER_TIGRFAM
					Cytosolic domain: T287-R371	TMHMMER
					Transmembrane domains: W264-F286, I372-Y389	
					Non-cytosolic domains: M1-D263, L390-P400	
					Neurotransmitter-gated ion-channels proteins BL00236: V68-K105, I121-N130, D151-Y189	BLIMPS_BLOCKS
					Neurotransmitter-gated ion-channels signature: L146-T199	PROFILESCAN
					Neurotransmitter-gated ion channel family signature PR00252: T88-F104, K120-G131, C166-C180	BLIMPS_PRINTS
					Gamma-aminobutyric acid (GABA) receptor signature PR00253: E228-A249, M262-V283, M369-Y389	BLIMPS_PRINTS

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					Gamma-aminobutyric-acid receptor alpha subunit signature PR01079: T40-D51, G60-F77, F104-L116, Y196-V208, S213-G235, K255-V268, T359-R371, V384-V395	BLIMPS_PRINTS
					CHANNEL IONIC TRANSMEMBRANE GLYCOPROTEIN POSTSYNAPTIC MEMBRANE RECEPTOR PRECURSOR SIGNAL PROTEIN PD000153: R44-T241, G235-Y285	BLAST_PRODOM
					GAMMAAMINOBUTYRICACID RECEPTOR SUBUNIT PRECURSOR GABAA POSTSYNAPTIC MEMBRANE IONIC CHANNEL GLYCOPROTEIN PD000235: K288-P349	BLAST_PRODOM
					GAMMAAMINOBUTYRICACID RECEPTOR ALPHA2 SUBUNIT PRECURSOR GABAA POSTSYNAPTIC MEMBRANE IONIC CHANNEL PD151117: M1-T43	BLAST_PRODOM
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00560 P08219 14-456: E32-T241, I225-L396	BLAST_DOMO
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00560 P20237 20-556: F42-M242, I225-T287, P353-E393	BLAST_DOMO
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00560 P16305 4-443: L14-M242, I225-E393	BLAST_DOMO

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00560 P23574 26-465: T43-M242, I225-V309, V363-L390 ATP/GTP-binding site motif A (P-loop): G290-S297	BLAST_DOMO MOTIFS
					Neurotransmitter-gated ion-channels signature: C166-C180	MOTIFS
42	7506959CD1	403	S64 S81 S251 S367 T83 T157 T263 T290 T344	N38 N138 N329	signal_cleavage: M1-L25 Signal Peptide: M10-A28 Neurotransmitter-gated ion-channel ligand binding domain: F42-N254 Neurotransmitter-gated ion-channel transmembrane domain: T209-W389 LIC: Cation transporter family protein: F12-Y392	SPSCAN HMMER HMMER_PFAM HMMER_PFAM HMMER_TIGRFAM
					Cytosolic domains: N227-P232, T290-R374 Transmembrane domains: Y204-L226, A233-A252, W267-F289, I375-Y392 Non-cytosolic domains: M1-G203, R253-D266, L393-P403	TMHMMER
					Neurotransmitter-gated ion-channels proteins BL00236: V68-K105, I121-N130, D151-Y189, Y189-S230	BLIMPS_BLOCKS
					Neurotransmitter-gated ion-channels signature: L146-R200	PROFILES SCAN

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					Neurotransmitter-gated ion channel family signature PR00252: T88-F104, K120-G131, C166-C180, F196-Q208	BLIMPS_PRINTS
					Gamma-aminobutyric acid (GABA) receptor signature PR00253: F205-W225, V231-A252, M265-V286, M372-Y392	BLIMPS_PRINTS
					Gamma-aminobutyric-acid receptor alpha subunit signature PR01079: T40-D51, G60-F77, F104-L116, K258-V271, T362-R374, V387-V398	BLIMPS_PRINTS
					CHANNEL IONIC TRANSMEMBRANE GLYCOPROTEIN POSTSYNAPTIC MEMBRANE RECEPTOR PRECURSOR SIGNAL PROTEIN PD000153: R44-K201, L182-Y288	BLAST_PRODOM
					GAMMAAMINOBUTYRICACID RECEPTOR SUBUNIT PRECURSOR GABAA POSTSYNAPTIC MEMBRANE IONIC CHANNEL GLYCOPROTEIN PD000235: K291-P352	BLAST_PRODOM
					GAMMAAMINOBUTYRICACID RECEPTOR ALPHA2 SUBUNIT PRECURSOR GABAA POSTSYNAPTIC MEMBRANE IONIC CHANNEL PD151117: M1-T43	BLAST_PRODOM
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00560 P08219 14-456: E32-T190, E188-L399	BLAST_DOMO
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00560 P20237 20-556: F42-Y189, E188-T290, P356-E396	BLAST_DOMO

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00560 P16305 4-443: L14-Y189, L155-E396	BLAST_DOMO
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00560 P23574 26-465: T43-Y189, S186-V312, V366-L393	BLAST_DOMO
					ATP/GTP-binding site motif A (P-loop): G293-S300	MOTIFS
					Neurotransmitter-gated ion-channels signature: C166-C180	MOTIFS
43	7506960CD1	66		N38	signal_cleavage: M1-L25	SPSCAN
					Signal Peptide: M10-A28	HMMER
					Gamma-aminobutyric-acid receptor alpha subunit signature PR01079: T40-D51	BLIMPS_PRINTS
					GAMMAAMINOBUTYRICACID RECEPTOR ALPHA2 SUBUNIT PRECURSOR GABAA POSTSYNAPTIC MEMBRANE IONIC CHANNEL PD151117: M1-T43	BLAST_PRODROM
44	7510540CD1	89	S42 S51	N37	signal_cleavage: M1-G20	SPSCAN
					Cytosolic domain: A33-R89	TMHMMER
					Transmembrane domain: L10-N32	
					Non-cytosolic domain: M1-T9	
					Sugar transporter signature PR00171: S21-I31	BLIMPS_PRINTS
					GLUCOSE TRANSPORTER TYPE LIVER	BLAST_PRODROM
					DUPLICATION TRANSMEMBRANE SUGAR TRANSPORT GLYCOPROTEIN MULTIGENE PD002509: M1-Q36	
45	7510545CD1	146	S100 T8 T73	N19	signal_cleavage: M1-P62	SPSCAN
					Signal Peptide: M46-A63	HMMER

Table 3

SEQ ID NO.	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					Cytosolic domain: T73-G146 Transmembrane domain: V50-G72 Non-cytosolic domain: M1-S49	TMHMMER
					E1-E2 ATPases phosphorylation site proteins BL00154: I57-G93, T95-V113	BLIMPS_BLOCKS
					E1-E2 ATPases phosphorylation site: A81-R129	PROFILES SCAN
					P-type cation-transporting atpase superfamily signature PR00119: C99-V113	BLIMPS_PRINTS
					Sodium/potassium-transporting ATPase signature PR00121: L92-V113	BLIMPS_PRINTS
					ATPASE HYDROLASE TRANSMEMBRANE PHOSPHORYLATION ATPBINDING TRANSPORT PUMP CALCIUM MAGNESIUM MEMBRANE PD000132: P36-I118	BLAST_PROD OM
					E1-E2 ATPASES PHOSPHORYLATION SITE DM00115 P18596 43-795: E22-S49, S49-E123	BLAST_DOMO
					E1-E2 ATPASES PHOSPHORYLATION SITE DM00115 P04191 43-795: S49-E123	BLAST_DOMO
					E1-E2 ATPASES PHOSPHORYLATION SITE DM00115 P22700 43-795: E2-E123	BLAST_DOMO
					E1-E2 ATPASES PHOSPHORYLATION SITE DM00115 P35316 43-799: E2-A127	BLAST_DOMO
					E1-E2 ATPases phosphorylation site: D101-T107	MOTIFS
46	7510654CD1	353	S99 T2 T205 T281		signal_cleavage: M1-G41	SPSCAN
					Signal Peptide: M1-G41	HMMER
					Sugar (and other) transporter: A29-P353	HMMER_PFAM
					SP: Sugar transporter: M1-V350	HMMER_TIGRFAM

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					Cytosolic domains: M1-V26, D92-K97, Y150-G155, P206-P256, D314-R319 Transmembrane domains: F27-P49, A69-V91, L98-A117, R127-A149, L156-V178, W183-T205, F257-A279, A294-M313, L320-H342 Non-cytosolic domains: A50-A68, Q118-G126, L179-R182, E280-L293, L343-P353	TMHMMER
					Sugar transport proteins BL00216: L123-A172	BLIMPS_BLOCKS
					Sugar transport proteins signatures: V108-L174, L293-Q344	PROFLESCAN
					Sugar transporter signature PR00171: G41-I51, L124-V143, Q267-F277	BLIMPS_PRINTS
					Glucose transporter signature PR00172: F257-Y278, S292-M313	BLIMPS_PRINTS
					SUGAR TRANSPORT PROTEINS DM00135[P47843]104-456: G110-L341	BLAST_DOMO
					SUGAR TRANSPORT PROTEINS DM00135[P32037]104-456: G110-L341	BLAST_DOMO
					SUGAR TRANSPORT PROTEINS DM00135[Q07647]104-456: G110-L341	BLAST_DOMO
					SUGAR TRANSPORT PROTEINS DM00135[P47842]104-456: G110-L341	BLAST_DOMO
					Sugar transport proteins signature 1: G87-S104, A309-S325	MOTIFS
					Sugar transport proteins signature 2: L129-R154	MOTIFS

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
47	7510660CD1	1155	S205 S224 S306 S328 S612 S634 S734 S757 S809 S887 S1085 S1110 T66 T438 T567 T596 T603 T868 T871 T919 T1148	N150 N287 N420 N502 N1058	haloacid dehalogenase-like hydrolase: V527-A843	HMMER_Pfam
					Cytosolic domains: M1-T66, V122-T444, L1030-P1054, S1110-S1155 Transmembrane domains: V67-W89, A99-S121, F445-I464, I1007-Y1029, S1055-Y1077, L1092-G1109 Non-cytosolic domains: G90-E98, E465-N1006, K1078-P1091	TMHMMER
					E1-E2 ATPases phosphorylation site proteins BL00154: V489-G525, V527-V545, E681-F721, T817-L840, A912-M945	BLIMPS_BLOCKS
					P-type cation-transporting atpase superfamily signature PR00119: D348-E362, C531-V545, T697-D707, C820-L839	BLIMPS_PRINTS
					PROBABLE CALCIUMTRANSPORTING ATPASE HYDROLASE CALCIUM TRANSPORT TRANSMEMBRANE PHOSPHORYLATION MAGNESIUM ATPBINDING PD023991: D901-G1147	BLAST_PRODROM

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					ATPASE PROBABLE CALCIUM TRANSPORTING HYDROLASE CALCIUM TRANSPORT TRANSMEMBRANE PHOSPHORYLATION MAGNESIUM ATP BINDING PD150086: G208-V267	BLAST_PRODROM
					ATPASE HYDROLASE TRANSMEMBRANE PHOSPHORYLATION ATP BINDING TRANSPORT PUMP CALCIUM MAGNESIUM MEMBRANE PD000132: I312-V548, I674-L719	BLAST_PRODROM
					E1-E2 ATPASES PHOSPHORYLATION SITE DM00115 P37367 60-746: I312-V390, V414-G550, D581-L839	BLAST_DOMO
					E1-E2 ATPASES PHOSPHORYLATION SITE DM00115 A46284 47-821: E316-E566, L595-L839	BLAST_DOMO
					E1-E2 ATPASES PHOSPHORYLATION SITE DM00115 S27763 47-821: E316-E566, L595-L839	BLAST_DOMO
					E1-E2 ATPASES PHOSPHORYLATION SITE DM00115 P39168 83-733: W309-V391, T388-L839	BLAST_DOMO
					E1-E2 ATPases phosphorylation site: D533-T539	MOTIFS
48	7510661CD1	606	S205 S224 S306 S328 T66 T438 T567 T596	N150 N287 N420 N502	signal_cleavage: M1-G46	SPSCAN
					Cytosolic domains: M1-T66, V122-T444 Transmembrane domains: V67-W89, A99-S121, F445-I464	TMHMMER
					Non-cytosolic domains: G90-E98, E465-P606 E1-E2 ATPases phosphorylation site proteins BL00154: V489-G525, V527-V545	BLIMPS_BLOCKS

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					E1-E2 ATPases phosphorylation site: I521-S561 ATPASE PROBABLE CALCIUMTRANSPORTING HYDROLASE CALCIUM TRANSPORT TRANSMEMBRANE PHOSPHORYLATION MAGNESIUM ATPBINDING PD150086: G208-V267	PROFILESCAN BLAST_PRODOM
					ATPASE HYDROLASE TRANSMEMBRANE PHOSPHORYLATION ATPBINDING TRANSPORT PUMP CALCIUM MAGNESIUM MEMBRANE PD000132: I312-V548	BLAST_PRODOM
					E1-E2 ATPases phosphorylation site: D533-T539	MOTIFS
49	7510680CD1	462	S13 S18 S225 S314 S373 T33 T323 T351	N229 N249	2A0119: cation transport protein: M1-Q460 Cytosolic domains: M1-I48, D109-S120, R202-Q283, R370-T381, I451-K462 Transmembrane domains: A49-V71, V86-A108, F121-L143, V179-W201, I284-L306, M347-G369, A382-L404, I428-P450 Non-cytosolic domains: S72-Q85, R144-Q178, E307-T346, R405-S427	HMMER_TIGRFAM TMHMMER
					SUGAR TRANSPORT PROTEINS DM00032[P30638]80-152: R45-K115 do VESICLE; SYNAPTIC; SV2; FORM; DM08835[S34961]180-344: I119-N249	BLAST_DOMO BLAST_DOMO
50	7505145CD1	366	S271 S287 S317 T10 T136 Y61	N156	2_A_01_02: Multidrug resistance protein: G90-T225	HMMER_TIGRFAM

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					Cytosolic domains: P47-S85, T136-Q175, P223-R274 Transmembrane domains: V24-L46, V86-G108, P118-A135, G176-L198, A203-L222, L275-T297 Non-cytosolic domains: M1-R23, A109-R117, P199-M202, H298-A366	TMHMMER
					Tetracycline resistance protein signature PR01035: L34-L50, M177-P199, A203-P223	BLIMPS_PRINTS
					TETRACYCLINE TRANSPORTERLIKE PROTEIN TRANSPORT MRNA PD023345: L226-S304	BLAST_PRODROM
					TETRACYCLINE TRANSPORTERLIKE PROTEIN TRANSPORT MRNA PD029169: E51-G89	BLAST_PRODROM
					TETRACYCLINE TRANSPORTERLIKE PROTEIN TRANSPORT MRNA PD025998: M1-F29	BLAST_PRODROM
51	7505162CD1	295	S37 S75 S164 S210 T216		2A0104: phosphoglycerate transporter protein: F18-V285 Cytosolic domains: M1-Y6, D72-R77, T157-T168, K240-Q295 Transmembrane domains: G7-F26, L49-S71, W78-V100, F134-A156, L169-H188, L220-V239 Non-cytosolic domains: N27-D48, P101-Q133, N189-E219	HMMER_TIGRFAM TMHMMER
					glpT family of transporters proteins BL00942: M17-K29, L44-L86, W128-L147, L169-E205, S210-F250	BLIMPS_BLOCKS

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					GLPT FAMILY OF TRANSPORTERS DM02439 P09836 1-401: Y6-W281	BLAST_DOMO
					GLPT FAMILY OF TRANSPORTERS DM02439 P37948 1-403: Y6-S258	BLAST_DOMO
					GLPT FAMILY OF TRANSPORTERS DM02439 P08194 1-403: Y6-K255	BLAST_DOMO
					GLPT FAMILY OF TRANSPORTERS DM02439 P12681 1-405: Y6-T216	BLAST_DOMO
52	7505469CD1	229	S22 S66 Y197	N18	Cytosolic domains: M1-E44, E100-S111, K186-Y197 Transmembrane domains: I45-P67, Y77-A99, Y112-V134, Y163-V185, A198-P220 Non-cytosolic domains: K68-S76, V135-P162, W221-L229	TMHMMER
					Amino acid permeases proteins BL00218: L48-S76, S80-S111, V180-V208	BLIMPS_BLOCKS
					MYELOBLAST KIAA0245 PD078048: M1-Q40	BLAST_PRODOM
					do ANTIPTORTER; ORNITHINE; PUTRESCINE; TRANSPORT; DM01125 P45539 1-318: T38-L211	BLAST_DOMO
53	7505475CD1	637	S30 S50 S134 S249 S353 S491 T111 T206 T558 T572 T624	N71 N84 N91 N109 N130 N241 N436 N544 N576	Signal Peptide: M26-A45, M26-M51	HMMER
					ABC transporter: G507-K637	HMMER_PFAM

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					Cytosolic domains: M1-E29, K244-F263, S319-K324, D418-K637 Transmembrane domains: S30-S49, E221-T243, W264-I286, G296-L318, A325-F347, T395-F417 Non-cytosolic domains: S50-N220, T287-T295, Y348-Y394	TMHMMER
					ABC TRANSPORTERS FAMILY DM00008 P41233 839-1045: I478-I635	BLAST_DOMO
					ABC TRANSPORTERS FAMILY DM00008 P34358 611-816: I478-I635	BLAST_DOMO
					ABC TRANSPORTERS FAMILY DM00008 P41233 1851-2058: I478-I635	BLAST_DOMO
					ABC TRANSPORTERS FAMILY DM00008 P44785 2-216: I478-I635	BLAST_DOMO
					ATP/GTP-binding site motif A (P-loop): G514-S521	MOTIFS
54	7505568CD1	90		N74	signal_cleavage: M1-G66 Cytosolic domain: M1-S55 Transmembrane domain: L56-V78 Non-cytosolic domain: N79-Q90 Sugar transporter signature PR00171: S68-V78	SPSCAN TMHMMER BLIMPS_PRINTS
55	7506953CD1	327	S109 S175 S291 T66 T105 T187 T214 T268	N38 N77 N253	signal_cleavage: M1-L25 Signal Peptide: M10-A28 Neurotransmitter-gated ion-channel transmembrane domain: T133-W313 LIC: Cation transporter family protein: F12-Y316	SPSCAN HMMER HMMER_PFAM HMMER_TIGRFAM

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					Cytosolic domains: M1-K125, T214-R298 Transmembrane domains: I126-F148, W191-F213, I299-Y316 Non-cytosolic domains: W149-D190, L317-P327 Neurotransmitter-gated ion-channels proteins BL00236: Y113-S154 Gamma-aminobutyric acid (GABA) receptor signature PR00253: F129-W149, V155-A176, M189-V210, M296-Y316 Gamma-aminobutyric-acid receptor alpha subunit signature PR01079: Y72-V84, S89-G111, K182-V195, T286-R298, V311-V322 CHANNEL IONIC TRANSMEMBRANE GLYCOPROTEIN POSTSYNAPTIC MEMBRANE RECEPTOR PRECURSOR SIGNAL PROTEIN PD000153: Y65-Y212 GAMMAAMINOBTYRICACID RECEPTOR SUBUNIT PRECURSOR GABAA POSTSYNAPTIC MEMBRANE IONIC CHANNEL GLYCOPROTEIN PD000235: K215-P276	TMHMMER
						BLIMPS_BLOCKS
						BLIMPS_PRINTS
						BLIMPS_PRINTS
						BLAST_PRODUM
						BLAST_PRODUM
					GAMMAAMINOBTYRICACID RECEPTOR ALPHA2 SUBUNIT PRECURSOR GABAA POSTSYNAPTIC MEMBRANE IONIC CHANNEL PD151117: M1-T43 NEUROTRANSMITTER-GATED ION-CHANNELS DM00560 P08219 14-456: E32-T66, A64-L323	BLAST_PRODUM
						BLAST_DOMO

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00560 P20237 20-556: R44-T214, P280-E320	BLAST_DOMO
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00560 P16305 4-443: R44-E320	BLAST_DOMO
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00560 P23574 26-465: T43-V84, Y65-V236, V290-L317	BLAST_DOMO
					ATP/GTP-binding site motif A (P-loop): G217-S224	MOTIFS
56	7510176CD1	40			signal_cleavage: M1-T32	SPSCAN
					Cytosolic domain: M1-R12	TMHMMER
					Transmembrane domain: F13-I35	
					Non-cytosolic domain: L36-R40	
57	7510541CD1	104	S41 T60	N74	Cytosolic domain: H101-L104	TMHMMER
					Transmembrane domain: A78-L100	
					Non-cytosolic domain: M1-N77	
					TRANSPORTER PROTEIN PD182518: M1-M70	BLAST_PRODROM
58	7510923CD1	296	S41 S254 T60 Y134	N74 N247 N248 N252	Cytosolic domains: A90-G95, K165-D184, K234-Q296	TMHMMER
					Transmembrane domains: S67-Y89, I96-L118, L143-I164, W185-M207, G211-Y233	
					Non-cytosolic domains: M1-T66, K119-K142, R208-L210	
					TRANSPORTER PROTEIN PD182518: M1-M70	BLAST_PRODROM
					TRANSPORTER PROTEIN PD138403: Y233-Q285	BLAST_PRODROM

Table 3

SEQ ID	Incye Polypeptide	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
NO:	ID				ACID AMINO PROTEIN TRANSPORTER PERMEASE TRANSMEMBRANE INTERGENIC REGION PUTATIVE PROLINE PD001875: D61-Y233	BLAST_PRODUM
59	7510984CD1	1364	S55 S347 S408 S487 S532 S615 S742 S774 S858 S961 S980 S1138 S1342 T151 T200 T304 T520 T524 T525 T600 T700 T758 T760 T783 T888 T913 T943 T945 T950 T1213 T1321	N10 N406 N698 N781 N829 N985 N1050	Cytosolic domains: S53-N72, H125-L135, R191-L301, Q369-Q427, A478-A537, R598-V1063, Q1179-E1249, N1296-Y1364 Transmembrane domains: A30-G52, L73-S95, H105-Y124, L136-L158, R168-I190, S302-V324, F351-L368, L428-I450, I455-V477, I538-V560, V575-V597, Y1064-V1086, V1156-I1178, V1250-L1272, L1276-L1295 Non-cytosolic domains: M1-D29, D96-L104, D159-L167, D325-E350, L451-Y454, G561-S574, E1087-A1155, H1273-E1275	TMHMMER
					ABC transporter transmembrane region.: L1012-V1299, L318-L590	HMMER_PFAM
					ABC transporter: G706-G906	HMMER_PFAM
					ATPases associated with a variety of cellular proteins: R705-L914	HMMER_SMART
					ABC transporters family proteins BL00211: I711-L722, L830-D861	BLIMPS_BLOCKS
					ABC transporters family signature: I812-D861	PROFILES CAN
					Presenilin 1 signature PR01073: D964-E975	BLIMPS_PRINTS
					Sulphonylurea receptor family signature PR01092: G25-G52, W65-F79, V122-L136, V204-K227, V357-V379	BLIMPS_PRINTS

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					Sulphonylurea receptor type 1 family signature PR01093: E9-Q19, A269-D277, A617-P629, Y638-E654, A1047-C1057	BLIMPS_PRINTS
					SULFONYLUREA RECEPTOR ATPBINDING TRANSPORT 2B 2A TRANSMEMBRANE PHOSPHORYLATION GLYCOPROTEIN 1B PD005449: M1-R297	BLAST_PRODOM
					SULFONYLUREA RECEPTOR ATPBINDING TRANSPORT TRANSMEMBRANE PHOSPHORYLATION GLYCOPROTEIN 1B ALTERNATIVE SPLICING PD011659: F591-T695	BLAST_PRODOM
					SULFONYLUREA RECEPTOR ATPBINDING TRANSPORT 2B 2A TRANSMEMBRANE PHOSPHORYLATION GLYCOPROTEIN 1B PD005248: T913-I1010	BLAST_PRODOM
					SULFONYLUREA RECEPTOR ATPBINDING TRANSPORT TRANSMEMBRANE PHOSPHORYLATION GLYCOPROTEIN 1B PD151487: R298-Y356	BLAST_PRODOM
					do RESISTANCE; MULTIDRUG; SAUROLEISHMANIA; C3F10.11C; DM01525 Q09427 906-1342: T907-L1334	BLAST_DOMO
					do RESISTANCE; MULTIDRUG; SAUROLEISHMANIA; C3F10.11C; DM01742 Q09427 213-630: G214-Q632	BLAST_DOMO
					ABC TRANSPORTERS FAMILY DM00008 Q09427 690-904: D691-G906	BLAST_DOMO

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					do RESISTANCE; MULTIDRUG; SAUROLEISHMANIA; C3F10.11C; DM01525[P33527/868-1291: L967-S1325	BLAST_DOMO
					ABC transporters family signature: L830-L844	MOTIFS
					ATP/GTP-binding site motif A (P-loop): G713-S720	MOTIFS

Table 4

Polynucleotide SEQ ID NO./ Incyte ID/ Sequence Length	Sequence Fragments
60/7509332CB1/895	1-895, 4-444, 26-450, 55-264, 133-264, 133-505, 133-849, 229-505, 354-495, 406-503
61/7509102CB1/1623	1-932, 1-986, 1-1623, 447-748, 451-653, 630-1189, 981-1215, 981-1326, 981-1342, 981-1379, 981-1419, 981-1425, 984-1395, 1515-1611
62/7509132CB1/1802	1-477, 39-850, 61-1802, 581-1046, 659-889, 662-1278, 662-1286, 712-1634, 716-1634, 736-1280, 750-1240, 750-1634, 802-1634, 816-1055, 818-923, 825-1468, 862-1280, 930-1634, 958-1233, 959-1634, 961-1236, 963-1524, 1086-1327, 1123-1418, 1139-1634, 1178-1455, 1182-1262, 1182-1409, 1182-1423, 1182-1436, 1373-1609, 1373-1770, 1412-1649
63/7509136CB1/2139	1-177, 1-250, 1-374, 1-457, 1-468, 1-495, 1-2139, 77-667, 77-690, 77-693, 77-841, 78-705, 111-316, 216-333, 242-443, 357-459, 559-1332, 703-1007, 703-1176, 703-1332, 704-1330, 705-1332, 721-1332, 723-1239, 730-943, 763-1332, 781-1320, 787-1364, 796-954, 804-1373, 804-1418, 807-895, 815-1062, 817-1359, 827-1365, 838-1000, 842-1017, 866-1389, 871-1315, 888-1385, 901-1397, 936-1497, 956-1223, 973-1509, 976-1303, 977-1526, 977-1565, 985-1510, 986-1521, 987-1843, 998-1326, 1002-1542, 1022-1717, 1033-1563, 1060-1537, 1080-1689, 1081-1655, 1082-1608, 1096-1612, 1106-1719, 1121-1682, 1130-1652, 1145-1666, 1184-1446, 1189-1675, 1202-1462, 1202-1566, 1205-1577, 1207-1502, 1207-1552, 1214-1552, 1305-1802, 1320-1800, 1322-1775, 1338-1633, 1338-1635, 1339-1801, 1354-1848, 1371-2110, 1399-1552, 1419-1641, 1419-1661, 1445-2098, 1451-1709, 1459-1753, 1470-1768, 1477-2105, 1567-1672, 1567-1674, 1567-1681, 1567-1687, 1567-1688, 1572-2139, 1688-2139, 1741-2105, 1808-2010, 1808-2134, 1861-2105, 1986-2093, 1986-2105, 1991-2105, 1992-2105, 1996-2105
64/7509178CB1/1461	1-252, 1-703, 1-913, 1-1459, 24-252, 248-804, 288-523, 351-1163, 361-1164, 419-1164, 420-1164, 444-1164, 452-699, 463-1098, 465-1165, 505-1163, 506-1034, 506-1036, 509-1164, 523-1164, 528-830, 528-897, 540-1164, 570-1420, 571-1461, 575-1461, 578-1112, 594-1461, 601-1434, 602-1461, 620-1461, 629-1460, 653-914, 670-1173, 672-1164, 684-1190, 687-906, 688-906, 716-1160, 716-1359, 716-1376, 726-1321, 773-1289, 798-1461, 799-1461, 811-1343, 833-1106, 833-1428, 953-1395, 1037-1223, 1144-1293, 1204-1459

Table 4

Polynucleotide SEQ ID NO./ Incyte ID/ Sequence Length	Sequence Fragments
65/7509214CB1/738	1-562, 1-738, 5-116, 41-139, 135-289, 135-305, 135-324, 135-359, 135-382, 135-386, 135-415, 135-430, 135-579, 135-623, 135-727, 136-386, 138-561, 141-415, 142-393, 146-634, 146-738, 147-612, 149-384, 149-394, 149-434, 150-372, 151-405, 151-417, 151-440, 152-576, 164-324, 165-383, 166-359, 166-738, 167-324, 170-398, 184-296, 186-442, 187-398, 187-433, 190-463, 203-434, 203-651, 204-468, 204-738, 205-470, 205-475, 209-482, 209-738, 213-481, 214-350, 216-475, 217-468, 221-738, 222-725, 230-506, 231-720, 233-728, 234-737, 238-496, 245-540, 246-479, 246-728, 249-736, 250-536, 254-723, 256-705, 256-730, 261-722, 261-723, 263-724, 269-738, 270-719, 271-505, 272-525, 273-726, 275-728, 277-725, 278-449, 278-550, 280-485, 280-738, 281-724, 282-508, 282-738, 283-542, 283-722, 283-725, 283-728, 284-699, 284-728, 286-580, 289-533, 289-554, 289-643, 291-556, 292-721, 296-722, 296-738, 298-724, 302-730, 303-721, 304-738, 305-720, 308-721, 308-722, 309-542, 309-722, 309-728, 310-734, 310-738, 311-588, 312-736, 313-738, 314-385, 314-573, 315-571, 318-723, 320-553, 322-721, 324-637, 325-722, 327-732, 328-592, 328-709, 328-738, 329-722, 330-727, 330-728, 331-738, 334-723, 335-723, 335-725, 337-723, 338-722, 341-606, 342-573, 342-640, 344-510, 345-725, 345-734, 347-581, 347-660, 347-726, 348-719, 350-721, 352-721, 352-738, 354-654, 355-651, 358-588, 358-703, 360-687, 361-726, 363-724, 364-716, 366-722, 369-725, 370-726, 371-581, 374-703, 380-718, 381-589, 381-722, 382-720, 382-723, 382-725, 384-725, 385-661, 385-728, 389-638, 390-539, 390-618, 393-725, 393-738, 409-720, 413-722, 413-723, 414-696, 414-737, 418-722, 421-726, 426-676, 426-683, 426-685, 426-711, 426-722, 427-721, 427-728, 428-696, 428-719, 429-645, 429-736, 431-726, 431-736, 432-722, 432-723, 432-724, 433-728, 434-722, 434-727, 436-722, 437-722, 437-725, 440-738, 443-722, 444-713, 446-728, 447-722, 447-725, 448-718, 448-721, 448-725, 448-728, 449-724, 450-722, 462-727, 462-728, 467-722, 472-728, 473-722, 474-737, 476-711, 477-721, 478-728, 479-722, 479-723, 482-721, 483-719, 487-722, 489-720, 497-724, 498-723, 501-722, 501-737, 502-738, 503-722, 505-727, 510-722, 511-723, 512-728, 599-731, 610-738, 611-722, 628-728, 629-738, 648-722, 671-722

Table 4

Polynucleotide SEQ ID NO./ Incyte ID/ Sequence Length	Sequence Fragments
66/7509244CB1/2106	1-177, 1-250, 1-374, 1-457, 1-468, 1-495, 1-2106, 77-667, 77-690, 77-693, 77-819, 77-820, 77-832, 77-838, 77-871, 77-878, 77-886, 77-893, 77-896, 77-980, 77-988, 77-999, 77-1002, 78-714, 78-758, 78-857, 78-858, 78-896, 111-316, 216-333, 241-888, 242-443, 508-1299, 705-737, 726-994, 989-1509, 996-1684, 1000-1530, 1027-1504, 1047-1656, 1048-1622, 1049-1575, 1063-1579, 1073-1686, 1088-1649, 1097-1619, 1112-1633, 1151-1413, 1156-1642, 1169-1429, 1169-1533, 1172-1544, 1174-1469, 1174-1519, 1181-1519, 1272-1769, 1287-1767, 1289-1742, 1305-1600, 1305-1602, 1306-1768, 1321-1815, 1338-2077, 1366-1519, 1386-1608, 1386-1628, 1412-2065, 1418-1676, 1426-1720, 1437-1735, 1444-2072, 1534-1639, 1534-1641, 1534-1648, 1534-1654, 1534-1655, 1539-2106, 1655-2106, 1708-2072, 1775-1977, 1775-2101, 1828-2072, 1953-2060, 1953-2072, 1958-2072, 1959-2072, 1963-2072
67/7509256CB1/2334	1-236, 1-2334, 18-115, 18-142, 18-143, 18-178, 18-255, 18-281, 18-339, 18-352, 18-394, 18-428, 18-480, 18-487, 18-644, 19-199, 22-357, 51-190, 51-654, 54-653, 72-204, 85-366, 85-373, 85-593, 85-690, 85-842, 86-636, 86-719, 86-826, 90-610, 97-357, 104-733, 127-448, 127-877, 127-887, 127-912, 128-672, 128-825, 128-826, 128-861, 128-876, 128-888, 128-889, 128-894, 128-906, 128-936, 128-949, 128-950, 128-983, 128-991, 128-992, 128-993, 128-997, 128-1008, 128-1030, 128-1037, 128-1039, 128-1058, 128-1066, 128-1070, 138-884, 138-907, 138-949, 138-977, 138-1058, 138-1087, 138-1102, 189-713, 190-543, 222-728, 255-980, 262-453, 354-997, 363-638, 412-1081, 421-1122, 444-1125, 450-886, 456-733, 469-872, 527-955, 529-627, 535-1525, 556-1527, 557-1000, 585-1152, 585-1154, 587-1203, 590-1148, 596-816, 599-918, 599-1173, 613-856, 626-1236, 639-1020, 646-1206, 660-1526, 662-1213, 662-1525, 670-1230, 671-1525, 675-1150, 676-1230, 679-1193, 701-1005, 715-1526, 721-1526, 727-1527, 732-1526, 733-1525, 734-1106, 734-1481, 736-1527, 738-1525, 745-1527, 750-1051, 773-1020, 775-1527, 785-864, 785-1202, 792-1525, 805-1525, 806-1356, 808-1247, 840-1067, 861-1241, 881-1571, 884-1391, 897-1459, 927-1525, 929-1462, 948-1561, 963-1106, 988-1071, 994-1328, 1023-1569, 1029-1300, 1056-1631, 1070-1297, 1075-1917, 1080-1696, 1085-1709, 1100-1262, 1110-1349, 1116-1378, 1116-1381, 1140-1356, 1145-1405, 1147-1455, 1150-1870, 1164-1743, 1176-1878, 1185-1856, 1211-1801, 1215-1448, 1220-1534, 1235-1506, 1235-1626, 1246-1766, 1253-1800, 1260-1875, 1266-1549, 1285-1532, 1351-1451, 1352-1882, 1353-2170, 1356-2170, 1366-1642, 1386-1669, 1400-1808, 1407-2170, 1408-2170, 1409-1647, 1415-1888, 1416-2170, 1418-2169, 1418-2170, 1423-2167, 1454-1885, 1456-2172, 1468-1575, 1475-2170, 1486-1791, 1504-1928, 1508-1928, 1523-1928, 1524-2020, 1526-1928, 1527-1925, 1547-1926, 1555-1776, 1558-1888, 1562-1849, 1562-1927, 1595-1925, 1600-1859, 1682-1919, 1708-1925, 1714-1927, 1766-1928, 1807-2076, 1839-2170, 1849-1925, 1862-2330, 1928-2334

Table 4

Polynucleotide SEQ ID NO./ Incyte ID/ Sequence Length	Sequence Fragments
68/7509395CB1/1475	1-717, 28-927, 30-1473, 53-266, 267-818, 302-537, 365-1177, 375-1178, 433-1178, 434-1178, 458-1178, 466-713, 477-1112, 479-1179, 519-1177, 520-1048, 520-1050, 523-1178, 537-1178, 542-844, 542-911, 554-1178, 584-1434, 585-1475, 589-1475, 592-1126, 608-1475, 615-1448, 616-1475, 634-1475, 643-1474, 667-928, 684-1187, 686-1178, 698-1204, 701-920, 702-920, 730-1174, 730-1373, 730-1390, 740-1335, 787-1303, 812-1475, 813-1475, 825-1357, 847-1120, 847-1442, 967-1409, 1051-1237, 1158-1307, 1218-1473
69/7503287CB1/1295	1-278, 1-423, 1-552, 1-1295, 17-667, 19-623, 35-667, 37-471, 37-593, 37-709, 37-763, 37-816, 37-870, 37-877, 37-880, 37-883, 37-885, 37-886, 63-669, 76-886, 81-884, 89-886, 105-886, 106-886, 126-495, 126-662, 126-768, 126-771, 128-768, 149-886, 277-644, 284-768, 800-976, 800-1044, 800-1295, 869-1146, 911-1164, 921-1166, 921-1175, 955-1230
70/7503320CB1/1386	1-575, 1-758, 1-855, 1-1386, 146-998, 152-997, 214-997, 236-865, 237-997, 238-998, 239-997, 243-997, 249-1070, 250-514, 252-997, 280-998, 283-997, 399-641, 407-643, 413-998, 530-775, 531-703, 572-793, 572-795, 587-1222, 668-1222, 702-927, 723-1149, 724-1261, 731-1240, 778-1230, 799-1376, 811-1230, 836-953, 836-1248, 865-970, 879-1169, 891-1312, 893-1353, 904-1359, 905-1386, 916-1365, 984-1222, 992-1222, 998-1240, 1002-1204, 1051-1219, 1118-1365, 1163-1376, 1172-1366
71/7503335CB1/2213	1-323, 5-794, 7-298, 7-452, 16-607, 20-216, 20-2008, 21-284, 32-607, 33-309, 33-369, 33-373, 33-457, 33-539, 33-613, 33-712, 33-729, 33-754, 35-284, 39-626, 43-520, 43-669, 68-699, 71-707, 74-306, 74-331, 74-367, 77-530, 95-489, 113-608, 142-802, 189-553, 241-761, 243-794, 260-696, 269-529, 277-839, 286-597, 299-810, 317-783, 357-547, 397-517, 412-913, 612-690, 700-942, 984-1650, 989-1538, 997-1318, 1005-1288, 1010-1262, 1014-1610, 1014-1705, 1074-1302, 1115-1342, 1123-1392, 1151-1420, 1153-1638, 1164-1436, 1167-1459, 1167-1500, 1167-1833, 1169-1971, 1188-1400, 1224-1482, 1249-1438, 1274-1957, 1280-1786, 1287-1744, 1287-1961, 1295-1597, 1295-1804, 1323-1899, 1365-1992, 1371-1650, 1382-2213, 1389-1945, 1394-1852, 1399-2025, 1408-1564, 1439-1966, 1467-1948, 1481-1728, 1481-1907, 1509-1664, 1510-2025, 1613-1733
72/7503952CB1/1289	1-1289, 295-852, 354-893

Table 4

Polynucleotide SEQ ID NO./ Incyte ID/ Sequence Length	Sequence Fragments
73/7504530CB1/1358	1-356, 3-295, 3-688, 3-690, 3-698, 3-731, 3-863, 17-242, 17-290, 17-457, 17-459, 31-356, 33-356, 33-1358, 36-356, 38-196, 45-503, 50-346, 60-295, 60-513, 60-668, 60-859, 62-363, 73-356, 75-835, 80-229, 80-364, 93-353, 101-356, 109-353, 109-356, 111-356, 206-699, 206-915, 206-945, 206-946, 206-948, 231-356, 231-363, 231-469, 234-1192, 249-948, 259-750, 302-1191, 333-948, 334-1191, 365-858, 385-1191, 390-1191, 407-518, 412-544, 421-670, 435-713, 476-1192, 534-849, 591-1191, 602-1178, 610-1139, 614-1229, 622-866, 622-948, 669-1230, 691-904, 706-958, 706-960, 733-1230, 765-1226, 766-1230, 826-1211, 867-1221, 926-1230, 927-1125, 932-1230, 947-1221, 947-1230, 993-1264, 1000-1272, 1058-1230, 1146-1358
74/7509303CB1/2232	1-634, 15-2217, 29-436, 29-673, 29-679, 29-682, 29-683, 29-690, 29-697, 29-713, 29-891, 33-644, 61-341, 209-718, 212-491, 223-462, 255-700, 260-671, 335-557, 616-718, 718-1010, 719-1022, 719-1271, 719-1279, 719-1294, 719-1339, 719-1359, 728-1316, 729-1202, 746-1386, 747-1246, 750-882, 750-983, 756-1143, 770-1398, 772-1263, 774-1325, 779-1417, 788-1460, 798-1314, 801-1414, 805-1404, 823-938, 826-1376, 837-1389, 840-1461, 846-1401, 857-1507, 864-1383, 886-1560, 893-1500, 895-1419, 895-1601, 898-1376, 900-1398, 902-1544, 909-1372, 910-1540, 912-1565, 917-1563, 918-1565, 920-1195, 923-1544, 928-1581, 932-1526, 932-1546, 936-1437, 938-1904, 943-1159, 953-1904, 960-1385, 965-1904, 967-1406, 967-1536, 983-1904, 985-1566, 991-1255, 991-1637, 992-1221, 992-1255, 1001-1490, 1004-1568, 1004-1616, 1006-1904, 1007-1904, 1008-1904, 1017-1262, 1017-1372, 1021-1638, 1022-1387, 1025-1315, 1026-1387, 1033-1630, 1038-1361, 1038-1581, 1043-1904, 1044-1439, 1044-1904, 1049-1302, 1051-1417, 1053-1457, 1053-1527, 1053-1602, 1053-1680, 1061-1397, 1067-1703, 1068-1694, 1085-1588, 1087-1584, 1088-1588, 1095-1904, 1097-1627, 1098-1716, 1099-1741, 1104-1419, 1107-1904, 1108-1598, 1108-1700, 1108-1724, 1108-1785, 1108-1904, 1109-1387, 1110-1723, 1111-1651, 1123-1904, 1131-1549, 1131-1683, 1149-1657, 1158-1604, 1158-1716, 1161-1734, 1162-1731, 1175-1744, 1195-1733, 1195-1750, 1198-1904, 1199-1631, 1203-1876, 1203-1904, 1214-1904, 1218-1584, 1222-1309, 1229-1484, 1233-1673, 1281-1523, 1286-1496, 1290-1578, 1307-1674, 1311-1594, 1315-1420, 1315-1582, 1315-1672, 1315-1874, 1315-1928, 1325-1988, 1327-1665, 1360-1661, 1367-1904, 1367-2042, 1370-1574, 1379-1665, 1382-1530, 1382-1624, 1384-1732, 1385-1529, 1390-1592, 1391-1667, 1393-1961, 1400-1930, 1401-1897, 1407-1657, 1407-1665, 1435-1904, 1440-1678, 1440-1734, 1440-2015, 1441-1656, 1443-1933, 1443-1992, 1444-1989, 1445-2095, 1451-1615, 1451-1663, 1451-1960, 1453-1971, 1463-1705, 1466-2061, 1467-2023, 1471-1731, 1480-1761, 1480-2123, 1483-2116, 1484-1938, 1485-2123, 1487-2013, 1501-1785, 1511-2065, 1526-1773, 1542-2081, 1543-2033, 1550-1680,

Table 4

Polynucleotide SEQ ID NO./ Incye ID/ Sequence Length	Sequence Fragments
	1555-1939, 1558-2143, 1566-2139, 1568-2204, 1569-2189, 1573-2200, 1577-2186, 1587-2199, 1591-2197, 1593-2168, 1594-2191, 1606-2181, 1611-2205, 1613-2217, 1617-2088, 1664-2139, 1678-2217, 1681-2027, 1689-2158, 1703-2100, 1704-1948, 1704-1949, 1704-1963, 1704-2069, 1704-2113, 1724-2206, 1725-1986, 1727-2021, 1759-2139, 1768-1971, 1769-2211, 1786-2097, 1791-2021, 1791-2130, 1796-2056, 1796-2159, 1813-1995, 1816-2130, 1820-2072, 1821-1994, 1822-2071, 1825-2058, 1831-2040, 1832-2058, 1832-2108, 1851-2232, 1856-2118, 1867-2129, 1871-2133, 1871-2154, 1881-2080, 1891-2168, 1910-2168, 1918-2165, 1927-2218, 1941-2186, 1941-2232, 1946-2231, 1953-2209, 1980-2200, 1980-2218, 1981-2231
75/7509910CB1/2230	1-323, 5-796, 7-298, 7-413, 10-822, 16-607, 20-216, 20-2230, 21-284, 32-607, 33-309, 33-369, 33-373, 33-457, 33-539, 33-613, 33-712, 33-729, 33-754, 40-808, 43-520, 43-669, 71-707, 74-306, 74-331, 74-367, 77-530, 87-531, 95-489, 142-803, 189-553, 260-696, 267-1048, 269-529, 286-597, 299-811, 317-783, 337-797, 357-547, 397-517, 518-1226, 522-1226, 522-1230, 528-1230, 549-1300, 570-1226, 581-1300, 587-932, 587-1215, 588-1226, 605-1215, 668-1215, 689-1226, 725-1230, 742-1229, 783-1300, 793-1226, 896-1300, 962-1732, 965-1432, 982-1585, 1021-1580, 1048-1863, 1071-1392, 1078-1600, 1102-1392, 1114-1870, 1114-1872, 1124-1863, 1124-1872, 1159-1478, 1211-1760, 1219-1540, 1227-1510, 1232-1484, 1236-1832, 1236-1854, 1296-1524, 1337-1564, 1345-1614, 1373-1642, 1375-1860, 1386-1658, 1389-1681, 1389-1722, 1410-1622, 1446-1704, 1471-1660, 1496-2179, 1502-2008, 1509-1966, 1509-2183, 1517-1819, 1517-1958, 1545-2121, 1593-1872, 1601-1955, 1611-1955, 1611-2167, 1612-1955, 1616-2074, 1630-1786, 1638-1955, 1661-2188, 1689-2170, 1703-1950, 1703-1991, 1732-2230, 1835-1955
76/7509982CB1/5966	1-273, 1-5966, 7-483, 24-272, 28-299, 42-317, 42-524, 42-551, 42-607, 42-623, 42-638, 42-643, 42-674, 42-675, 42-680, 42-681, 45-273, 45-317, 45-425, 48-358, 49-330, 58-319, 83-327, 87-544, 87-600, 95-364, 95-652, 821-1394, 821-1421, 821-1438, 1174-1697, 1174-1880, 1274-2027, 1283-1569, 1283-1705, 1283-1904, 1292-1896, 1318-1869, 1397-1967, 1403-1904, 1432-2031, 1459-2160, 1468-2410, 1476-1904, 1494-2023, 1494-2024, 1494-2073, 1494-2076, 1494-2110, 1494-2142, 1494-2171, 1501-1904, 1503-1904, 1508-2226, 1509-1904, 1519-1904, 1520-2008, 1525-2159, 1528-2354, 1532-2277, 1542-2401, 1560-2374, 1571-1797, 1571-2357, 1583-2383, 1630-2198, 1630-2227, 1632-2201, 1654-2092, 1659-2078, 1659-2150, 1659-2159, 1659-2160, 1659-2161, 1662-2160, 1694-2527, 1720-2440, 1750-2526, 1751-2160, 1774-1952, 1783-2411, 1786-2416, 1786-2425, 1794-2527, 1810-2527, 1825-2527, 1827-2481, 1831-2160, 1837-2527, 1841-2400, 1859-2527, 1878-2527, 1883-2154, 1883-2156, 1883-2160, 1896-2527, 1908-2527, 1912-2527, 1924-2527, 1926-2527, 1936-2528, 1939-2527, 1941-2418, 1942-2761,

Table 4

Polynucleotide SEQ ID NO./ Incyte ID/ Sequence Length	Sequence Fragments
	1950-2418, 1983-2527, 1991-2527, 2002-2527, 2043-2436, 2077-2354, 2087-2527, 2088-2287, 2088-2526, 2088-2527, 2107-2418, 2117-2527, 2128-2527, 2168-2527, 2178-2527, 2191-2407, 2208-2527, 2218-3008, 2223-2899, 2223-2968, 2223-3008, 2223-3046, 2223-3053, 2235-2419, 2236-2419, 2237-2527, 2269-2426, 2274-2526, 2279-2469, 2279-2526, 2279-2527, 2285-2419, 2286-2419, 2287-2419, 2302-2419, 2305-2594, 2370-2527, 2379-2970, 2379-3030, 2458-2909, 2458-2968, 2458-3046, 2458-3052, 2458-3061, 2458-3080, 2458-3095, 2458-3113, 2458-3170, 2556-2610, 2572-2610, 2588-2610, 2628-2968, 2629-2843, 2629-2979, 2629-3035, 2629-3144, 2651-3169, 2671-3271, 2677-3145, 2722-3419, 2813-3431, 2827-3325, 2827-3353, 2827-3385, 2827-3395, 2827-3412, 2827-3429, 2827-3448, 2827-3489, 2829-3316, 2830-3343, 2833-3407, 2833-3445, 2833-3557, 2833-3560, 2868-3562, 2880-3445, 2881-3149, 2881-3366, 2881-3428, 2881-3445, 2881-3562, 2883-3560, 2885-3437, 2887-3583, 2896-3554, 2898-3562, 2902-3562, 2903-3549, 2904-3510, 2914-3562, 2918-3562, 2923-3562, 2928-3562, 2929-3562, 2942-3333, 2942-3336, 2942-3400, 2942-3462, 2942-3474, 2942-3547, 2942-3562, 2943-3562, 2945-3242, 2945-3562, 2947-3562, 2953-3562, 2959-3562, 2965-3562, 2983-3484, 2983-3516, 2983-3558, 2983-3561, 2983-3562, 2985-3562, 2987-3562, 2990-3562, 2991-3562, 3007-3561, 3007-3562, 3030-3562, 3033-3561, 3034-3515, 3034-3534, 3034-3561, 3034-3562, 3036-3562, 3038-3562, 3044-3535, 3044-3562, 3045-3562, 3059-3562, 3060-3562, 3076-3557, 3084-3562, 3091-3561, 3096-3562, 3113-3562, 3121-3562, 3155-3562, 3273-3562, 3297-3562, 3319-3561, 3319-3562, 3320-3562, 3330-3552, 3330-3745, 3338-3561, 3338-3562, 3400-3675, 3400-3846, 3400-3873, 3400-3959, 3400-3960, 3400-4002, 3400-4060, 3400-4062, 3469-3562, 3569-3952, 3569-4044, 3569-4146, 3569-4152, 3592-4627, 3602-3791, 3639-4117, 3645-4287, 3650-4133, 3682-4066, 3712-4598, 3722-3969, 3739-4356, 3742-4357, 3751-4245, 3754-4048, 3754-4346, 3789-4460, 3824-4489, 3853-4554, 3887-4370, 3887-4384, 3888-4214, 3889-4381, 3896-4474, 3897-4223, 3904-4153, 3914-4428, 3916-4489,

Table 4

Polynucleotide SEQ ID NO./ Incyte ID/ Sequence Length	Sequence Fragments
	3928-4463, 3932-4607, 3935-4542, 3938-4486, 3940-4574, 3955-4192, 3959-4422, 3959-4522, 3959-4621, 3963-4514, 3964-4520, 3970-4403, 3973-4526, 3973-4603, 3997-4485, 4003-4672, 4018-4613, 4028-4296, 4028-4542, 4045-4608, 4047-4397, 4048-4566, 4049-4462, 4049-4500, 4049-4520, 4049-4560, 4049-4628, 4050-4594, 4058-4326, 4063-4310, 4064-4624, 4069-4635, 4070-4331, 4073-4570, 4079-4753, 4080-4600, 4088-4535, 4089-4822, 4095-4759, 4097-4684, 4102-4720, 4103-4366, 4116-4778, 4122-4765, 4126-4740, 4128-4338, 4131-4744, 4136-4378, 4141-4611, 4142-4450, 4154-4666, 4156-4617, 4156-4730, 4159-4347, 4161-4744, 4167-4852, 4168-4671, 4168-4799, 4171-4933, 4178-4853, 4182-4662, 4184-4853, 4189-4719, 4190-4746, 4192-4632, 4192-4721, 4195-4761, 4198-4849, 4205-4681, 4213-4473, 4213-4714, 4213-4804, 4220-4831, 4225-4892, 4228-4878, 4229-4732, 4233-4706, 4234-4705, 4235-4871, 4238-4498, 4238-4521, 4238-4719, 4238-4738, 4238-4857, 4240-4714, 4240-4822, 4241-4595, 4253-4926, 4254-4598, 4262-4769, 4266-5226, 4270-4864, 4275-4966, 4276-4619, 4276-4894, 4278-4784, 4287-4409, 4302-4808, 4304-4800, 4307-4740, 4340-4455, 4346-4938, 4349-4985, 4351-4907, 4355-4576, 4360-4566, 4371-4563, 4371-4852, 4373-4938, 4377-4707, 4381-4910, 4417-5036, 4420-4938, 4422-5035, 4424-4879, 4429-5048, 4430-5184, 4440-5059, 4445-5044, 4453-5013, 4463-4854, 4464-4715, 4468-4609, 4481-4932, 4486-5131, 4487-4659, 4489-5095, 4491-5034, 4493-5041, 4495-5141, 4509-5121, 4512-5036, 4518-4937, 4518-5147, 4527-5130, 4529-4630, 4532-5110, 4555-5125, 4559-5074, 4559-5125, 4571-5151, 4571-5192, 4572-5151, 4578-5151, 4579-5153, 4589-5279, 4599-5243, 4603-5194, 4606-4709, 4609-5168, 4613-4945, 4627-5102, 4636-5204, 4638-5058, 4638-5125, 4638-5160, 4663-5151, 4691-5001, 4710-5361, 4712-5197, 4716-4980, 4716-5190, 4717-4995, 4721-5266, 4726-5151, 4727-5360, 4738-5151, 4754-5048, 4757-5273, 4765-5151, 4767-5151, 4770-5146, 4778-5042, 4800-5219, 4823-5148, 4826-4972, 4840-5242, 4843-5146, 4858-5160, 4858-5175, 4888-5180, 4902-5241, 4906-5353, 4908-5361, 4935-5153, 4939-5362, 4956-5241, 4958-5073, 4958-5112, 4970-5361, 4990-5327, 5020-5357, 5025-5361, 5029-5267, 5029-5325, 5035-5370, 5067-5328, 5067-5333, 5067-5523, 5067-5569, 5110-5378, 5123-5273, 5153-5625, 5237-5423, 5273-5364, 5332-5584, 5334-5569, 5418-5853, 5427-5569, 5492-5569

Table 4

Polynucleotide SEQ ID NO./ Incyte ID/ Sequence Length	Sequence Fragments
77/7510082CB1/2071	1-704, 1-2071, 119-449, 277-950, 309-949, 401-954, 411-610, 411-616, 484-1178, 485-697, 498-1161, 563-789, 580-838, 580-1374, 581-1184, 581-1246, 689-1258, 705-1129, 707-830, 715-972, 727-924, 760-834, 762-834, 777-1035, 781-1026, 797-1098, 812-1111, 818-1018, 818-1304, 819-1102, 822-1402, 824-1100, 824-1123, 832-1243, 837-1121, 841-1260, 854-1108, 861-1159, 863-1677, 873-1142, 875-1130, 878-1131, 907-1582, 914-1183, 920-1144, 925-1234, 949-1134, 949-1156, 949-1420, 949-1436, 949-1451, 949-1469, 949-1481, 949-1486, 949-1497, 949-1521, 949-1533, 949-1590, 949-1605, 949-1613, 949-1666, 949-1729, 949-1756, 951-1571, 953-1515, 953-1599, 953-1655, 956-1200, 959-1577, 972-1247, 1001-1603, 1024-1282, 1024-1326, 1035-1334, 1052-1750, 1073-1355, 1077-1244, 1077-1302, 1079-1811, 1084-1311, 1085-1757, 1102-1373, 1102-1381, 1102-1900, 1123-1318, 1145-1344, 1145-1400, 1145-1404, 1145-1416, 1145-1820, 1146-1384, 1147-1374, 1148-1331, 1149-1442, 1151-1444, 1159-1639, 1161-2023, 1193-1444, 1205-1443, 1215-1450, 1215-1472, 1215-1727, 1219-1453, 1232-1438, 1253-1481, 1271-1852, 1276-1563, 1293-1589, 1298-1563, 1342-1984, 1351-1562, 1371-1651, 1371-1903, 1389-2064, 1398-1677, 1403-1647, 1405-1678, 1423-1900, 1443-1699, 1444-1924, 1450-1908, 1463-1722, 1475-1672, 1475-1727, 1475-1744, 1475-1766, 1479-1768, 1493-1764, 1544-1775, 1570-1713, 1570-1784
78/7510367CB1/3703	1-227, 1-3703, 86-856, 86-879, 2641-2911, 2671-2885, 2686-3033, 2751-3043, 2790-2999, 2790-3014, 2790-3036, 2843-3042, 2866-3497, 2902-3497, 2941-3703
79/7510413CB1/1171	1-1171, 229-762, 229-830, 498-987, 558-978, 579-977, 594-977, 619-977, 621-952, 646-977, 718-974, 718-987, 727-987, 753-969
80/1721303CB1/323	1-313, 5-290, 5-312, 35-323, 54-319, 130-323, 185-315, 186-311, 192-313, 206-312
81/7502007CB1/1221	1-281, 2-1086, 2-1096, 33-126, 33-212, 41-681, 41-719, 41-731, 41-758, 41-760, 41-789, 41-804, 41-821, 41-907, 41-908, 41-1048, 71-212, 71-219, 72-325, 74-212, 79-212, 93-804, 115-606, 158-1047, 189-804, 221-714, 241-1047, 246-1047, 263-374, 291-569, 390-705, 447-1047, 458-1034, 466-995, 470-1100, 478-722, 478-804, 525-1135, 547-788, 562-814, 562-816, 589-1188, 621-1101, 622-1150, 682-1067, 723-1077, 782-1221, 783-981, 788-1089, 803-1077, 803-1104, 803-1111, 914-1098

Table 4

Polynucleotide SEQ ID NO./ Incyte ID/ Sequence Length	Sequence Fragments
82/7506439CB1/2008	1-251, 1-393, 1-2003, 94-852, 100-907, 100-920, 559-946, 559-947, 559-968, 559-991, 559-1018, 559-1098, 564-808, 565-1462, 565-1463, 570-991, 576-1462, 587-720, 604-1463, 633-1228, 635-1164, 642-1462, 676-1462, 681-1462, 714-1462, 730-1462, 732-1462, 780-1463, 816-1463, 841-1463, 857-1322, 884-1322, 897-991, 897-1466, 898-1394, 935-1213, 935-1358, 935-1390, 935-1413, 935-1441, 935-1454, 935-1471, 935-1485, 935-1504, 936-1495, 938-1470, 950-1440, 969-1164, 970-1470, 977-1196, 1034-1379, 1035-1454, 1042-1607, 1050-1576, 1067-1164, 1086-1555, 1095-1720, 1109-1676, 1124-1591, 1125-1383, 1128-1404, 1146-1904, 1146-1939, 1161-1677, 1165-1648, 1166-1677, 1167-1640, 1167-1641, 1179-1807, 1198-1607, 1219-1987, 1241-1905, 1259-1677, 1260-1673, 1281-1922, 1285-1939, 1287-1818, 1297-1769, 1303-1962, 1303-1977, 1323-1616, 1327-1971, 1334-1795, 1334-1858, 1335-1858, 1356-1873, 1361-1858, 1362-1913, 1362-1926, 1369-1633, 1396-1698, 1402-1983, 1407-1859, 1418-2008, 1424-2008, 1434-2006, 1438-1752, 1438-1792, 1455-1858, 1477-2005, 1507-2005, 1512-2008, 1516-2008, 1524-1991, 1530-2005, 1543-1991, 1554-2005, 1563-1991, 1569-2005, 1582-2005, 1585-2008, 1591-2005, 1612-1986, 1622-1991, 1625-1991, 1631-1991, 1640-2008, 1646-1991, 1656-1991, 1667-1929, 1684-1944, 1687-2002, 1692-1991, 1740-2007, 1771-2005, 1812-1980
83/7509243CB1/1080	1-337, 1-338, 1-1080, 19-338, 20-78, 20-133, 20-150, 20-197, 20-337, 20-338, 20-1080, 21-338, 22-338, 26-338, 29-338, 60-338, 67-338, 158-338, 171-338, 177-338, 181-338, 219-1080
84/7509404CB1/2412	1-236, 1-2401, 17-2402, 18-115, 18-142, 18-143, 18-178, 18-255, 18-266, 18-280, 18-281, 18-288, 19-199, 51-190, 72-204, 90-288, 127-886, 350-733, 350-780, 350-886, 350-887, 350-903, 350-922, 350-937, 350-938, 350-948, 350-949, 350-955, 350-997, 350-1010, 350-1011, 350-1038, 350-1041, 350-1044, 350-1053, 350-1058, 350-1091, 350-1119, 350-1127, 350-1163, 351-774, 415-1058, 424-699, 473-1142, 482-1183, 505-1186, 511-947, 517-795, 530-933, 588-886, 590-688, 596-1586, 617-1588, 618-1061, 646-1213, 646-1215, 651-1209, 657-877, 658-1264, 660-979, 660-1234, 674-917, 687-1297, 700-1081, 707-1267, 721-1587, 723-1274, 723-1586, 731-1291, 732-1586, 736-1211, 737-1291, 740-1254, 762-1066, 776-1587, 782-1587, 788-1588, 793-1542, 793-1586, 793-1587, 795-1167, 797-1588, 799-1586, 806-1588, 811-1112, 834-1081, 836-1588, 846-925, 846-1263, 857-1586, 866-1586, 867-1417, 869-1308, 900-1128, 922-1302, 942-1632, 945-1452, 958-1520, 988-1586, 990-1523, 1009-1622, 1024-1167, 1055-1389, 1084-1630, 1090-1361, 1117-1692, 1131-1358, 1136-1978, 1141-1757, 1146-1770, 1171-1410,

Table 4

Polynucleotide SEQ ID NO./ Incyte ID/ Sequence Length	Sequence Fragments
	1177-1439, 1177-1442, 1201-1417, 1206-1466, 1208-1516, 1211-1931, 1225-1804, 1237-1928, 1246-1917, 1272-1862, 1276-1509, 1281-1595, 1296-1567, 1296-1687, 1307-1827, 1314-1861, 1321-1936, 1327-1610, 1346-1593, 1412-1512, 1413-1943, 1414-2231, 1417-2231, 1427-1703, 1447-1730, 1461-1869, 1468-2231, 1469-2231, 1470-1708, 1476-1949, 1477-2231, 1479-2230, 1479-2231, 1484-2228, 1515-1946, 1517-2233, 1529-1636, 1536-2231, 1547-1852, 1565-1989, 1569-1988, 1584-1989, 1585-2081, 1587-1988, 1588-1986, 1608-1987, 1616-1837, 1619-1949, 1623-1910, 1623-1988, 1656-1982, 1661-1920, 1743-1980, 1769-1982, 1775-1988, 1827-1988, 1868-2137, 1900-2231, 1910-1982, 1923-2391, 1989-2412
85/7509439CB1/1004	1-477, 70-479, 70-729, 77-491, 78-382, 373-1004
86/7510202CB1/5231	1-603, 1-747, 1-748, 1-770, 1-5226, 321-801, 394-1125, 402-982, 426-1125, 465-1126, 512-1198, 521-1118, 557-1125, 749-904, 753-1125, 1009-1419, 1009-1468, 1011-1568, 1020-1486, 1123-1569, 1123-1570, 1960-2222, 1960-2224, 2001-2382, 2002-2467, 2039-2467, 2061-2450, 2091-2454, 2151-2845, 2151-2847, 2153-2813, 2264-2917, 2329-2426, 2329-2450, 2330-2967, 2407-2781, 2407-2994, 2407-3022, 2407-3060, 2407-3100, 2407-3161, 2436-3100, 2436-3105, 2469-2987, 2636-3019, 2651-3163, 2832-3285, 2878-3258, 2958-3623, 3270-3941, 3301-3941, 3452-4125, 3577-4128, 3906-4454, 3914-4564, 4033-4638, 4143-4390, 4239-4357, 4259-4500, 4275-4523, 4342-5226, 4375-4648, 4411-4660, 4454-4890, 4719-5231
87/7510203CB1/3269	1-505, 1-3251, 35-625, 130-656, 132-407, 134-734, 176-653, 216-915, 217-505, 217-783, 360-416, 360-420, 360-421, 419-463, 419-479, 514-1224, 543-1147, 544-1143, 567-1078, 707-1334, 737-1224, 747-990, 747-1032, 747-1196, 747-1202, 747-1222, 862-1209, 889-1154, 932-1207, 953-1555, 968-1249, 968-1388, 968-1535, 1012-1567, 1065-1529, 1085-1256, 1132-1705, 1134-1826, 1136-1413, 1194-1842, 1195-1772, 1217-1380, 1247-1381, 1248-1773, 1267-1815, 1287-1545, 1287-1634, 1287-1792, 1287-1839, 1287-1862, 1300-1790, 1381-1943, 1381-1999, 1396-1621, 1412-1909, 1469-1686, 1472-1731, 1475-1920, 1498-2208, 1508-1704, 1527-1999, 1547-2199, 1728-2254, 1745-2291, 1756-1959, 1795-2385, 1803-2443, 1848-2429, 1851-2410, 1956-2632, 1960-2535, 1990-2656, 2009-2663, 2010-2247, 2022-2485, 2049-2543, 2058-2346, 2071-2600, 2085-2367, 2099-2778, 2104-2581, 2106-2514, 2107-2387, 2150-2395, 2159-2635, 2169-2784, 2175-2714, 2179-2549, 2185-2823, 2186-2732, 2209-2676, 2213-2867, 2246-2490, 2246-2921, 2285-2782, 2298-2824, 2298-2879, 2302-2955, 2303-2842, 2308-2600.

Table 4

Polynucleotide SEQ ID NO./ Incyte ID/ Sequence Length	Sequence Fragments
	2316-2427, 2330-2593, 2351-2645, 2351-2647, 2351-2659, 2360-2863, 2365-2957, 2367-2866, 2396-2845, 2404-2659, 2415-2961, 2417-3045, 2418-2858, 2421-2948, 2427-3000, 2462-3162, 2466-2983, 2512-3162, 2524-3064, 2544-3206, 2570-3193, 2578-3160, 2586-3174, 2592-3038, 2595-3236, 2603-2793, 2633-3224, 2634-3177, 2636-3093, 2645-3251, 2648-2913, 2648-2913, 2648-3195, 2650-3224, 2650-3236, 2655-3080, 2655-3131, 2658-3245, 2671-3224, 2672-3138, 2675-3133, 2678-3261, 2688-3215, 2701-3173, 2701-3250, 2706-2966, 2706-2982, 2706-2987, 2706-2997, 2706-3000, 2706-3005, 2706-3006, 2706-3007, 2706-3011, 2706-3018, 2708-3199, 2719-3070, 2726-3224, 2727-3249, 2727-3254, 2747-3179, 2750-3016, 2750-3147, 2753-3203, 2755-3253, 2758-3224, 2766-3214, 2772-3215, 2775-3233, 2788-3045, 2791-3123, 2795-3018, 2797-3070, 2797-3254, 2814-3256, 2814-3269, 2819-3241, 2823-3241, 2829-3236, 2834-3236, 2835-3072, 2866-3236, 2868-3201, 2877-3224, 2889-3222, 2891-3224, 2903-3237, 2906-3162, 2920-3224, 2926-3238, 2976-3238, 2987-3224, 2992-3236, 2999-3231, 3014-3242, 3014-3251, 1-635, 1-7706, 5-618, 20-353, 20-630, 22-623, 24-514, 25-545, 26-542, 26-574, 26-655, 26-659, 26-694, 29-673, 29-791, 30-139, 30-463, 30-466, 30-564, 30-566, 30-583, 30-591, 30-613, 30-623, 31-584, 31-764, 32-587, 32-655, 33-558, 35-462, 45-415, 57-690, 61-659, 62-470, 72-615, 73-230, 73-392, 75-397, 75-533, 76-567, 77-572, 77-621, 79-612, 79-647, 79-758, 80-710, 82-435, 82-628, 84-524, 84-645, 95-709, 97-678, 101-365, 171-274, 294-751, 305-670, 430-774, 492-1113, 507-987, 516-904, 536-1148, 539-1080, 582-1208, 599-1160, 660-1225, 699-998, 724-1164, 741-1305, 813-1471, 834-1478, 873-1340, 892-1482, 897-1620, 941-1452, 947-1522, 997-1375, 1058-1446, 1121-1751, 1145-1375, 1145-1452, 1145-1471, 1145-1495, 1145-1500, 1145-1521, 1145-1523, 1145-1527, 1145-1560, 1145-1598, 1145-1600, 1145-1614, 1145-1653, 1145-1661, 1145-1681, 1145-1718, 1145-1777, 1145-1830, 1203-1798, 1245-1719, 1273-1375, 1308-1507, 1376-1864, 1376-2060, 1377-2061, 1377-2061, 1379-2060, 1382-1989, 1382-2061, 1385-2063, 1391-2061, 1395-2063, 1398-2061, 1402-2061, 1403-2025, 1403-2061, 1404-2061,
88/7510208CB1/7706	

Table 4

Polynucleotide SEQ ID NO./ Incyte ID/ Sequence Length	Sequence Fragments
	1404-2063, 1408-2061, 1409-2061, 1414-2061, 1414-2063, 1417-2061, 1418-2061, 1422-2061, 1423-2061, 1426-2063, 1429-2061, 1433-2061, 1439-2061, 1442-1924, 1442-1933, 1442-1989, 1442-2030, 1442-2035, 1443-2061, 1443-2063, 1447-2061, 1447-2063, 1451-2061, 1452-2061, 1452-2063, 1453-2061, 1455-2061, 1458-2061, 1462-2061, 1467-1742, 1467-1743, 1471-2061, 1472-2061, 1474-2061, 1480-2061, 1487-2060, 1487-2061, 1487-2063, 1488-2061, 1489-2061, 1494-2061, 1496-2061, 1498-2061, 1500-2061, 1503-2060, 1504-2061, 1506-2061, 1510-2061, 1512-2061, 1515-1994, 1515-2000, 1515-2061, 1520-2061, 1524-2061, 1525-2061, 1528-2061, 1534-1992, 1541-2063, 1546-2061, 1547-2061, 1550-2061, 1557-2063, 1561-1835, 1561-1864, 1561-2061, 1564-2060, 1564-2061, 1566-2009, 1570-2061, 1572-2061, 1574-2061, 1577-2028, 1577-2061, 1580-2060, 1581-2009, 1583-2061, 1589-2066, 1596-2060, 1598-2061, 1600-2061, 1604-2060, 1610-2061, 1634-2061, 1639-2060, 1644-2060, 1644-2061, 1646-2063, 1654-2061, 1667-2060, 1684-2058, 1690-2060, 1710-2060, 1711-2060, 1736-1912, 1789-2064, 1790-2061, 1792-2059, 1850-1909, 1869-2061, 1941-2060, 1962-2061, 2068-2191, 2068-2669, 2070-2291, 2070-2606, 2071-2247, 2071-2291, 2071-2395, 2071-2451, 2071-2508, 2071-2513, 2071-2568, 2071-2576, 2071-2632, 2071-2687, 2071-2691, 2071-2715, 2071-2747, 2275-3049, 2334-2631, 2427-2543, 2662-3148, 2770-3383, 2882-3433, 2918-3447, 2979-3494, 3007-3488, 3021-3482, 3077-3576, 3078-3518, 3636-3672, 3636-3703, 3636-3704, 3643-3704, 3667-4087, 4538-5095, 4538-5381, 4580-5166, 4580-5375, 4601-5139, 4622-5204, 4638-5235, 4661-5225, 4667-5255, 4708-5336, 4711-5255, 4738-5373, 4743-5279, 4783-5295, 4784-5306, 4800-5401, 4859-5408, 4880-5279, 4884-5443, 4905-5429, 4906-5428, 4907-5392, 4911-5439, 4922-5431, 4931-5511, 4932-5539, 4943-5513, 4954-5510, 4957-5560, 4969-5513, 4990-5641, 4997-5521, 5040-5353, 5040-5427, 5041-5428, 5045-5279, 5045-5544, 5045-5772, 5054-5270, 5084-5630, 5085-5630, 5095-5545, 5117-5526, 5146-5403, 5150-5764, 5173-5458, 5174-5828, 5194-5822, 5214-5824, 5226-5872, 5234-5863, 5245-5451, 5245-5452, 5263-5869, 5267-5803,

Table 4

Polynucleotide SEQ ID NO./ Incye ID/ Sequence Length	Sequence Fragments
	5269-5803, 5300-5963, 5303-5825, 5315-5482, 5315-5545, 5330-5598, 5347-5494, 5363-5985, 5376-6040, 5393-5701, 5406-5883, 5420-5784, 5420-5982, 5431-5662, 5432-5790, 5433-5678, 5449-5996, 5455-6083, 5479-6046, 5485-6220, 5507-6146, 5511-5861, 5511-6131, 5518-5800, 5554-5792, 5554-6341, 5563-5858, 5572-6335, 5582-6076, 5589-6214, 5629-5967, 5632-5813, 5665-5870, 5707-6218, 5707-6417, 5709-6233, 5731-5969, 5741-6316, 5758-6068, 5773-6039, 5773-6051, 5790-6444, 5816-6050, 5842-6403, 5846-6459, 5848-6045, 5855-6084, 5855-6091, 5855-6181, 5877-5931, 5882-6240, 5882-6381, 5885-6198, 5930-6401, 5958-6243, 5960-6226, 5968-6491, 5974-6252, 6014-6272, 6017-6502, 6032-6345, 6051-6303, 6137-6738, 6162-6360, 6163-6626, 6163-6745, 6163-6843, 6232-6660, 6248-6501, 6255-6510, 6258-6585, 6261-6536, 6277-6458, 6302-6899, 6304-6567, 6305-6784, 6307-6589, 6312-6527, 6334-6728, 6338-6595, 6338-6773, 6338-6822, 6338-6850, 6338-6892, 6338-6909, 6338-6922, 6338-6931, 6338-6990, 6338-7007, 6338-7110, 6338-7119, 6339-6937, 6339-6945, 6339-7014, 6339-7083, 6342-6898, 6342-6899, 6347-6430, 6362-6599, 6363-7043, 6366-7088, 6370-6893, 6370-6906, 6378-6847, 6387-6847, 6393-6583, 6402-6707, 6402-6847, 6402-7039, 6402-7048, 6403-6870, 6407-6671, 6412-6878, 6422-6691, 6423-6660, 6423-6673, 6424-6948, 6436-7093, 6442-7164, 6446-6908, 6446-6940, 6447-7153, 6469-6847, 6480-6729, 6484-6774, 6484-7058, 6485-6685, 6491-7000, 6492-6758, 6492-6760, 6507-7247, 6513-7239, 6515-6631, 6522-6786, 6525-7113, 6526-7057, 6549-7113, 6556-7082, 6557-6931, 6558-6831, 6558-7180, 6565-7391, 6568-7165, 6583-6691, 6587-7007, 6593-7134, 6600-6830, 6600-6845, 6600-7138, 6604-7391, 6616-7287, 6626-6855, 6626-6880, 6643-6925, 6645-6943, 6670-7202, 6678-7242, 6691-6938, 6691-7304, 6700-6982, 6702-7297, 6704-7334, 6718-6950, 6718-6951, 6729-6860, 6740-6997, 6751-7037, 6759-7327, 6764-7286, 6768-7484, 6778-7411, 6781-7335, 6781-7340, 6782-6899, 6785-7451, 6792-7055, 6820-7364, 6826-6894, 6833-7296, 6839-7239, 6839-7581, 6839-7586, 6839-7623, 6839-7663, 6839-7699, 6845-7114, 6873-7440, 6880-7256, 6882-7434, 6887-7530,

Table 4

Polynucleotide SEQ ID NO./ Incyte ID/ Sequence Length	Sequence Fragments
	6890-7113, 6892-7394, 6898-7706, 6902-7150, 6902-7158, 6902-7333, 6910-7696, 6911-7177, 6911-7180, 6911-7509, 6920-7339, 6928-7068, 6937-7196, 6937-7516, 6942-7254, 6943-7193, 6943-7220, 6944-7483, 6944-7706, 6947-7706, 6955-7317, 6956-7508, 6977-7258, 6983-7230, 6992-7328, 6995-7251, 7004-7514, 7005-7220, 7005-7591, 7007-7694, 7007-7706, 7010-7659, 7015-7552, 7016-7706, 7022-7219, 7022-7466, 7022-7497, 7030-7272, 7030-7277, 7046-7621, 7048-7266, 7051-7343, 7051-7588, 7055-7335, 7062-7545, 7068-7349, 7068-7353, 7069-7360, 7082-7706, 7096-7629, 7098-7706, 7114-7457, 7115-7398, 7115-7706, 7119-7662, 7137-7341, 7152-7644, 7153-7664, 7156-7706, 7162-7373, 7166-7706, 7186-7655, 7210-7507, 7223-7388, 7226-7701, 7228-7515, 7230-7444, 7237-7516, 7240-7481, 7264-7584, 7265-7579, 7266-7557, 7286-7523, 7294-7560, 7302-7501, 7304-7481, 7306-7687, 7311-7562, 7311-7596, 7330-7626, 7345-7583, 7359-7602, 7385-7622, 7397-7653, 7399-7668, 7408-7654, 7409-7574, 7427-7692, 7430-7706, 7434-7676, 7435-7643, 7438-7671, 7440-7545, 7446-7683, 7450-7621, 7480-7706, 7502-7536, 7502-7537, 7502-7539, 7515-7539, 7540-7575, 7540-7577, 7541-7568, 7544-7577, 7553-757
89/7510446CB1/3159	1-730, 1-773, 1-3135, 1839-2568, 2165-2402, 2165-2513, 2165-2597, 2165-2628, 2165-2697, 2165-2701, 2165-2709, 2165-2725, 2165-2741, 2165-2745, 2165-2775, 2192-2671, 2196-2820, 2204-2837, 2209-2807, 2221-2959, 2236-2775, 2237-2793, 2339-3135, 2347-3002, 2380-2601, 2387-3135, 2423-2729, 2425-3135, 2426-3135, 2427-3135, 2439-2957, 2469-3135, 2475-3133, 2490-3134, 2525-3135, 2525-3154, 2550-3137, 2567-3133, 2580-3135, 2594-2811, 2615-3101, 2640-3159, 2642-2862, 2658-3133, 2665-2823, 2668-3159, 2794-2895, 2918-3089, 2992-3159
90/7505294CB1/1821	1-263, 1-1813, 29-558, 46-193, 110-266, 112-264, 124-485, 139-661, 254-484, 295-607, 330-646, 350-626, 365-610, 370-620, 370-848, 395-671, 426-832, 444-706, 496-704, 497-840, 507-619, 514-769, 520-800, 524-827, 566-919, 566-922, 566-1085, 581-849, 617-828, 621-870, 631-864, 641-814, 641-870, 642-858, 642-870, 643-868, 643-870, 643-928, 644-748, 644-870, 645-869, 646-870, 646-892, 648-870, 649-865, 649-870, 650-764, 651-870, 654-870, 673-870, 689-870, 691-795, 716-870, 770-870, 771-1032, 785-1060, 870-1255, 871-1439, 875-1226, 875-1257, 879-1458, 895-1100, 902-1423, 903-1140, 920-1481, 923-1257, 924-1191, 930-1407, 950-1214, 952-1215, 955-1219, 958-1225, 960-1171, 962-1226, 963-1105, 966-1206, 967-1229, 967-1252, 972-1182, 972-1428, 995-1294, 1010-1472, 1034-1202, 1041-1223, 1044-1328, 1064-1314, 1067-1311, 1071-1340, 1071-1698, 1074-1618, 1089-1328, 1089-1724, 1089-1731, 1093-1338, 1110-1373, 1110-1433, 1118-1458, 1123-1408, 1132-1325, 1132-1329, 1142-1762, 1145-1394, 1147-1668, 1148-1427, 1149-1766, 1158-1417, 1158-1745, 1160-1745, 1161-1765,

Table 4

Polynucleotide SEQ ID NO./ Incyte ID/ Sequence Length	Sequence Fragments
	1162-1813, 1166-1440, 1169-1331, 1182-1458, 1188-1742, 1189-1413, 1191-1731, 1192-1503, 1195-1799, 1196-1478, 1200-1746, 1200-1748, 1203-1662, 1222-1497, 1233-1799, 1261-1707, 1288-1734, 1290-1390, 1316-1821, 1317-1813, 1336-1564, 1336-1622, 1344-1821, 1346-1819, 1349-1601, 1349-1718, 1353-1803, 1359-1552, 1359-1819, 1360-1633, 1360-1815, 1362-1639, 1363-1621, 1363-1768, 1366-1772, 1374-1803, 1374-1810, 1379-1761, 1389-1648, 1395-1821, 1401-1816, 1404-1698, 1406-1815, 1409-1815, 1409-1819, 1417-1819, 1427-1814, 1428-1810, 1430-1816, 1430-1819, 1433-1815, 1437-1813, 1437-1815, 1448-1695, 1450-1691, 1451-1618, 1455-1704, 1456-1815, 1463-1821, 1465-1810, 1466-1780, 1467-1817, 1471-1810, 1472-1740, 1475-1756, 1476-1817, 1478-1701, 1478-1806, 1490-1724, 1490-1766, 1493-1787, 1498-1807, 1501-1623, 1511-1810, 1512-1821, 1514-1819, 1516-1746, 1542-1807, 1542-1817, 1543-1811, 1544-1816, 1547-1799, 1548-1818, 1552-1741, 1556-1821, 1557-1759, 1559-1819, 1563-1815, 1564-1820, 1567-1805, 1568-1818, 1570-1816, 1586-1819, 1609-1820, 1612-1821, 1754-1812, 1763-1817
91/7505631CB1/3526	1-126, 1-242, 1-268, 1-280, 1-678, 1-3526, 3-578, 6-247, 7-501, 7-786, 14-293, 15-239, 15-246, 15-286, 15-306, 15-555, 15-556, 15-560, 18-603, 30-315, 37-643, 41-841, 95-612, 116-740, 133-811, 134-592, 160-456, 164-781, 180-840, 208-764, 283-767, 301-909, 321-883, 321-1044, 332-765, 332-968, 332-969, 403-1060, 416-976, 450-987, 450-1057, 450-1124, 450-1183, 450-1198, 450-1203, 450-1204, 450-1220, 450-1226, 450-1228, 450-1233, 450-1260, 450-1292, 450-1327, 450-1346, 450-1353, 450-1362, 459-1355, 477-877, 477-1063, 477-1165, 477-1242, 481-1071, 481-1250, 481-1263, 500-1284, 562-921, 569-1370, 594-932, 614-1079, 678-1447, 694-795, 779-1013, 779-1115, 779-1120, 779-1283, 779-1331, 779-1380, 779-1390, 779-1419, 820-1403, 852-1447, 854-1260, 876-1329, 879-1403, 933-1244, 1002-1273, 1116-1431, 1169-1446, 1197-2004, 1199-1877, 1242-1447, 1440-1657, 1440-1679, 1440-1702, 1440-1737, 1440-1946, 1440-1998, 1440-2017, 1440-2037, 1440-2077, 1463-2139, 1474-1713, 1495-1738, 1536-1830, 1543-2081, 1547-1821, 1551-1867, 1568-1798, 1572-1767, 1572-2160, 1588-1807, 1604-1835, 1-441, 1-946, 23-447, 52-261, 52-893, 176-894, 226-759, 279-759, 317-747

Table 4

Polynucleotide SEQ ID NO./ Incyte ID/ Sequence Length	Sequence Fragments
93/7510733CB1/2737	1-153, 1-313, 1-356, 1-384, 1-423, 1-447, 1-459, 1-490, 1-503, 1-542, 1-2737, 443-1360, 444-1360, 446-1360, 447-1360, 460-1360, 478-1360, 486-1360, 502-1361, 503-1360, 504-1360, 539-1360, 608-1100, 612-1360, 623-1360, 624-1358, 624-1360, 689-1360, 727-1124, 823-1360, 868-1088, 885-1141, 918-1143, 1015-1261, 1044-1308, 1044-1651, 1072-1676, 1107-1375, 1117-1392, 1169-1429, 1259-1760, 1282-1713, 1290-1565, 1290-1575, 1290-1776, 1290-1802, 1290-1810, 1290-1819, 1290-1871, 1290-1872, 1290-1875, 1290-1903, 1310-1947, 1319-1548, 1327-1611, 1332-1825, 1368-1615, 1369-1578, 1397-1575, 1442-1681, 1442-2013, 1456-2032, 1484-1706, 1521-1925, 1526-2057, 1567-1808, 1580-2066, 1592-1796, 1593-1924, 1599-1822, 1626-1825, 1626-1833, 1629-1867, 1648-2226, 1649-2154, 1649-2173, 1681-1917, 1681-1921, 1682-1944, 1687-1964, 1689-1896, 1689-2141, 1690-1858, 1723-2155, 1736-2226, 1747-2154, 1749-2151, 1749-2249, 1749-2304, 1750-1913, 1750-2155, 1750-2211, 1759-2464, 1760-2431, 1777-2052, 1783-2008, 1805-2027, 1805-2050, 1807-2036, 1807-2073, 1825-2093, 1827-2049, 1842-2155, 1846-2120, 1846-2155, 1847-2110, 1859-2173, 1859-2333, 1859-2356, 1859-2620, 1859-2649, 1859-2669, 1864-2672, 1868-2104, 1892-2333, 1897-2156, 1920-2162, 1944-2537, 1947-2737, 1951-2206, 1963-2457, 1980-2278, 1993-2422, 2004-2737, 2006-2737, 2018-2737, 2028-2422, 2047-2266, 2047-2287, 2047-2319, 2048-2737, 2060-2719, 2063-2294, 2072-2737, 2098-2585, 2098-2735, 2106-2657, 2108-2351, 2115-2369, 2119-2371, 2121-2548, 2122-2422, 2130-2394, 2156-2422, 2156-2636, 2156-2641, 2156-2673, 2157-2422, 2157-2673, 2172-2690, 2186-2737, 2190-2492, 2197-2443, 2207-2734, 2231-2737, 2247-2483, 2252-2732, 2253-2505, 2260-2733, 2272-2723, 2273-2730, 2273-2732, 2275-2724, 2277-2737, 2284-2556, 2284-2730, 2285-2521, 2289-2730, 2298-2731, 2313-2546, 2317-2598, 2321-2730, 2327-2732, 2333-2733, 2334-2422, 2334-2737, 2335-2737, 2336-2422, 2336-2737, 2337-2578, 2347-2730, 2347-2732, 2348-2595, 2354-2729, 2358-2578, 2361-2732, 2362-2585, 2368-2634, 2390-2733, 2403-2665, 2450-2737, 2461-2716, 2461-2729, 2476-2733, 2525-2737, 2553-2673, 2554-2696, 2560-2719, 2576-2737, 2581-2737, 2603-2729, 2675-2732, 2675-2737

Table 4

Polynucleotide SEQ ID NO./ Incyte ID/ Sequence Length	Sequence Fragments
94/7510734CB1/2821	1-153, 1-313, 1-356, 1-384, 1-444, 1-472, 1-2821, 66-643, 70-643, 74-628, 158-1016, 228-562, 552-1445, 702-1445, 708-1445, 709-1443, 709-1445, 774-1445, 812-1209, 908-1445, 953-1173, 970-1226, 1003-1228, 1100-1346, 1129-1393, 1129-1736, 1157-1761, 1192-1460, 1202-1477, 1254-1514, 1344-1845, 1367-1798, 1375-1650, 1375-1660, 1375-1861, 1375-1887, 1375-1895, 1375-1904, 1375-1956, 1375-1957, 1375-1960, 1375-1988, 1395-2032, 1404-1633, 1412-1696, 1417-1910, 1453-1700, 1454-1663, 1482-1660, 1527-1766, 1527-2098, 1541-2117, 1569-1791, 1606-2010, 1611-2142, 1652-1893, 1665-2151, 1677-1881, 1678-2009, 1684-1907, 1711-1910, 1711-1918, 1714-1952, 1733-2311, 1734-2239, 1734-2258, 1766-2002, 1766-2006, 1767-2029, 1772-2049, 1774-1981, 1774-2226, 1775-1943, 1808-2240, 1821-2311, 1832-2239, 1834-2236, 1834-2334, 1834-2389, 1835-1998, 1835-2240, 1835-2296, 1844-2549, 1845-2516, 1862-2137, 1868-2093, 1890-2112, 1890-2135, 1892-2121, 1892-2158, 1910-2178, 1912-2134, 1927-2240, 1931-2205, 1931-2240, 1932-2195, 1944-2258, 1944-2418, 1944-2441, 1944-2705, 1944-2734, 1944-2754, 1949-2757, 1953-2189, 1977-2418, 1982-2241, 2005-2247, 2029-2622, 2032-2821, 2036-2291, 2048-2542, 2065-2363, 2078-2507, 2089-2821, 2091-2821, 2103-2821, 2113-2507, 2132-2351, 2132-2372, 2132-2404, 2133-2821, 2145-2804, 2148-2379, 2157-2821, 2183-2670, 2183-2820, 2191-2742, 2193-2436, 2200-2454, 2204-2456, 2206-2633, 2207-2507, 2215-2479, 2241-2507, 2241-2721, 2241-2726, 2241-2758, 2242-2507, 2242-2758, 2257-2775, 2271-2821, 2275-2577, 2282-2528, 2292-2819, 2316-2821, 2332-2568, 2337-2817, 2338-2590, 2345-2818, 2357-2808, 2358-2815, 2358-2817, 2360-2809, 2362-2821, 2369-2641, 2369-2815, 2370-2606, 2374-2815, 2383-2816, 2398-2631, 2402-2683, 2406-2815, 2412-2817, 2418-2818, 2419-2507, 2419-2821, 2420-2821, 2421-2507, 2421-2821, 2422-2663, 2432-2815, 2432-2817, 2433-2680, 2439-2814, 2443-2663, 2446-2817, 2447-2670, 2453-2719, 2475-2818, 2488-2750, 2535-2821, 2546-2801, 2546-2814, 2561-2818, 2610-2821, 2638-2758, 2639-2781, 2645-2804, 2661-2821, 2666-2821, 2688-2814, 2760-2817, 2760-2821

Table 4

Polynucleotide SEQ ID NO./ Incyte ID/ Sequence Length	Sequence Fragments
95/7503977CBI/3583	1-674, 9-531, 28-538, 45-665, 47-3531, 94-761, 110-444, 117-452, 129-812, 137-752, 147-424, 147-432, 147-446, 147-448, 163-674, 217-929, 222-506, 232-523, 235-443, 247-929, 252-452, 268-893, 271-509, 288-833, 288-893, 288-896, 310-531, 310-820, 312-807, 326-787, 331-812, 377-920, 382-516, 474-802, 564-1199, 819-1110, 889-1134, 911-1384, 921-1079, 923-1099, 928-1517, 963-1110, 976-1651, 994-1110, 994-1490, 998-1110, 1023-1480, 1046-1658, 1077-1640, 1145-1710, 1166-1421, 1166-1527, 1166-1626, 1166-1703, 1166-1705, 1167-1505, 1184-1598, 1192-1833, 1196-1862, 1197-1704, 1210-1659, 1213-1789, 1216-1906, 1230-1900, 1241-1730, 1244-1955, 1245-1911, 1252-1910, 1254-1829, 1265-1802, 1270-1516, 1274-1922, 1275-1940, 1278-1802, 1281-1590, 1288-1923, 1292-1913, 1296-1876, 1303-1872, 1304-1868, 1306-1913, 1309-1563, 1312-1573, 1331-1854, 1337-1989, 1342-1910, 1356-1980, 1376-1998, 1382-2041, 1396-1959, 1403-2063, 1406-1787, 1421-1979, 1421-1989, 1421-2024, 1428-2101, 1433-1687, 1458-1666, 1473-1981, 1475-1730, 1479-2103, 1492-2155, 1493-2206, 1496-2190, 1510-1883, 1523-1919, 1533-2064, 1533-2185, 1535-2002, 1539-1951, 1539-2064, 1541-2138, 1542-2223, 1550-2178, 1551-2167, 1556-1930, 1576-1865, 1576-1929, 1576-2310, 1577-1930, 1577-2040, 1578-2208, 1580-2255, 1584-1955, 1584-1975, 1584-2245, 1587-2167, 1595-2242, 1598-2144, 1601-2110, 1601-2242, 1601-2348, 1602-1857, 1602-1925, 1602-1929, 1602-2086, 1602-2101, 1602-2123, 1602-2137, 1602-2221, 1602-2243, 1602-2244, 1602-2282, 1602-2289, 1602-2355, 1604-2094, 1605-2365, 1609-1865, 1615-2172, 1618-2281, 1621-2312, 1622-2169, 1622-2258, 1623-2195, 1628-2214, 1630-2342, 1638-1896, 1644-2216, 1644-2487, 1648-1974, 1649-1911, 1649-2229, 1651-2341, 1663-2113, 1664-2272, 1664-2350, 1667-1838, 1671-1838, 1678-1902, 1679-2375, 1684-1929, 1684-2120, 1684-2290, 1684-2305, 1684-2348, 1684-2395, 1685-2143, 1686-1935, 1688-2312, 1689-2429, 1692-2366, 1694-1923, 1694-2206, 1710-2217, 1722-2075, 1727-1942, 1734-2104, 1737-2330, 1739-2255, 1747-2379, 1748-2338, 1753-2447, 1754-1904, 1755-2391, 1756-2423, 1757-2072, 1757-2453, 1760-2142, 1763-2424,

Table 4

Polynucleotide SEQ ID NO./ Incyte ID/ Sequence Length	Sequence Fragments
	1767-2001, 1767-2442, 1770-2316, 1772-2462, 1775-2453, 1781-2430, 1782-2363, 1790-1854, 1796-2105, 1817- 2500, 1823-2342, 1831-2110, 1836-2501, 1837-2496, 1837-2529, 1856-2545, 1865-2005, 1876-2415, 1881-2322, 1888-2106, 1888-2120, 1893-2562, 1898-2218, 1902-2334, 1919-2535, 1920-2636, 1923-2500, 1924-2266, 1933- 2141, 1936-2146, 1943-2601, 1945-2064, 1948-2076, 1954-2587, 1956-2558, 1963-2115, 1965-2425, 1970-2648, 1971-2299, 1982-2646, 1989-2684, 1995-2631, 2000-2334, 2003-2550, 2003-2652, 2004-2455, 2004-2535, 2004- 2655, 2006-2624, 2007-2358, 2011-2415, 2012-2658, 2014-2249, 2014-2730, 2019-2119, 2019-2625, 2022-2355, 2025-2695, 2027-2497, 2029-2323, 2029-2662, 2031-2669, 2038-2703, 2039-2557, 2042-2529, 2047-2714, 2051- 2678, 2055-2332, 2065-2593, 2068-2655, 2069-2296, 2073-2338, 2080-2408, 2082-2352, 2082-2380, 2082-2529, 2082-2544, 2082-2716, 2082-2847, 2085-2581, 2107-2335, 2110-2334, 2138-2397, 2139-2720, 2141-2360, 2146- 2402, 2155-2634, 2164-2798, 2171-2519, 2175-2735, 2182-3014, 2196-2455, 2208-2662, 2225-2879, 2226-2699, 2226-2826, 2226-2845, 2235-2867, 2241-2718, 2252-2695, 2263-2601, 2274-2655, 2275-2507, 2276-2867, 2282- 2936, 2285-2915, 2296-2509, 2297-2580, 2304-2948, 2309-2867, 2309-2997, 2310-2844, 2310-2956, 2312-2525, 2312-2834, 2321-2418, 2331-2866, 2335-2540, 2339-2635, 2341-2498, 2343-2590, 2346-2936, 2362-2601, 2364- 3036, 2366-2601, 2366-2646, 2366-2649, 2370-2657, 2371-2575, 2371-2597, 2372-3176, 2374-2624, 2374-2646, 2374-2658, 2374-2672, 2376-2588, 2376-2644, 2376-2651, 2377-2610, 2378-2633, 2378-2696, 2378-2729, 2379- 2609, 2379-3044, 2381-2649, 2381-2650, 2386-2589, 2390-2673, 2396-2679, 2396-2686, 2398-2672, 2398-3084, 2418-3064, 2421-2662, 2421-2781, 2440-3147, 2445-2654, 2445-2665, 2448-2724, 2452-2985, 2454-3000, 2455- 2688, 2458-2691, 2458-2739, 2459-2703, 2459-3201, 2462-3050, 2468-3031, 2472-2688, 2479-2985, 2482-2737, 2482-3040, 2483-2744, 2484-2737, 2494-2749, 2495-2607, 2496-3092, 2507-2796, 2522-2745, 2522-2748, 2527- 2781, 2529-3090, 2542-3085, 2576-2815, 2582-3134, 2586-3108, 2623-2829, 2629-3142, 2635-3253, 2640-2906,

Table 4

Polynucleotide SEQ ID NO./ Incye ID/ Sequence Length	Sequence Fragments
	2654-3369, 2660-2917, 2670-3209, 2672-2990, 2672-3004, 2692-2906, 2699-2946, 2700-3042, 2710-2951, 2710-3281, 2716-2980, 2716-3014, 2716-3327, 2716-3339, 2717-2957, 2718-2964, 2718-3004, 2718-3316, 2718-3322, 2720-3337, 2723-2806, 2730-2993, 2730-3056, 2731-2975, 2737-3019, 2738-2978, 2756-3067, 2765-3074, 2765-3084, 2768-3022, 2769-3538, 2785-3467, 2786-3042, 2790-3551, 2811-3085, 2819-3121, 2819-3269, 2838-3137, 2845-3432, 2855-3081, 2863-3553, 2865-3096, 2875-3180, 2880-3173, 2887-3425, 2890-3552, 2893-3176, 2894-3524, 2900-3327, 2905-3552, 2907-3530, 2911-3170, 2911-3424, 2916-3465, 2920-3395, 2923-3553, 2924-3496, 2932-3553, 2936-3006, 2936-3212, 2938-3194, 2942-3523, 2944-3231, 2944-3552, 2945-3382, 2959-3198, 2960-3499, 2964-3196, 2970-3550, 2972-3153, 2985-3235, 2985-3252, 2990-3552, 2992-3243, 2997-3551, 2998-3242, 3003-3276, 3008-3554, 3016-3519, 3028-3550, 3032-3323, 3035-3496, 3054-3313, 3054-3328, 3060-3545, 3066-3479, 3066-3480, 3066-3553, 3071-3328, 3072-3541, 3073-3553, 3075-3553, 3082-3551, 3084-3245, 3085-3300, 3085-3339, 3088-3552, 3093-3538, 3096-3312, 3111-3543, 3112-3541, 3113-3552, 3113-3554, 3114-3530, 3126-3399, 3129-3583, 3154-3542, 3156-3540, 3166-3535, 3167-3468, 3188-3438, 3192-3338, 3196-3434, 3204-3558, 3223-3436, 3224-3504, 3226-3537, 3233-3541, 3234-3506, 3235-3539, 3239-3523, 3243-3510, 3260-3482, 3260-3492, 3265-3549, 3268-3538, 3276-3535, 3279-3537, 3298-3524, 3298-3538, 3325-3538, 3327-3517, 3370-3582
96/7505084CB1/2125	1-210, 1-372, 1-383, 1-412, 1-418, 1-456, 1-479, 1-499, 1-500, 1-2125, 18-611, 408-872, 551-1187, 567-1115, 603-1138, 636-916, 636-1077, 636-1107, 636-1124, 636-1210, 636-1288, 639-1288, 688-1149, 745-1352, 878-1429, 1060-1230, 1060-1249, 1104-1966, 1184-1678, 1184-1689, 1184-1738, 1228-1825, 1230-1595, 1241-1858, 1294-1664, 1298-1799, 1302-1920, 1388-2125, 1419-1728, 1420-1936, 1449-2125, 1463-2111, 1470-1920, 1487-1739, 1496-2076, 1547-2116, 1550-2015, 1559-1719, 1559-1849, 1579-2125, 1664-2121, 1715-1949, 1732-2103, 1732-2121, 1738-1997, 1780-1933, 1792-2122, 1798-2121, 1836-2086, 1888-2125, 1929-2120
97/7506950CB1/1517	1-479, 1-1517, 37-229, 37-849, 98-1037, 240-490, 507-881, 518-1033, 519-1033, 542-1037, 796-1285, 838-1248, 838-1331, 840-1095, 1053-1403
98/7506951CB1/1694	1-479, 1-1694, 37-229, 37-596, 37-603, 37-657, 37-676, 37-698, 37-699, 37-701, 37-711, 37-723, 37-730, 37-740, 37-741, 37-747, 37-754, 37-755, 37-765, 37-776, 37-778, 37-782, 37-819, 37-847, 37-865, 37-877, 37-880, 37-907, 38-728, 39-744, 40-662, 240-490, 303-766, 427-1214, 436-1213, 491-1214, 568-1214, 973-1462, 1015-1425, 1015-1508, 1017-1272, 1230-1580
99/7506954CB1/1102	1-1102, 114-310, 114-622, 381-870, 423-833, 423-916, 425-680, 638-988

Table 4

Polynucleotide SEQ ID NO./ Incyte ID/ Sequence Length	Sequence Fragments
100/7506956CB1/1744	1-479, 1-1744, 37-231, 37-270, 37-596, 37-603, 37-657, 37-676, 37-698, 37-699, 37-701, 37-723, 37-730, 37-740, 37-741, 37-747, 37-763, 37-766, 37-903, 38-728, 39-744, 40-662, 240-490, 303-747, 331-1264, 434-1264, 553-1264, 622-644, 743-1260, 746-1260, 769-1264, 1023-1512, 1065-1475, 1065-1558, 1067-1322, 1280-1630
101/7506959CB1/1753	1-479, 1-1753, 37-231, 37-270, 37-596, 37-913, 240-490, 476-1273, 598-1269, 603-974, 603-1269, 603-1273, 607-1273, 648-1213, 651-1273, 682-1273, 754-1269, 755-1269, 778-1273, 1032-1521, 1074-1484, 1074-1567, 1076-1331, 1289-1639
102/7506960CB1/1609	1-1609, 114-323, 114-744, 114-914, 114-926, 114-942, 114-981, 114-982, 206-1125, 307-1129, 368-1129, 394-1129, 397-1129, 612-1125, 634-1129, 888-1377, 930-1340, 930-1423, 932-1187, 1145-1495
103/7510540CB1/1930	1-133, 1-134, 1-742, 1-874, 1-1930, 229-892, 328-772, 440-835, 454-720, 465-1137, 524-761, 541-960, 567-752, 613-1194, 616-1218, 623-974, 649-770, 656-981, 684-1488, 735-956, 790-1605, 804-963, 807-963, 815-1607, 861-1607, 950-1345, 975-1607, 1028-1449, 1179-1453, 1234-1511, 1363-1647, 1363-1893, 1384-1652, 1414-1814, 1441-1704, 1482-1815, 1515-1786, 1646-1899
104/7510545CB1/1205	1-789, 4-1205, 429-640, 429-644, 429-650, 429-654, 429-661, 429-666, 429-669, 429-704, 429-799, 429-900, 429-989, 429-1060, 429-1084, 435-716, 435-1036, 436-818, 450-605, 454-992, 454-1150, 456-706, 456-710, 471-996, 509-1083, 519-795, 532-1156, 539-1056, 553-751, 553-796, 553-805, 556-811, 556-1064, 556-1135, 558-822, 559-834, 564-1069, 569-853, 570-1012, 572-849, 582-855, 583-802, 583-1107, 588-858, 598-1071, 599-831, 604-904, 610-855, 627-913, 630-873, 631-839, 634-859, 635-832, 635-905, 640-804, 644-948, 652-850, 672-892, 676-961, 678-952, 682-1038, 687-848, 691-887, 691-957, 691-980, 704-985, 707-980, 707-985, 713-951, 719-948, 730-964, 732-914, 732-1147, 735-991, 735-1018, 748-1003, 749-1143, 750-988, 757-1142, 766-1021, 777-1043, 777-1080, 779-1030, 780-1052, 783-1036, 799-1030, 799-1040, 800-1046, 801-934, 803-1067, 807-1155, 813-1071, 815-1082, 815-1104, 823-1113, 827-1018, 833-1114, 838-1107, 838-1111, 843-1110, 843-1112, 851-1088, 851-1089, 851-1116, 859-1056, 859-1151, 859-1155, 865-1054, 866-1114, 871-1155, 883-1155, 887-1057, 940-1113, 950-1071

Table 4

Polynucleotide SEQ ID NO./ Incyte ID/ Sequence Length	Sequence Fragments
105/7510654CBI/1790	1-260, 2-313, 2-1789, 20-595, 20-732, 20-772, 40-447, 41-763, 41-838, 41-942, 43-788, 43-811, 43-900, 43-944, 111-335, 111-449, 121-258, 129-501, 129-592, 156-610, 222-595, 222-716, 222-983, 279-860, 360-593, 360-893, 420-747, 452-753, 455-575, 524-919, 529-941, 530-1104, 544-772, 583-832, 645-848, 663-935, 663-1023, 675-990, 703-966, 711-973, 720-1023, 731-946, 766-999, 776-914, 831-1023, 843-871, 919-1023, 1022-1330, 1022-1544, 1027-1579, 1029-1287, 1029-1492, 1029-1519, 1029-1566, 1029-1570, 1029-1598, 1034-1277, 1040-1578, 1041-1317, 1045-1579, 1048-1578, 1055-1579, 1060-1266, 1060-1337, 1063-1256, 1063-1309, 1065-1434, 1065-1579, 1069-1372, 1073-1214, 1073-1286, 1073-1300, 1074-1533, 1076-1311, 1079-1578, 1081-1579, 1082-1579, 1089-1574, 1090-1347, 1093-1291, 1093-1729, 1097-1579, 1105-1573, 1108-1557, 1108-1576, 1116-1339, 1125-1391, 1130-1408, 1132-1579, 1138-1308, 1157-1385, 1161-1401, 1161-1579, 1173-1404, 1196-1394, 1204-1576, 1211-1454, 1221-1576, 1228-1345, 1243-1519, 1244-1655, 1259-1529, 1259-1710, 1272-1789, 1277-1578, 1278-1579, 1381-1789, 1395-1579, 1396-1578, 1397-1579, 1422-1576, 1451-1579, 1480-1579, 1712-1786
106/7510660CB/3824	1-3820, 119-822, 124-917, 140-548, 140-813, 149-617, 166-895, 168-718, 501-1113, 705-1045, 751-1354, 758-994, 768-1517, 787-1528, 816-1535, 850-1078, 850-1138, 850-1303, 850-1436, 850-1489, 850-1491, 850-1541, 853-1499, 883-1266, 883-1406, 883-1423, 883-1467, 883-1470, 903-1470, 909-1444, 971-1692, 991-1664, 1010-1262, 1057-1604, 1070-1814, 1104-1465, 1104-1470, 1105-1470, 1115-1470, 1126-1470, 1164-1465, 1174-1470, 1178-1465, 1190-1470, 1199-1461, 1199-1470, 1214-1470, 1218-1470, 1220-1470, 1220-1841, 1226-1470, 1239-1465, 1284-1812, 1303-1799, 1333-1891, 1340-1958, 1368-1986, 1376-1465, 1398-1951, 1399-1780, 1399-1873, 1399-1913, 1399-1944, 1399-2015, 1401-1998, 1401-2002, 1403-2175, 1404-1576, 1415-2104, 1418-2059, 1489-2107, 1497-1941, 1506-2095, 1525-1769, 1525-2028, 1525-2054, 1529-1622, 1529-1768, 1529-1775, 1529-2124, 1529-2135, 1536-2082, 1543-1794, 1543-1827, 1546-1711, 1548-1831, 1563-2137, 1576-2159, 1590-1850, 1629-1941, 1653-2228, 1657-1823, 1687-1930, 1687-2150, 1687-2173, 1687-2229, 1699-2228, 1703-1848, 1727-2001,

Table 4

Polynucleotide SEQ ID NO./ Incyte ID/ Sequence Length	Sequence Fragments
	1748-2229, 1753-1941, 1787-2192, 1788-2036, 1824-2105, 1851-1941, 1967-2212, 1974-2229, 1985-2169, 2001- 2207, 2010-2317, 2010-2353, 2010-2403, 2010-2614, 2010-2819, 2096-2858, 2106-2621, 2116-2718, 2168-2821, 2172-2859, 2193-2801, 2214-2888, 2228-2484, 2228-2496, 2229-2825, 2233-2726, 2234-2695, 2236-2854, 2237- 2904, 2239-2584, 2243-2569, 2249-2501, 2262-2797, 2262-2853, 2271-2768, 2272-2601, 2274-2756, 2274-2785, 2278-2808, 2280-2623, 2288-2448, 2294-2876, 2296-2887, 2301-2895, 2302-2695, 2308-2588, 2321-2982, 2352- 2628, 2360-3029, 2364-3005, 2367-2948, 2367-3028, 2368-2671, 2421-2971, 2421-2985, 2424-2852, 2425-2597, 2427-3098, 2439-3064, 2446-2710, 2452-2734, 2452-2769, 2453-2921, 2459-2780, 2461-3130, 2462-3135, 2467- 2672, 2468-3065, 2473-3067, 2481-2883, 2482-2883, 2487-2862, 2488-3089, 2495-3097, 2497-3221, 2502-2765, 2510-3255, 2518-2998, 2520-3207, 2521-3017, 2522-2769, 2536-2807, 2536-3026, 2537-3053, 2541-3046, 2541- 3052, 2541-3080, 2542-3320, 2543-2810, 2544-2784, 2545-3156, 2546-2839, 2551-3164, 2555-3137, 2557-3065, 2557-3068, 2563-2746, 2566-3245, 2570-3102, 2575-2971, 2580-3183, 2589-3050, 2589-3296, 2590-3277, 2593- 3296, 2596-2888, 2611-2949, 2612-2871, 2615-3184, 2616-2918, 2617-3282, 2620-2809, 2620-3195, 2626-3136, 2636-2925, 2649-3124, 2654-3130, 2658-3168, 2666-2991, 2669-3137, 2672-2902, 2675-2933, 2678-2951, 2684- 3175, 2689-3342, 2690-2961, 2699-2968, 2701-3310, 2721-3355, 2722-3151, 2723-3199, 2725-3282, 2727-3116, 2728-3233, 2729-3116, 2734-3212, 2737-2999, 2739-3233, 2755-3395, 2756-3330, 2758-3018, 2760-3056, 2761- 2931, 2764-2901, 2770-3076, 2794-3169, 2794-3285, 2794-3401, 2795-3047, 2795-3050, 2795-3086, 2811-3303, 2812-3368, 2813-3679, 2820-3304, 2826-3397, 2827-3339, 2833-3067, 2841-3091, 2841-3244, 2841-3307, 2847- 3408, 2855-3267, 2885-3125, 2894-3134, 2894-3141, 2912-3161, 2912-3363, 2918-3263, 2918-3458, 2920-3291, 2927-3242, 2949-3360, 2949-3431, 2953-3425, 2958-3293, 2958-3506, 2967-3206, 2972-3259, 2975-3289, 2975- 3294, 2986-3102, 2988-3609, 2988-3686, 3009-3288, 3024-3250, 3029-3815, 3038-3506, 3059-3318, 3059-3649,

Table 4

Polynucleotide SEQ ID NO./ Incyte ID/ Sequence Length	Sequence Fragments
	3059-3660, 3061-3298, 3062-3275, 3064-3327, 3071-3311, 3071-3615, 3078-3361, 3082-3574, 3086-3374, 3089-3329, 3089-3355, 3095-3506, 3102-3506, 3116-3643, 3125-3689, 3130-3306, 3132-3815, 3135-3578, 3139-3419, 3141-3815, 3145-3764, 3149-3459, 3153-3391, 3160-3807, 3161-3466, 3162-3413, 3164-3815, 3165-3374, 3165-3415, 3165-3509, 3168-3824, 3170-3460, 3172-3278, 3173-3442, 3174-3424, 3174-3824, 3181-3401, 3184-3792, 3185-3474, 3187-3394, 3197-3461, 3197-3719, 3212-3411, 3212-3459, 3225-3815, 3227-3387, 3228-3685, 3229-3469, 3230-3535, 3240-3478, 3245-3743, 3245-3777, 3247-3773, 3250-3779, 3277-3794, 3287-3742, 3287-3824, 3296-3824, 3300-3685, 3303-3815, 3308-3778, 3312-3824, 3315-3449, 3323-3814, 3325-3506, 3326-3506, 3329-3824, 3331-3506, 3340-3506, 3344-3824, 3357-3572, 3360-3824, 3367-3824, 3369-3815, 3371-3620, 3372-3824, 3377-3506, 3377-3598, 3377-3667, 3377-3763, 3377-3798, 3377-3815, 3386-3821, 3388-3629, 3388-3816, 3392-3646, 3392-3815, 3402-3652, 3407-3815, 3411-3775, 3411-3815, 3417-3606, 3418-3817, 3420-3659, 3420-3824, 3426-3822, 3426-3824, 3429-3816, 3430-3816, 3437-3505, 3438-3503, 3441-3506, 3441-3687, 3441-3702, 3441-3704, 3441-3705, 3441-3706, 3441-3733, 3442-3506, 3444-3506, 3446-3506, 3457-3506, 3461-3506, 3463-3506, 3465-3506, 3466-3506, 3468-3506, 3470-3506, 3473-3506, 3474-3755, 3475-3506, 3478-3506, 3486-3506, 3488-3510, 3505-3525, 3505-3544, 3505-3546, 3505-3554, 3505-3565, 3505-3566, 3505-3567, 3505-3658, 3505-3684, 3505-3685, 3505-3689, 3505-3696, 3505-3699, 3505-3702, 3505-3704, 3505-3707, 3505-3716, 3505-3718, 3505-3720, 3505-3724, 3505-3734, 3505-3735, 3505-3752, 3505-3778, 3505-3800, 3505-3811, 3505-3815, 3505-3818, 3505-3819, 3505-3820, 3505-3821, 3505-3822, 3505-3824, 3506-3816, 3507-3769, 3507-3801, 3524-3820, 3531-3816, 3536-3815, 3539-3777, 3549-3796, 3554-3776, 3561-3815, 3566-3784, 3566-3820, 3573-3775, 3589-3815, 3598-3816, 3620-3815, 3647-3816, 3648-3818, 3649-3776, 3649-3815, 3651-3815, 3674-3815, 3674-3821, 3705-3824, 3708-3824, 3736-3819

Table 4

Polynucleotide SEQ ID NO./ Incyte ID/ Sequence Length	Sequence Fragments
107/7510661CB1/3770	<p>1-3770, 119-822, 124-917, 140-548, 140-813, 149-617, 166-895, 168-718, 501-1113, 705-1045, 751-1354, 758-994, 768-1517, 787-1528, 816-1535, 850-1078, 850-1138, 850-1303, 850-1436, 850-1489, 850-1491, 850-1541, 853-1499, 883-1266, 883-1406, 883-1423, 883-1467, 883-1470, 903-1470, 909-1444, 971-1692, 991-1664, 1010-1262, 1057-1604, 1070-1814, 1104-1465, 1104-1470, 1105-1470, 1115-1470, 1126-1470, 1164-1465, 1174-1470, 1178-1465, 1190-1470, 1199-1461, 1199-1470, 1214-1470, 1218-1470, 1220-1470, 1220-1841, 1226-1470, 1239-1465, 1284-1812, 1303-1799, 1333-1891, 1340-1941, 1354-2064, 1368-1997, 1376-1465, 1399-1780, 1399-1873, 1399-1913, 1399-1941, 1404-1576, 1445-2098, 1489-2247, 1525-1769, 1529-1622, 1529-1768, 1529-1775, 1543-1794, 1543-1827, 1546-1711, 1548-1831, 1590-1850, 1629-2283, 1657-1823, 1686-2379, 1687-1930, 1703-1848, 1753-2333, 1843-2476, 1849-2545, 1851-2544, 1886-2540, 1914-2573, 1939-2749, 1940-2099, 1940-2137, 2026-2788, 2036-2551, 2046-2648, 2098-2751, 2102-2789, 2123-2731, 2144-2818, 2158-2414, 2158-2426, 2159-2755, 2163-2656, 2164-2625, 2166-2784, 2167-2834, 2169-2514, 2173-2499, 2179-2431, 2192-2727, 2192-2783, 2201-2698, 2202-2531, 2204-2686, 2204-2715, 2208-2738, 2210-2553, 2218-2378, 2224-2806, 2226-2817, 2231-2825, 2232-2625, 2238-2518, 2251-2912, 2282-2558, 2290-2959, 2294-2935, 2297-2878, 2297-2958, 2298-2601, 2351-2901, 2351-2915, 2354-2782, 2355-2527, 2357-3028, 2369-2994, 2376-2640, 2382-2664, 2382-2699, 2383-2851, 2389-2710, 2391-3060, 2392-3065, 2397-2602, 2398-2995, 2403-2997, 2411-2813, 2412-2813, 2417-2792, 2418-3019, 2425-3027, 2427-3151, 2432-2695, 2440-3185, 2448-2928, 2450-3137, 2451-2947, 2452-2699, 2466-2737, 2466-2956, 2467-2983, 2471-2976, 2471-2982, 2471-3010, 2472-3250, 2473-2740, 2474-2714, 2475-3086, 2476-2769, 2481-3094, 2485-3067, 2487-2995, 2487-2998, 2493-2676, 2496-3175, 2500-3032, 2505-2901, 2510-3113, 2519-2980, 2519-3226, 2520-3207, 2523-3226, 2526-2818, 2541-2879, 2542-2801, 2545-3114, 2546-2848, 2547-3212, 2550-2739, 2550-3125, 2556-3066, 2566-2855, 2579-3054, 2584-3060, 2588-3098, 2596-2921, 2599-3067,</p>

Table 4

Polynucleotide SEQ ID NO./ Incyte ID/ Sequence Length	Sequence Fragments
	2602-2832, 2605-2863, 2608-2881, 2614-3105, 2619-3272, 2620-2891, 2629-2898, 2631-3240, 2651-3285, 2652-3081, 2653-3129, 2655-3212, 2657-3046, 2658-3163, 2659-3046, 2664-3142, 2667-2929, 2669-3163, 2685-3325, 2686-3260, 2688-2948, 2690-2986, 2691-2861, 2694-2831, 2700-3006, 2724-3099, 2724-3215, 2724-3331, 2725-2977, 2725-2980, 2725-3016, 2741-3233, 2742-3298, 2743-3630, 2750-3234, 2756-3327, 2757-3269, 2763-2997, 2771-3021, 2771-3174, 2771-3237, 2777-3338, 2785-3197, 2815-3055, 2824-3064, 2824-3071, 2842-3091, 2842-3293, 2848-3193, 2848-3388, 2850-3221, 2857-3172, 2879-3290, 2879-3361, 2883-3355, 2888-3223, 2888-3437, 2897-3136, 2902-3189, 2905-3219, 2905-3224, 2916-3032, 2918-3560, 2918-3637, 2939-3218, 2954-3180, 2959-3766, 2968-3520, 2989-3248, 2989-3600, 2989-3611, 2991-3228, 2992-3205, 2994-3257, 3001-3241, 3001-3566, 3008-3291, 3012-3525, 3016-3304, 3019-3259, 3019-3285, 3025-3453, 3032-3518, 3046-3594, 3055-3640, 3062-3766, 3069-3349, 3071-3766, 3075-3715, 3079-3389, 3083-3321, 3090-3758, 3091-3396, 3092-3343, 3094-3766, 3095-3304, 3095-3345, 3095-3440, 3098-3770, 3100-3390, 3102-3208, 3103-3372, 3104-3354, 3104-3770, 3111-3331, 3114-3743, 3115-3404, 3117-3324, 3127-3391, 3127-3670, 3142-3341, 3142-3389, 3155-3766, 3157-3317, 3158-3636, 3159-3399, 3160-3432, 3170-3408, 3175-3694, 3175-3728, 3177-3724, 3180-3730, 3207-3745, 3217-3693, 3217-3767, 3226-3770, 3230-3636, 3233-3766, 3238-3729, 3242-3770, 3253-3765, 3255-3495, 3256-3497, 3259-3770, 3261-3516, 3270-3505, 3271-3402, 3274-3770, 3287-3523, 3290-3770, 3297-3770, 3299-3766, 3301-3571, 3302-3770, 3307-3476, 3307-3618, 3307-3714, 3307-3749, 3307-3766, 3316-3770, 3318-3580, 3318-3767, 3322-3597, 3322-3766, 3332-3603, 3337-3766, 3341-3726, 3347-3557, 3348-3768, 3350-3610, 3350-3770, 3356-3768, 3356-3770, 3359-3767, 3360-3767, 3367-3770, 3368-3770, 3371-3638, 3371-3647, 3371-3653, 3371-3655, 3371-3656, 3371-3657, 3371-3684, 3372-3655, 3372-3658, 3372-3685, 3372-3703, 3374-3653, 3376-3729, 3387-3762, 3391-3766, 3393-3770, 3395-3766, 3396-3769, 3398-3669, 3400-3609, 3400-3636, 3400-3650, 3403-3766, 3403-3770, 3405-3667, 3405-3671, 3408-3517, 3410-3770, 3416-3640, 3418-3769, 3428-3751, 3431-3635, 3433-3770, 3435-3766, 3435-3769, 3437-3766, 3438-3770, 3440-3766, 3440-3770, 3442-3686, 3445-3770, 3446-3766, 3447-3766, 3447-3770, 3449-3675, 3452-3770, 3457-3767, 3458-3720, 3458-3752, 3475-3770, 3482-3767, 3487-3766, 3490-3728, 3500-3747, 3505-3727, 3512-3766, 3517-3735, 3517-3770, 3524-3726, 3540-3766, 3549-3767, 3571-3766, 3598-3767, 3599-3769, 3600-3727, 3600-3766, 3602-3766, 3625-3766, 3625-3770, 3656-3770, 3659-3770, 3687-3770

Table 4

Polynucleotide SEQ ID NO./ Incyte ID/ Sequence Length	Sequence Fragments
108/7510680CB1/1978	1-350, 12-308, 12-1976, 131-408, 140-507, 521-651, 521-652, 521-782, 521-892, 521-972, 521-982, 521-1005, 521-1086, 594-866, 598-652, 618-1152, 654-1072, 703-1311, 721-1280, 740-929, 755-1354, 771-1310, 786-1382, 792-1096, 798-1267, 801-1389, 807-1294, 809-1078, 809-1452, 822-1497, 858-1322, 859-1246, 864-1427, 871-1349, 873-1155, 873-1159, 882-1472, 893-1241, 896-1443, 902-1315, 937-1513, 1028-1427, 1034-1330, 1061-1310, 1118-1375, 1298-1513, 1335-1830, 1510-1856, 1510-1870, 1510-1883, 1510-1972, 1510-1975, 1510-1976, 1510-1978, 1534-1962, 1560-1949, 1618-1961
109/7505145CB1/1622	1-153, 1-236, 1-1612, 7-243, 9-238, 9-491, 9-570, 14-257, 14-289, 14-320, 21-228, 21-268, 25-284, 27-228, 27-238, 27-279, 30-319, 32-265, 32-272, 32-288, 33-275, 33-290, 36-328, 39-219, 39-232, 39-369, 40-307, 40-501, 41-264, 41-324, 41-331, 41-348, 42-308, 42-310, 44-312, 44-548, 44-626, 45-229, 45-282, 47-335, 51-199, 51-307, 56-312, 60-303, 71-683, 74-654, 76-331, 83-339, 90-303, 91-242, 94-321, 99-326, 106-375, 126-427, 151-640, 157-887, 159-435, 177-627, 189-447, 198-480, 199-442, 272-521, 304-881, 326-533, 354-577, 357-603, 357-859, 357-902, 359-774, 360-522, 361-630, 363-884, 377-638, 390-645, 395-637, 398-676, 408-579, 427-648, 429-614, 430-923, 430-994, 443-701, 451-639, 456-699, 456-715, 461-679, 465-719, 477-740, 477-755, 487-681, 493-954, 493-965, 512-777, 528-794, 532-743, 538-1070, 548-815, 553-691, 560-879, 577-804, 583-963, 615-839, 618-861, 624-835, 643-809, 644-872, 655-971, 671-933, 694-979, 699-994, 702-970, 702-994, 728-994, 746-976, 754-977, 764-1019, 767-994, 773-862, 777-915, 783-992, 797-971, 811-954, 949-1603, 994-1218, 994-1240, 994-1274, 994-1278, 994-1331, 994-1568, 994-1616, 995-1614, 996-1256, 996-1564, 997-1212, 997-1274, 1004-1318, 1005-1261, 1005-1519, 1008-1555, 1013-1612, 1014-1318, 1025-1622, 1037-1294, 1037-1622, 1058-1312, 1062-1248, 1068-1621, 1071-1622, 1074-1622, 1087-1379, 1094-1325, 1097-1350, 1103-1594, 1105-1615, 1114-1333, 1114-1418, 1116-1251, 1116-1569, 1117-1360, 1123-1360, 1124-1389, 1133-1436, 1135-1611, 1142-1622, 1143-1440, 1153-1622, 1162-1387, 1164-1614, 1171-1622, 1177-1622, 1182-1622, 1192-1611, 1194-1614, 1195-1459, 1195-1467, 1196-1622, 1198-1526, 1199-1610, 1200-1609, 1201-1610, 1206-1614, 1209-1610, 1212-1610, 1214-1610, 1215-1609, 1218-1610, 1220-1612, 1221-1610, 1224-1600, 1230-1610, 1232-1375, 1235-1609, 1235-1612, 1236-1415, 1238-1609, 1239-1622, 1240-1610, 1246-1622, 1248-1589, 1258-1510, 1268-1614, 1270-1517, 1270-1609, 1270-1622, 1273-1599, 1277-1611, 1282-1609, 1283-1620, 1284-1613, 1284-1622, 1292-1542, 1295-1561, 1300-1571, 1301-1609, 1302-1438, 1304-1619, 1309-1609, 1313-1564, 1319-1581, 1330-1578, 1337-1616, 1346-1607, 1571, 1301-1609, 1302-1438, 1304-1619, 1309-1609, 1313-1564, 1319-1581, 1330-1578, 1337-1616, 1346-1607,

Table 4

Polynucleotide SEQ ID NO./ Incyte ID/ Sequence Length	Sequence Fragments
110/7505162CBI/1982	<p>1350-1582, 1353-1611, 1363-1610, 1371-1611, 1371-1622, 1399-1608, 1399-1609, 1407-1622, 1412-1610, 1415-1619, 1415-1622, 1416-1609, 1417-1599, 1418-1615, 1419-1614, 1421-1609, 1422-1611, 1422-1612, 1424-1611, 1431-1576, 1436-1603, 1444-1619, 1444-1622, 1453-1583, 1453-1596, 1454-1622, 1476-1611, 1479-1615, 1496-1613, 1521-1615, 1522-1622</p> <p>1-256, 1-294, 1-439, 1-472, 1-486, 1-490, 1-533, 1-545, 1-663, 2-275, 4-775, 5-212, 5-292, 5-1982, 7-245, 7-253, 7-279, 7-280, 7-339, 9-264, 10-689, 14-308, 18-299, 19-258, 33-287, 60-338, 89-327, 106-409, 113-413, 113-495, 113-672, 114-371, 116-350, 139-671, 153-399, 157-668, 158-422, 159-562, 173-342, 180-342, 189-720, 192-467, 229-870, 263-755, 285-628, 289-547, 315-873, 333-592, 333-692, 335-602, 342-579, 354-858, 369-590, 369-839, 375-983, 382-652, 401-631, 401-999, 443-1052, 446-958, 505-754, 529-999, 594-748, 594-856, 602-781, 602-804, 605-919, 609-827, 609-830, 637-910, 640-972, 671-999, 697-949, 704-961, 788-1349, 815-963, 839-1186, 953-1092, 981-1531, 997-1251, 1003-1336, 1006-1537, 1007-1300, 1016-1323, 1023-1694, 1024-1240, 1026-1438, 1036-1295, 1038-1537, 1040-1291, 1049-1587, 1069-1500, 1075-1295, 1081-1699, 1084-1324, 1090-1360, 1098-1344, 1103-1699, 1105-1641, 1106-1645, 1124-1584, 1124-1673, 1131-1771, 1133-1333, 1138-1311, 1139-1422, 1157-1740, 1165-1304, 1172-1403, 1174-1678, 1176-1830, 1179-1466, 1180-1851, 1182-1398, 1183-1442,</p> <p>1184-1505, 1189-1483, 1190-1628, 1192-1759, 1197-1478, 1206-1702, 1210-1768, 1210-1891, 1215-1491, 1218-1600, 1220-1710, 1220-1817, 1226-1813, 1238-1701, 1239-1549, 1240-1872, 1247-1724, 1253-1506, 1256-1432, 1256-1588, 1256-1932, 1257-1861, 1268-1590, 1271-1593, 1272-1801, 1273-1544, 1275-1954, 1277-1900, 1288-1982, 1290-1489, 1295-1478, 1305-1733, 1309-1733, 1311-1812, 1312-1609, 1313-1982, 1315-1782, 1327-1454, 1329-1973, 1333-1951, 1335-1913, 1345-1949, 1348-1900, 1368-1952, 1374-1982, 1375-1982, 1377-1552, 1384-1666, 1389-1975, 1395-1982, 1397-1696, 1400-1672, 1400-1676, 1401-1785, 1401-1961, 1413-1748, 1413-1874, 1415-1847, 1420-1671, 1421-1723, 1430-1979, 1445-1662, 1445-1665, 1446-1965, 1466-1982, 1476-1982, 1482-1893, 1483-1972, 1483-1977, 1485-1971, 1486-1601, 1486-1737, 1494-1955, 1496-1972, 1508-1682, 1508-1726, 1508-1972, 1509-1977, 1513-1982, 1521-1982, 1523-1643, 1534-1972, 1534-1978, 1535-1976, 1538-1972, 1539-1977, 1540-1982, 1542-1776, 1543-1972, 1546-1978, 1548-1967, 1548-1972, 1550-1971, 1550-1972, 1561-1972,</p>

Table 4

Polynucleotide SEQ ID NO./ Incyte ID/ Sequence Length	Sequence Fragments
111/7505469CB1/2231	1578-1900, 1580-1972, 1584-1975, 1588-1972, 1590-1972, 1593-1972, 1598-1973, 1610-1976, 1613-1974, 1623-1897, 1625-1972, 1630-1971, 1636-1777, 1636-1925, 1638-1982, 1645-1753, 1646-1972, 1647-1891, 1648-1972, 1659-1972, 1662-1873, 1667-1972, 1669-1964, 1670-1978, 1671-1971, 1671-1974, 1672-1979, 1674-1972, 1678-1973, 1680-1975, 1682-1972, 1687-1973, 1702-1972, 1707-1971, 1709-1974, 1717-1973, 1717-1974, 1743-1978, 1768-1947, 1770-1973, 1779-1971, 1837-1974, 1838-1972, 1861-1982, 1899-1972 1-593, 4-307, 4-668, 4-753, 4-825, 4-2221, 32-606, 39-105, 91-392, 120-254, 126-410, 149-764, 156-756, 169-620, 178-684, 258-784, 271-717, 279-810, 289-789, 306-741, 402-665, 518-686, 533-686, 563-681, 665-779, 665-929, 665-936, 665-1058, 665-1095, 665-1116, 665-1297, 666-1155, 792-1131, 810-1039, 810-1418, 882-1241, 912-1463, 1038-1476, 1039-1633, 1073-1362, 1112-1560, 1125-1673, 1130-1401, 1135-1658, 1151-2012, 1167-1283, 1169-2012, 1174-2012, 1197-1673, 1204-1522, 1207-2012, 1208-2012, 1209-2012, 1212-2009, 1212-2012, 1226-2012, 1233-1673, 1242-1822, 1252-1758, 1253-2012, 1277-2012, 1296-1673, 1299-2012, 1335-2012, 1342-1745, 1344-2012, 1357-2012, 1368-2011, 1376-1673, 1382-2012, 1383-2012, 1390-2012, 1414-1712, 1423-2096, 1438-2099, 1450-1687, 1646-2221, 1668-2012, 1712-1952, 1712-1985, 1712-2192, 1712-2231, 1768-2231, 1780-2231, 1782-2231, 1814-2089, 1829-2231, 1840-2231, 1870-2004, 1880-2197, 1881-2231, 1900-2152, 1901-2145, 1909-2152, 1921-2231, 1928-2152, 1935-2153, 1950-2155, 1976-2147, 1982-2192, 2017-2231, 2034-2139
112/7505475CB1/5170	1-229, 1-255, 1-273, 1-420, 1-480, 1-507, 1-515, 1-563, 1-579, 1-594, 1-599, 1-630, 1-631, 1-636, 1-637, 1-5070, 4-314, 5-286, 14-275, 39-283, 43-500, 43-556, 51-320, 777-1350, 777-1377, 777-1394, 1130-1653, 1130-1836, 1230-1983, 1239-1525, 1239-1860, 1248-1852, 1274-1825, 1353-1923, 1359-1860, 1388-1987, 1432-1860, 1450-1979, 1450-1980, 1450-2029, 1450-2032, 1450-2066, 1450-2081, 1457-1860, 1459-1860, 1465-1860, 1475-1860, 1476-1964, 1527-1753, 1610-2048, 1615-2034, 1730-1908, 1838-2486, 1898-2343, 1898-2344, 2086-2243, 2091-2343, 2096-2286, 2096-2343, 2096-2344, 2102-2236, 2103-2236, 2104-2236, 2122-2411, 2187-2344, 2196-2769, 2196-2829, 2275-2673, 2275-2708, 2275-2767, 2275-2845, 2275-2851, 2275-2860, 2275-2879, 2275-2894, 2275-2912, 2275-2969, 2371-2778, 2389-2834, 2402-2943, 2405-2642, 2428-2767, 2450-2968, 2470-3070, 2476-2944, 2521-3218, 2612-3230, 2626-3124, 2626-3152, 2626-3184, 2626-3194, 2626-3211, 2626-3228, 2626-3247, 2626-3288, 2628-3115, 2629-3142, 2632-3206, 2632-3244, 2632-3356, 2632-3359, 2667-3361, 2679-3244, 2680-2948,

Table 4

Polynucleotide SEQ ID NO./ Incyte ID/ Sequence Length	Sequence Fragments
	2680-3165, 2680-3227, 2680-3244, 2680-3361, 2682-3359, 2684-3236, 2695-3353, 2697-3361, 2701-3361, 2702-3348, 2703-3309, 2713-3361, 2722-3361, 2727-3361, 2728-3361, 2730-3361, 2732-3361, 2733-3189, 2733-3317, 2733-3323, 2733-3361, 2738-3361, 2741-2985, 2741-3022, 2741-3132, 2741-3135, 2741-3199, 2741-3261, 2741-3273, 2741-3346, 2741-3361, 2742-3361, 2744-3041, 2744-3361, 2746-3361, 2752-3361, 2758-3361, 2764-3361, 2782-3283, 2782-3315, 2782-3357, 2782-3360, 2782-3361, 2784-3361, 2786-3361, 2789-3361, 2790-3361, 2806-3360, 2806-3361, 2829-3361, 2832-3360, 2833-3314, 2833-3333, 2833-3360, 2833-3361, 2835-3361, 2837-3361, 2843-3334, 2843-3361, 2844-3361, 2858-3361, 2859-3361, 2875-3356, 2883-3361, 2890-3360, 2895-3361, 2912-3361, 2920-3361, 2954-3361, 3072-3361, 3096-3361, 3118-3360, 3118-3361, 3119-3361, 3129-3351, 3129-3544, 3137-3360, 3137-3361, 3199-3474, 3199-3645, 3199-3672, 3199-3759, 3199-3781, 3199-3801, 3199-3859, 3199-3861, 3268-3361, 3368-3751, 3368-3843, 3368-3945, 3368-3951, 3391-4426, 3401-3590, 3438-3916, 3444-4086, 3449-3932, 3481-3865, 3511-4397, 3521-3768, 3538-4155, 3541-4156, 3550-4044, 3553-3847, 3553-4145, 3588-4259, 3623-4288, 3652-4353, 3674-4356, 3683-4169, 3684-4183, 3687-4013, 3688-4180, 3695-4273, 3696-4022, 3703-3952, 3713-4227, 3715-4288, 3727-4262, 3731-4406, 3734-4341, 3737-4285, 3739-4373, 3754-3991, 3758-4221, 3758-4321, 3758-4420, 3762-4313, 3763-4319, 3769-4202, 3772-4325, 3772-4402, 3796-4284, 3802-4471, 3817-4412, 3824-4341, 3825-4095, 3844-4407, 3846-4256, 3847-4365, 3848-4261, 3848-4299, 3848-4319, 3848-4353, 3848-4359, 3848-4427, 3849-4393, 3853-4203, 3857-4125, 3862-4109, 3863-4423, 3868-4434, 3869-4130, 3872-4369, 3878-4552, 3879-4399, 3887-4334, 3888-4621, 3894-4558, 3896-4483, 3901-4519, 3902-4165, 3915-4577, 3921-4564, 3925-4539, 3927-4137, 3930-4543, 3935-4177, 3940-4410, 3941-4249, 3953-4465, 3955-4416, 3955-4529, 3958-4146, 3960-4543, 3966-4651, 3967-4470, 3967-4598, 3970-4732, 3977-4652, 3978-4461, 3983-4652, 3988-4518, 3989-4545, 3991-4431, 3991-4520, 3994-4560, 3997-4648, 4004-4480, 4012-4272, 4012-4513, 4012-4709, 4019-4630, 4024-4691, 4027-4677, 4028-4531, 4032-4505, 4033-4504, 4034-4670, 4037-4297, 4037-4320, 4037-4518, 4037-4537, 4037-4656, 4039-4513, 4039-4621, 4040-4394, 4052-4725, 4053-4397, 4061-4568, 4065-5025, 4069-4663, 4074-4765, 4075-4418, 4075-4693, 4077-4583, 4086-4208, 4101-4607, 4103-4599, 4106-4539, 4139-4254, 4145-4757, 4148-4784, 4150-4706, 4154-4375, 4159-4365, 4170-4362, 4170-4651, 4172-4737, 4180-4709, 4183-4884, 4216-4835, 4219-4737, 4219-4934, 4221-4834, 4223-4678, 4228-4847, 4229-4983, 4239-4858, 4244-4843, 4252-4812, 4262-4653, 4263-4514, 4267-4408, 4280-4731, 4285-4930, 4286-4458, 4288-4894, 4290-4833, 4292-4840, 4294-4940, 4311-4835, 4317-4736, 4317-4946, 4326-4929, 4328-4429, 4331-4909, 4354-4924, 4358-4924, 4370-4950, 4370-4991, 4371-4950, 4377-4950, 4378-4952, 4388-5078,

Table 4

Polynucleotide SEQ ID NO./ Incyte ID/ Sequence Length	Sequence Fragments
	4437-4959, 4443-5115, 4462-4950, 4490-4800, 4490-5070, 4509-4705, 4509-4722, 4511-4996, 4515-4779, 4515-4989, 4516-4794, 4525-4950, 4537-4950, 4553-4847, 4564-4950, 4566-4950, 4569-4945, 4577-4841, 4579-5170, 4599-5018, 4622-4947, 4625-4771, 4639-5041, 4642-4945, 4657-4959, 4657-5076, 4687-4979, 4701-5040, 4734-4952, 4755-5040, 4757-4872, 4757-4911, 4828-5066, 4922-5072
113/7505568CB1/1876	1-204, 1-246, 1-576, 1-603, 1-750, 1-765, 1-783, 1-816, 1-867, 1-1876, 2-634, 5-685, 7-206, 10-244, 30-281, 48-115, 102-865, 142-836, 305-547, 305-571, 305-573, 305-875, 326-907, 342-1225, 349-1036, 368-882, 380-941, 381-879, 383-588, 383-943, 385-519, 387-1006, 407-612, 429-948, 437-952, 451-1273, 455-1062, 463-994, 470-938, 475-734, 475-1022, 484-1086, 513-1497, 514-1143, 520-1121, 522-1093, 531-1101, 544-847, 548-1022, 573-1079, 585-1025, 585-1095, 585-1444, 607-943, 617-940, 619-1155, 620-1176, 626-1273, 631-1404, 632-1138, 652-1234, 669-1184, 670-1185, 673-1182, 680-1223, 680-1242, 680-1303, 700-801, 700-926, 712-1313, 713-868, 713-899, 727-1394, 740-1012, 740-1157, 740-1230, 740-1300, 740-1319, 740-1321, 740-1350, 740-1383, 740-1399, 741-1475, 742-878, 742-909, 742-1069, 742-1400, 744-1571, 752-978, 756-1030, 756-1041, 756-1230, 756-1295, 766-1304, 771-1213, 775-1404, 778-1256, 779-979, 779-988, 789-1149, 799-1308, 806-1064, 808-1149, 821-1425, 825-1383, 832-1408, 834-1086, 836-1424, 873-1480, 876-1173, 894-1204, 912-1437, 915-1740, 918-1480, 940-1454, 951-1049-1412, 1054-1876, 1055-1876, 1079-1876, 1091-1876, 1123-1343, 1129-1876, 1143-1257, 1160-1876, 1185-1345, 1186-1729, 1191-1691, 1195-1876, 1239-1874, 1265-1753, 1270-1479, 1270-1497, 1270-1854, 1279-1820, 1325-1497, 1495-1875
114/7506953CB1/1602	1-1602, 114-308, 114-876, 308-1118, 308-1122, 311-1122, 324-805, 325-1122, 333-1122, 337-1122, 339-1121, 339-1122, 352-1122, 355-1122, 358-1122, 379-1118, 397-1122, 399-1118, 400-1121, 412-1122, 414-1122, 419-1118, 436-823, 441-823, 446-1118, 447-1118, 450-1122, 452-1118, 456-1122, 497-1062, 500-1122, 531-1122, 603-1118, 604-966, 604-1118, 627-1122, 881-1370, 923-1333, 923-1416, 925-1180, 1138-1488
115/7510176CB1/2173	1-398, 1-569, 1-644, 1-656, 1-724, 1-729, 1-736, 18-115, 18-124, 18-2173, 112-736, 410-952, 576-1116, 656-1460, 683-1618, 691-1607, 933-1870, 1053-1977, 1173-1814, 1373-2173, 1449-2173, 1453-2173, 1463-2173, 1465-2173, 1471-2173, 1823-1985

Table 4

Polynucleotide SEQ ID NO./ Incyte ID/ Sequence Length	Sequence Fragments
116/7510541CBI/1826	1-237, 1-1826, 40-464, 49-371, 58-301, 59-713, 61-313, 66-206, 67-382, 71-341, 464-946, 464-1028, 467-946, 492-911, 498-1102, 499-1102, 508-1102, 517-782, 522-845, 524-822, 547-685, 580-877, 608-882, 743-1384, 822-1056, 822-1154, 822-1294, 822-1315, 826-1258, 842-1456, 870-1418, 892-1379, 922-1448, 939-1580, 953-1228, 958-1466, 1074-1280, 1086-1364, 1086-1393, 1091-1659, 1137-1750, 1138-1706, 1146-1488, 1175-1442, 1180-1458, 1180-1586, 1180-1678, 1180-1703, 1180-1826, 1182-1406, 1200-1775, 1243-1680, 1247-1784, 1294-1458, 1368-1650, 1374-1516, 1389-1789, 1459-1666, 1488-1773, 1584-1826
117/7510923CBI/2052	1-237, 1-2052, 40-466, 49-371, 50-813, 51-664, 51-785, 58-301, 60-637, 61-313, 67-382, 71-341, 71-666, 73-665, 203-778, 436-1008, 532-1019, 566-985, 596-919, 621-759, 654-951, 682-956, 915-1464, 987-1584, 1093-1730, 1103-1378, 1108-1616, 1224-1430, 1236-1514, 1236-1543, 1241-1809, 1287-1900, 1288-1856, 1296-1638, 1325-1592, 1330-1608, 1330-1736, 1330-1828, 1330-1853, 1330-1981, 1332-1556, 1350-1925, 1393-1830, 1397-1934, 1444-1608, 1518-1800, 1524-1666, 1539-1939, 1609-1816, 1638-1923, 1734-2052
118/7510984CBI/5056	1-5053, 291-687, 1037-1504, 1251-1382, 1969-2443, 1978-2162, 2304-2666, 2457-2724, 2579-3381, 3662-4331, 3708-4226, 4331-4585, 4331-4810, 4341-4667, 4349-4591, 4350-4691, 4350-4812, 4368-4513, 4368-4667, 4368-4685, 4368-4771, 4368-4798, 4368-4805, 4368-4817, 4368-4819, 4368-4825, 4368-4841, 4375-4617, 4379-5053, 4399-4612, 4469-5027, 4613-5056, 4638-5056, 4683-5036, 4695-5053, 4769-5056, 4894-5049

Table 5

Polynucleotide SEQ ID NO:	Incyte Project ID:	Representative Library
60	7509332CB1	MONOTXN05
61	7509102CB1	PROSTUT10
62	7509132CB1	COLNNOT01
64	7509178CB1	MUSCNOT11
65	7509214CB1	DENDTNT01
66	7509244CB1	MUSCDIT06
67	7509256CB1	ISLTNOT01
68	7509395CB1	MUSCNOT11
69	7503287CB1	BRAUNOR01
70	7503320CB1	BSTMNON02
71	7503335CB1	BRATDIC01
73	7504530CB1	BRSTNOT04
74	7509303CB1	MIXDTME02
75	7509910CB1	BRACDIK08
76	7509982CB1	BRSTNOT01
77	7510082CB1	LIVRNON08
78	7510367CB1	BRAINON01
79	7510413CB1	MCLDTXN05
80	1721303CB1	SPLNNOT11
81	7502007CB1	DRGTNON04
82	7506439CB1	ADENINB01
84	7509404CB1	ISLTNOT01
85	7509439CB1	LIVRTMR01
86	7510202CB1	HEALDIR01
87	7510203CB1	FIBRTXS07
88	7510208CB1	BRAUNOR01
89	7510446CB1	BRAITUT21
90	7505294CB1	CORPNOT02
91	7505631CB1	HUVELPB01
93	7510733CB1	NEUTGMT01
94	7510734CB1	NEUTGMT01
95	7503977CB1	PROSTUT12
96	7505084CB1	SINTBST01
97	7506950CB1	BRAIHCT01
98	7506951CB1	BRAIHCT01
99	7506954CB1	BRAIHCT01
100	7506956CB1	BRAIHCT01
101	7506959CB1	BRAINOR03
102	7506960CB1	BRAIHCT01
103	7510540CB1	SINJNOT03
104	7510545CB1	LUNGNOT22
105	7510654CB1	BRAINOT12
106	7510660CB1	FIBRTXS07
107	7510661CB1	FIBRTXS07
108	7510680CB1	LNODNON02
109	7505145CB1	HEAONOT04
110	7505162CB1	PROSNOT06
111	7505469CB1	UTRSTUE01
112	7505475CB1	DRGCNOT01

Table 5

Polynucleotide SEQ ID NO:	Incyte Project ID:	Representative Library
113	7505568CB1	LIVRNON08
114	7506953CB1	BRAINOR03
115	7510176CB1	GBLADIT01
116	7510541CB1	MLP000060
117	7510923CB1	LIVRTMR01
118	7510984CB1	LIVRTUT13

Table 6

Library	Vector	Library Description
ADENINB01	PBLUESCRIPT	Library was constructed using RNA isolated from the inflamed adenoid tissue of a 3-year-old child. (RNA came from Clontech.)
BRACDIK08	PSPORT1	This amplified and normalized library was constructed using RNA isolated from diseased corpus callosum tissue removed from the brain of a 57-year-old Caucasian male who died from a cerebrovascular accident. Serologies were negative. Patient history included Huntington's disease, emphysema, and tobacco abuse (3-4 packs per day for 40 years).
BRAIHCT01	pINCY	Library was constructed using RNA isolated from diseased occipital lobe tissue removed from the brain of a 57-year-old Caucasian male, who died from a cerebrovascular accident. Patient history included Huntington's disease and emphysema.
BRAINON01	PSPORT1	Library was constructed and normalized from 4.88 million independent clones from a brain tissue library. RNA was made from brain tissue removed from a 26-year-old Caucasian male during cranioplasty and excision of a cerebralmeningeal lesion. Pathology for the associated tumor tissue indicated a grade 4 oligoastrocytoma in the right fronto-parietal part of the brain. The normalization and hybridization conditions were adapted from Soares et al., PNAS (1994) 91:9228, except that a significantly longer (48-hour) reannealing hybridization was used.
BRAINOR03	PBK-CMV	This random primed library was constructed using pooled cDNA from two donors. cDNA was generated using mRNA isolated from brain tissue removed from a Caucasian male fetus (donor A) who was stillborn with a hypoplastic left heart at 23 weeks' gestation and from brain tissue removed from a Caucasian male fetus (donor B), who died at 23 weeks' gestation from premature birth. Serologies were negative for both donors and family history for donor B included diabetes in the mother.
BRAINOT12	pINCY	Library was constructed using RNA isolated from brain tissue removed from the right frontal lobe of a 5-year-old Caucasian male during a hemispherectomy. Pathology indicated extensive polymicrogyria and mild to moderate gliosis (predominantly subpial and subcortical), which are consistent with chronic seizure disorder. Family history included a cervical neoplasm.
BRAITUT21	pINCY	Library was constructed using RNA isolated from brain tumor tissue removed from the midline frontal lobe of a 61-year-old Caucasian female during excision of a cerebral meningeal lesion. Pathology indicated subfrontal meningothelial meningioma with no atypia. One ehmoid and mucosal tissue sample indicated meningioma. Family history included cerebrovascular disease, senile dementia, hyperlipidemia, benign hypertension, atherosclerotic coronary artery disease, congestive heart failure, and breast cancer.

Table 6

Library	Vector	Library Description
BRATDIC01	pINCY	This large size-fractionated library was constructed using RNA isolated from diseased brain tissue removed from the left temporal lobe of a 27-year-old Caucasian male during a brain lobectomy. Pathology for the left temporal lobe, including the mesial temporal structures, indicated focal, marked pyramidal cell loss and gliosis in hippocampal sector CA1, consistent with mesial temporal sclerosis. The left frontal lobe showed a focal deep white matter lesion, characterized by marked gliosis, calcifications, and hemosiderin-laden macrophages, consistent with a remote perinatal injury. The frontal lobe tissue also showed mild to moderate generalized gliosis, predominantly subpial and subcortical, consistent with chronic seizure disorder. GFAP was positive for astrocytes. The patient presented with intractable epilepsy, focal epilepsy, hemiplegia, and unspecified brain injury. Patient history included cerebral palsy, abnormality of gait, depressive disorder, and tobacco abuse in remission. Previous surgeries included tendon transfer. Patient medications included minocycline, hydrochloride, Tegretol, phenobarbital, vitamin C, Pepcid, and Pevaryl. Family history included brain cancer
		in the father.
BRAUNOR01	pINCY	This random primed library was constructed using RNA isolated from striatum, globus pallidus and posterior putamen tissue removed from an 81-year-old Caucasian female who died from a hemorrhage and ruptured thoracic aorta due to atherosclerosis. Pathology indicated moderate atherosclerosis involving the internal carotids, bilaterally; microscopically of the frontal cortex and hippocampus, and scattered diffuse amyloid plaques and neurofibrillary tangles, consistent with age. Grossly, the leptomeninges showed only mild thickening and hyalinization along the superior sagittal sinus. The remainder of the leptomeninges was thin and contained some congested blood vessels. Mild atrophy was found mostly in the frontal poles and lobes, and temporal lobes, bilaterally. Microscopically, there were pairs of Alzheimer type II astrocytes within the deep layers of the neocortex. There was increased satellitosis around neurons in the deep gray matter in the middle frontal cortex. The amygdala contained rare diffuse plaques and neurofibrillary tangles. The
		posterior hippocampus contained a microscopic area of cystic cavitation with hemosiderin-laden macrophages surrounded by reactive gliosis. Patient history included sepsis, cholangitis, post-operative atelectasis, pneumonia CAD, cardiomegaly due to left ventricular hypertrophy, splenomegaly, arteriolonephrosclerosis, nodular colloidal goiter, emphysema, CHF, hypothyroidism, and peripheral vascular disease.
BRSTNOT01	PBLUESCRIPT	Library was constructed using RNA isolated from the breast tissue of a 56-year-old Caucasian female who died in a motor vehicle accident.

Table 6

Library	Vector	Library Description
BRSTNOT04	PSPORT1	Library was constructed using RNA isolated from breast tissue removed from a 62-year-old East Indian female during a unilateral extended simple mastectomy. Pathology for the associated tumor tissue indicated an invasive grade 3 ductal carcinoma. Patient history included benign hypertension, hyperlipidemia, and hematuria. Family history included cerebrovascular and cardiovascular disease, hyperlipidemia, and liver cancer.
BSTMNON02	PSPORT1	This normalized brain stem library was constructed from 2.84 million independent clones from a brain stem library. Starting RNA was made from the brain stem tissue of a 72-year-old Caucasian male who died from myocardial infarction. Patient history included coronary artery disease, insulin-dependent diabetes mellitus, and arthritis. Normalization and hybridization conditions were adapted from Soares et al. (PNAS (1994) 91:9228).
COLNNOT01	PSPORT1	Library was constructed using RNA isolated from colon tissue removed from a 75-year-old Caucasian male during a hemicolectomy.
CORFNOT02	pINCY	Library was constructed using RNA isolated from diseased corpus callosum tissue removed from the brain of a 74-year-old Caucasian male who died from Alzheimer's disease.
DENDTNT01	pINCY	Library was constructed using RNA isolated from treated dendritic cells from peripheral blood.
DRGCNOT01	pINCY	Library was constructed using RNA isolated from dorsal root ganglion tissue removed from the cervical spine of a 32-year-old Caucasian male who died from acute pulmonary edema and bronchopneumonia, bilateral pleural and pericardial effusions, and malignant lymphoma (natural killer cell type). Patient history included probable cytomegalovirus infection, hepatic congestion and steatosis, splenomegaly, hemorrhagic cystitis, thyroid hemorrhage, and Bell's palsy. Surgeries included colonoscopy, large intestine biopsy, adenotonsillectomy, and nasopharyngeal endoscopy and biopsy; treatment included radiation therapy.
DRGTN04	pINCY	The normalized dorsal root ganglion tissue library was constructed from 5.64 million independent clones from the a dorsal root ganglion library. Starting RNA was made from thoracic dorsal root ganglion tissue from a 32-year-old Caucasian male, who died from acute pulmonary edema, acute bronchopneumonia, pleural and pericardial effusion, and lymphoma. The patient presented with pyrexia, fatigue, and GI bleeding. Patient history included probable cytomegalovirus infection, liver congestion and steatosis, splenomegaly, hemorrhagic cystitis, thyroid hemorrhage, respiratory failure, pneumonia, natural killer cell lymphoma of the pharynx, Bell's palsy, and tobacco and alcohol abuse. The library was normalized in one round using conditions adapted from Soares et al., PNAS(1994) 91:9228 and Bonaldo et al., Genome Research 6 (1996):791, except that a significantly longer (48-hours/round) reannealing hybridization was used. The library was then linearized and recircularized to select for insert containing clones as follows: plasmid DNA was prepped from

Table 6

Library	Vector	Library Description
		approximately 1 million clones from the normalized dorsal root ganglion tissue library following soft agar transformation.
FIBRTXS07	pINCY	This subtracted library was constructed using 1.3 million clones from a dermal fibroblast library and was subjected to two rounds of subtraction hybridization with 2.8 million clones from an untreated dermal fibroblast tissue library. The starting library for subtraction was constructed using RNA isolated from treated dermal fibroblast tissue removed from the breast of a 31-year-old Caucasian female. The cells were treated with 9 CIS retinoic acid. The hybridization probe for subtraction was derived from a similarly constructed library from RNA isolated from untreated dermal fibroblast tissue from the same donor. Subtractive hybridization conditions were based on the methodologies of Swaroop et al., NAR (1991) 19:1954 and Bonaldo, et al., Genome Research (1996) 6:791.
GBLADIT01	pINCY	The library was constructed using RNA isolated from diseased gallbladder tissue removed from a 18-year-old Caucasian female during cholecystectomy and incidental appendectomy. Pathology indicated acute and chronic cholecystitis with cholelithiasis. The gallbladder contained multiple fragments of stony material. The appendix showed lymphoid hyperplasia. The patient presented with abdominal pain, nausea, and vomiting. Patient history included Chlamydia, extrinsic asthma, and cesarean delivery (x3). Family history included benign hypertension, acute myocardial infarction, and atherosclerotic coronary artery disease.
HEALDIR01	PCDNA2.1	This random primed library was constructed using RNA isolated from diseased left ventricle tissue removed from a 7-month old Caucasian male who died from cardiopulmonary arrest due to Pompe's disease. Patient history included Pompe's disease, left ventricular hypertrophy, pyrexia, right complete cleft lip, cleft palate, chronic serous otitis media, hypertrophic cardiomyopathy, congestive heart failure, and developmental delays. Family history included acute myocardial infarction, diabetes, cystic fibrosis and Down's syndrome.
HEAONOT04	pINCY	Library was constructed using RNA isolated from aortic tissue removed from a 12-year-old Caucasian female, who died from a closed head injury.
HUVELPB01	PBLUESCRIPT	Library was constructed using RNA isolated from HUV-EC-C (ATCC CRL 1730) cells that were stimulated with cytokine/LPS. RNA was isolated from two pools of HUV-EC-C cells that had been treated with either gamma IFN and TNF-alpha or IL-1 beta and LPS. In the first instance, HUV-EC-C cells were treated with 4 units/ml TNF and 2 units/ml IFNg for 96 hours. In the second instance, cells were treated with 1 units/ml IL-1 and 100 ng/ml LPS for 5 hours.
ISLTNOT01	pINCY	Library was constructed using RNA isolated from a pooled collection of pancreatic islet cells.

Table 6

Library	Vector	Library Description
LIVRNON08	pINCY	This normalized library was constructed from 5.7 million independent clones from a pooled liver tissue library. Starting RNA was made from pooled liver tissue removed from a 4-year-old Hispanic male who died from anoxia and a 16 week female fetus who died after 16-weeks gestation from anencephaly. Serologies were positive for cytomegalovirus in the 4-year-old. Patient history included asthma in the 4-year-old. Family history included taking daily prenatal vitamins and mitral valve prolapse in the mother of the fetus. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91:9228 and Bonaldo et al., Genome Research 6 (1996):791, except that a significantly longer (48hours/round) reannealing hybridization was used.
LIVRTMR01	PCDNA2.1	This random primed library was constructed using RNA isolated from liver tissue removed from a 62-year-old Caucasian female during partial hepatectomy and exploratory laparotomy. Pathology for the matched tumor tissue indicated metastatic intermediate grade neuroendocrine carcinoma, consistent with islet cell tumor, forming nodules ranging in size, in the lateral and medial left liver lobe. The pancreas showed fibrosis, chronic inflammation and fat necrosis consistent with pseudocyst. The gallbladder showed mild chronic cholecystitis. Patient history included malignant neoplasm of the pancreas tail, pulmonary embolism, hyperlipidemia, thrombophlebitis, joint pain in multiple joints, type II diabetes, benign hypertension, cerebrovascular disease, and normal delivery. Previous surgeries included distal pancreatectomy, total splenectomy, and partial hepatectomy. Family history included pancreas cancer with secondary liver cancer, benign hypertension, and hyperlipidemia.
LIVRTUT13	pINCY	Library was constructed using RNA isolated from liver tumor tissue removed from a 62-year-old Caucasian female during partial hepatectomy and exploratory laparotomy. Pathology indicated metastatic intermediate grade neuroendocrine carcinoma, consistent with islet cell tumor, forming nodules ranging in size, in the lateral and medial left liver lobe. The pancreas showed fibrosis, chronic inflammation and fat necrosis consistent with pseudocyst. The gall bladder showed mild chronic cholecystitis. Patient history included malignant neoplasm of the pancreas tail, pulmonary embolism, hyperlipidemia, thrombophlebitis, joint pain in multiple joints, type II diabetes, benign hypertension, and cerebrovascular disease. Family history included pancreas cancer, secondary liver cancer, benign hypertension, and hyperlipidemia.

Table 6

Library	Vector	Library Description
LNODNON02	pINCY	This normalized lymph node tissue library was constructed from .56 million independent clones from a lymph node tissue library. Starting RNA was made from lymph node tissue removed from a 16-month-old Caucasian male who died from head trauma. Serologies were negative. Patient history included bronchitis. Patient medications included Dopamine, Dobutamine, Vancomycin, Vasopressin, Proventil, and Atarax. The library was normalized in two rounds using conditions adapted from Soares et al., PNAS (1994) 91:9228-9932 and Bonaldo et al., Genome Research 6 (1996):791, except that a significantly longer (48 hours/round) reannealing hybridization was used.
LUNGNOT22	pINCY	Library was constructed using RNA isolated from lung tissue removed from a 58-year-old Caucasian female. The tissue sample used to construct this library was found to have tumor contaminant upon microscopic examination. Pathology for the associated tumor tissue indicated a caseating granuloma. Family history included congestive heart failure, breast cancer, secondary bone cancer, acute myocardial infarction and atherosclerotic coronary artery disease.
MCLDTXN05	pINCY	This normalized dendritic cell library was constructed from 1 million independent clones from a pool of two derived dendritic cell libraries. Starting libraries were constructed using RNA isolated from untreated and treated derived dendritic cells from umbilical cord blood CD34+ precursor cells removed from a male. The cells were derived with granulocyte/macrophage colony stimulating factor (GM-CSF), tumor necrosis factor alpha (TNF alpha), and stem cell factor (SCF). The GM-CSF was added at time 0 at 100 ng/ml, the TNF alpha was added at time 0 at 2.5 ng/ml, and the SCF was added at time 0 at 25 ng/ml. Incubation time was 13 days. The treated cells were then exposed to phorbol myristate acetate (PMA), and Ionomycin. The PMA and Ionomycin were added at 13 days for five hours. The library was normalized in two rounds using conditions adapted from Soares et al., PNAS (1994) 91:9228 and Bonaldo et al., Genome Research 6(1996):791, except that a significantly longer (48 hours/round) reannealing hybridization was used.

Table 6

Library	Vector	Library Description
MIXDTME02	PBK-CMV	<p>This 5' biased random primed library was constructed using pooled cDNA from five donors. cDNA was generated using mRNA isolated from heart tissue removed from a Caucasian male fetus who died after 20 weeks gestation from Patau's syndrome (donor A); adrenal gland removed from a 43-year-old Caucasian male (donor B) during nephroureterectomy, regional lymph node resection and unilateral adrenalectomy; kidney cortex removed from a 65-year-old male (donor C) during nephroureterectomy; lung tissue removed from a 14-month-old Caucasian female who died from drowning (donor D); and kidney tissue removed from an 8-year-old Caucasian female who died from a motor vehicle accident (donor E). For donor B, pathology for the associated tumor indicated grade 2 (of 4) renal cell carcinoma in the left kidney with invasion into the renal pelvis. Patient presented with hematuria and anemia. Patient history included benign hypertension and obesity. Previous surgeries included adenotomysilectomy and indirect inguinal hernia repair. The patient was</p> <p>not taking any medications. Family history included benign hypertension and atherosclerotic coronary artery disease in the father. For donor C pathology for the associated tumor shows grade 3 (of 4) renal cell carcinoma, clear cell type, within the mid-portion of the kidney. For donor D, serologies were negative. For donor E, medications included respiradol.</p> <p>MLP000060 PCR2-TOPO TA Library was constructed using pooled cDNA from different donors. cDNA was generated using mRNA isolated from the following: aorta, cerebellum, lymphnodes, muscle, tonsil (lymphoid hyperplasia), bladder tumor (invasive grade 3 transitional cell carcinoma), breast (proliferative fibrocystic changes without atypia characterized by epithelial ductal hyperplasia, testicle tumor (embryonal carcinoma), spleen, ovary, parathyroid, ileum, breast skin, sigmoid colon, penis tumor (fungating invasive grade 4 squamous cell carcinoma), fetal lung, breast, fetal small intestine, fetal liver, fetal pancreas, fetal lung, fetal skin, fetal penis, fetal bone, fetal ribs, frontal brain tumor (grade 4</p>
		<p>gemistocytic astrocytoma), ovary (stromal hyperthecosis), bladder, bladder tumor (invasive grade 3 transitional cell carcinoma), stomach, lymph node tumor (metastatic basaloid squamous cell carcinoma), tonsil (reactive lymphoid hyperplasia), periosteum from the tibia, fetal brain, fetal spleen, uterus tumor, endometrial (grade 3 adenocarcinoma), seminal vesicle, liver, aorta, adrenal gland, lymph node (metastatic grade 3 squamous cell carcinoma), glossal muscle, esophagus, esophagus tumor (invasive grade 3 adeno carcinoma), ileum, pancreas, soft tissue tumor from the skull (grade 3 ependymoma), transverse colon, (benign familial polyposis), rectum tumor (grade 3 colonic adenocarcinoma), rib tumor, (metastatic grade 3 osteosarcoma), lung, heart, placenta, thymus, stomach, spleen (splenomegaly with congestion), uterus, cervix (mild chronic cervicitis with focal squamous metaplasia), spleen tumor (malignant lymphoma, diffuse large cell type, B-cell phenotype with abundant reactive T-cells and marked granulomatous response), umbilical cord blood mononuclear cells,</p>

Table 6

Library	Vector	Library Description
		upper lobe lung tumor, (grade 3 squamous cell carcinoma), endometrium (secretory phase), liver, liver tumor (metastatic grade 2 neuroendocrine carcinoma), colon, umbilical cord blood, Th1 cells, nonactivated, umbilical cord blood, Th2 cells, nonactivated, coronary artery endothelial cells (untreated), coronary artery smooth muscle cells, (untreated), coronary artery smooth muscle cells (treated with TNF & IL-110ng/ml each for 20 hours), bladder (mild chronic cystitis), epiglottis, breast skin, small intestine, fetal prostate stroma fibroblasts, prostate epithelial cells (PrEC cells), fetal adrenal glands, fetal liver, kidney transformed embryonal cell line (293-EBNA) (untreated), kidney transformed embryonal cell line (293-EBNA) (treated with 5Aza-2deoxy cytidine for 72 hours), mammary epithelial cells, (HMEC cells), peripheral blood monocytes (treated with IL-10 at time 0, 10ng/ml, LPS was added at 1 hour at 5ng/ml. Incubation 24 hours), peripheral blood monocytes (treated with anti-IL-10 at time 0, 10ng/ml, LPS was added at 1 hour at 5ng/ml. Incubation 24 hours), spinal cord, base of
		medulla (Huntington's chorea), thigh and arm muscle (ALS), breast skin fibroblast (untreated), breast skin fibroblast (treated with 9CIS Retinoic Acid 1 μ M for 20 hours), breast skin fibroblast (treated with TNF-alpha & IL-1 beta, 10ng/ml each for 20 hours), fetal liver mast cells, hematopoietic (Mast cells prepared from human fetal liver hematopoietic progenitor cells (CD34+ stem cells) cultured in the presence of hIL-6 and hSCF for 18 days), epithelial layer of colon, bronchial epithelial cells (treated for 20 hours with 20% smoke conditioned media), lymph node, pooled peripheral blood mononuclear cells (untreated), pooled brain segments: striatum, globus pallidus and posterior putamen (Alzheimer's Disease), pituitary gland, umbilical cord blood, CD34+ derived dendritic cells (treated with SCF, GM-CSF & TNF alpha, 13 days), umbilical cord blood, CD34+ derived dendritic cells (treated with SCF, GM-CSF & TNFalpha, 13 days followed by PMA/Ionomycin for 5 hours), small intestine rectum, bone marrow neuroblastoma cell line (SH-SY5Y cells, treated with 6-Hydroxydopamine 100 uM for 8 hours), bone marrow, neuroblastoma cell line (SH-SY5Y cells, untreated), brain segments from one donor: amygdala, entorhinal cortex, globus pallidus, substantia innominata, striatum, dorsocaudate nucleus, dorsal putamen, ventral nucleus accumbens, archaocortex (hippocampus anterior and posterior), thalamus, nucleus raphe magnus, periaqueductal gray, midbrain, substantia nigra, and dentate nucleus, pineal gland (Alzheimer's Disease), preadipocytes (untreated), preadipocytes (treated with a peroxisome proliferator-activated receptor gamma agonist, ImicroM, 4 hours), pooled prostate (adenofibromatous hyperplasia), pooled kidney, pooled adipocytes (untreated), pooled adipocytes (treated with human insulin), pooled mesenteric and abdominal fat, pooled adrenal glands, pooled thyroid (normal and adenomatous hyperplasia), pooled spleen (normal and with changes consistent with idiopathic thrombocytopenic purpura), pooled right and left breast, pooled lung, pooled nasal polyps, pooled fat, pooled synovium (normal and rheumatoid arthritis), pooled brain

Table 6

Library	Vector	Library Description
		(meningioma, gemistocytic astrocytoma and Alzheimer's disease), pooled fetal colon, pooled fetal colon, pooled colon: ascending, descending (chronic ulcerative colitis), and rectal tumor (adenocarcinoma), pooled esophagus, normal and tumor (invasive grade 3 adenocarcinoma), pooled breast skin fibroblast (one treated w/ 9CIS Retinoic Acid and the other with TNF-alpha & IL-1 beta), pooled gallbladder (acute necrotizingcholecystitis with cholelithiasis (clinically hydrops), acute hemorrhagic cholecystitis with cholelithiasis, chronic cholecystitis and cholelithiasis), pooled fetal heart, (Patau's and fetal demise), pooled neurogenic tumor cell line, SK-N-MC, (neuroepithelioma, metastasis tosupra-orbital area, untreated) and neuron, NT-2 cell line, (treated with mouse leptin at 1 μ g/ml and 9cis retinoic acid at 3.3 μ M for 6 days), pooled ovary (normal and polycystic ovarian disease), pooled prostate, (adenofibromatous hyperplasia), pooled seminal vesicle, pooled small intestine, pooled fetal small intestine, pooled stomach and fetal stomach, prostate epithelial cells, pooled
		testis (normal and embryonal carcinoma), pooled uterus, pooled uterus tumor (grade 3 adenosquamous carcinoma and leiomyoma), pooled uterus, endometrium, and myometrium, (normal and adenomatous hyperplasia with squamous metaplasia and focal atypia), pooled brain: (temporal lobe meningioma, cerebellum and hippocampus (Alzheimer's Disease), pooled skin, fetal lung, adrenal tumor (adrenal cortical carcinoma), prostate tumor (adenocarcinoma), fetal heart, fetal small intestine, ovary tumor (mucinous cystadenoma), ovary, ovary tumor (transitional cell carcinoma), disease prostate (adenofibromatous hyperplasia), fetal colon, uterus tumor (leiomyoma), temporal brain, submandibular gland, colon tumor (adenocarcinoma), ascending and transverse colon, ovary tumor (endometrioid carcinoma), lung tumor (squamous cell carcinoma), fetal brain, fetal lung, ureter tumor (transitional cell carcinoma), untreated HNT cells, para-aortic soft tissue, testis, seminal vesicle, diseased ovary (endometriosis), temporal lobe, myometrium, diseased gallbladder
		(cholecystitis, cholelithiasis), placenta, breast tumor (ductal adenocarcinoma), breast, lung tumor (lipo sarcoma), endometrium, abdominal fat, cervical spine dorsal root ganglion, thoracic spine dorsal root ganglion, diseased thyroid (adenomatous hyperplasia), liver, kidney, fetal liver, NT-2 cells (treated with mouse leptin and 9 cisRA), K562 cells (treated with 9 cis RA), cerebellum, corpus callosum, hypothalamus, fetal brain astrocytes (treated with TNFa and IL-1b), inferior parietal cortex, posterior hippocampus, pons, thalamus, C3A cells (untreated), C3A cells (treated with 3-methylcholanthrene), testis, colon epithelial layer, pooled prostate, pooled liver, substantia nigra, thigh muscle, rib bone, fallopian tube tumor (endometrioid and serousadenocarcinoma), diseased lung (idiopathic pulmonary disease), cingulateanterior allocortex and neocortex, cingulate posterior allocortex, auditory neocortex, frontal neocortex, orbital inferior neocortex, parietal superior neocortex, visual primary neocortex, dentate nucleus, posterior cingulate, cerebellum, vermis,

Table 6

Library	Vector	Library Description
		inferior temporal cortex, medulla, posterior parietal cortex, colon polyp, pooled breast, anterior and posterior hippocampus, mesenteric and abdominal fat, pooled esophagus, pooled fetal kidney, pooled fetal liver, ileum, small intestine, pooled gallbladder, frontal and superior temporal cortex, pooled ovary, pooled endometrium, pooled prostate, pooled kidney, fetal femur, sacrum tumor (giant cell tumor), pooled kidney and kidney tumor (renal cell carcinoma clear-cell type), pooled liver and liver tumor (neuroendocrine carcinoma), pooled fetal liver, pooled lung, fetal pancreas, pancreas, parotid gland, parotid tumor (sebaceous lymphadenoma), retroperitoneal and supraglottic soft tissue, spleen, fetal spleen, spleen tumor (malignant lymphoma), diseased spleen (idiopathic thrombocytopenic purpura), parathyroid, thyroid, thymus, tonsil ureter tumor (transitional cell carcinoma), pooled adrenal gland and adrenal tumor (pheochromocytoma), pooled lymph node tumor (Hodgkin's disease and metastatic adenocarcinoma), pooled neck and calf muscles, and pooled bladder.
MONOTXN05	pINCY	This normalized treated monocyte cell tissue library was constructed from 1.03 million independent clones from a monocyte tissue library. Starting RNA was made from RNA isolated from treated monocytes from peripheral blood removed from a 42-year-old female. The cells were treated with interleukin-10 (IL-10) and lipopolysaccharide (LPS). The library was normalized in two rounds using conditions adapted from Soares et al., PNAS (1994) 91:9228-9232 and Bonaldo et al., Genome Research 6 (1996):791, except that a significantly longer (48 hours/round) reannealing hybridization was used.
MUSCDIT06	pINCY	Library was constructed using RNA isolated from skeletal muscle tissue removed from an 11-month-old Caucasian female who died from cardiopulmonary arrest. Patient history included Krabbe's disease.
MUSCNOT11	pINCY	The library was constructed using RNA isolated from diseased arm muscle tissue removed from a 74-year-old Caucasian female who died from respiratory arrest due to amyotrophic lateral sclerosis (ALS). Patient history included amyotrophic lateral sclerosis, hypertension, arthritis, and alcohol use.
NEUTGMT01	PSPORT1	Library was constructed using RNA isolated from peripheral blood granulocytes collected by density gradient centrifugation through Ficoll-Hypaque. The cells were isolated from buffy coat units obtained from 20 unrelated male and female donors. Cells were cultured in 10 nM GM-CSF for 1 hour before washing and harvesting for total RNA preparation.
PROSNOT06	PSPORT1	Library was constructed using RNA isolated from the diseased prostate tissue of a 57-year-old Caucasian male during radical prostatectomy, removal of both testes and excision of regional lymph nodes. Pathology indicated adenofibromatous hyperplasia. Pathology for the associated tumor tissue indicated adenocarcinoma (Gleason grade 3+3). Patient history included a benign neoplasm of the large bowel and type I diabetes. Family history included a malignant neoplasm of the prostate and type I diabetes.

Table 6

Library	Vector	Library Description
PROSTUT10	pINCY	Library was constructed using RNA isolated from prostatic tumor tissue removed from a 66-year-old Caucasian male during radical prostatectomy and regional lymph node excision. Pathology indicated an adenocarcinoma (Gleason grade 2+3). Adenofibromatous hyperplasia was also present. The patient presented with elevated prostate specific antigen (PSA). Family history included prostate cancer and secondary bone cancer.
PROSTUT12	pINCY	Library was constructed using RNA isolated from prostate tumor tissue removed from a 65-year-old Caucasian male during a radical prostatectomy. Pathology indicated an adenocarcinoma (Gleason grade 2+2). Adenofibromatous hyperplasia was also present. The patient presented with elevated prostate specific antigen (PSA).
SINJNOT03	pINCY	Library was constructed using RNA isolated from duodenum tissue removed from the small intestine of a 16-year-old Caucasian male who died from head trauma. Patient history included a kidney infection.
SINTBST01	pINCY	Library was constructed using RNA isolated from ileum tissue obtained from an 18-year-old Caucasian female during bowel anastomosis. Pathology indicated Crohn's disease of the ileum, involving 15 cm of the small bowel. Family history included cerebrovascular disease and atherosclerotic coronary artery disease.
SPLNNOT11	pINCY	Library was constructed using RNA isolated from diseased spleen tissue removed from a 14-year-old Asian male during a total splenectomy. Pathology indicated changes consistent with idiopathic thrombocytopenic purpura. The patient presented with bruising. Patient medications included Vincristine.
UTRSTUE01	PCDNA2.1	This 5' biased random primed library was constructed using RNA isolated from uterus tumor tissue removed from a 37-year-old Black female during myomectomy, dilation and curettage, right fimbrial region biopsy, and incidental appendectomy. Pathology indicated multiple (12) uterine leiomyomata. A fimbrial cyst was identified. The patient presented with deficiency anemia, an umbilical hernia, and premenopausal menorrhagia. Patient history included premenopausal menorrhagia and sarcoidosis of the lung. Previous surgeries included hysterectomy, dilation and curettage, and an endoscopic lung biopsy. Patient medications included Chromagen and Claritin. Family history included acute myocardial infarction and atherosclerotic coronary artery disease in the father.

Table 7

Program	Description	Reference	Parameter Threshold
ABI FACTURA	A program that removes vector sequences and masks ambiguous bases in nucleic acid sequences.	Applied Biosystems, Foster City, CA.	
ABI/PARACEL FDF	A Fast Data Finder useful in comparing and annotating amino acid or nucleic acid sequences.	Applied Biosystems, Foster City, CA; Paracel Inc., Pasadena, CA.	Mismatch <50%
ABI AutoAssembler	A program that assembles nucleic acid sequences.	Applied Biosystems, Foster City, CA.	
BLAST	A Basic Local Alignment Search Tool useful in sequence similarity search for amino acid and nucleic acid sequences. BLAST includes five functions: blastp, blastn, blastx, tblastn, and tblastx.	Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410; Altschul, S.F. et al. (1997) Nucleic Acids Res. 25:3389-3402.	ESTs: Probability value = 1.0E-8 or less; Full Length sequences: Probability value = 1.0E-10 or less
FASTA	A Pearson and Lipman algorithm that searches for similarity between a query sequence and a group of sequences of the same type. FASTA comprises at least five functions: fasta, tfasta, fastx, tfastx, and ssearch.	Pearson, W.R. and D.J. Lipman (1988) Proc. Natl. Acad. Sci. USA 85:2444-2448; Pearson, W.R. (1990) Methods Enzymol. 183:63-98; and Smith, T.F. and M.S. Waterman (1981) Adv. Appl. Math. 2:482-489.	ESTs: fasta E value = 1.0E-6; Assembled ESTs: fasta Identity = 95% or greater and Match length = 200 bases or greater; fastx E value = 1.0E-8 or less; Full Length sequences: fastx score = 100 or greater
BLIMPS	A BLocks IMProved Searcher that matches a sequence against those in BLOCKS, PRINTS, DOMO, PRODOM, and PFAM databases to search for gene families, sequence homology, and structural fingerprint regions.	Henikoff, S. and J.G. Henikoff (1991) Nucleic Acids Res. 19:6565-6572; Henikoff, J.G. and S. Henikoff (1996) Methods Enzymol. 266:88-105; and Attwood, T.K. et al. (1997) J. Chem. Inf. Comput. Sci. 37:417-424.	Probability value = 1.0E-3 or less

Table 7

Program	Description	Reference	Parameter Threshold
HMME	An algorithm for searching a query sequence against hidden Markov model (HMM)-based databases of protein family consensus sequences, such as PFAM, INCY, SMART and TIGRFAM.	Krogh, A. et al. (1994) J. Mol. Biol. 235:1501-1531; Sonnhammer, E.L.L. et al. (1988) Nucleic Acids Res. 26:320-322; Durbin, R. et al. (1998) Our World View, in a Nutshell, Cambridge Univ. Press, pp. 1-350.	PFAM, INCY, SMART or TIGRFAM hits: Probability value = 1.0E-3 or less; Signal peptide hits: Score = 0 or greater
ProfileScan	An algorithm that searches for structural and sequence motifs in protein sequences that match sequence patterns defined in Prosite.	Gribskov, M. et al. (1988) CABIOS 4:61-66; Gribskov, M. et al. (1989) Methods Enzymol. 183:146-159; Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221.	Normalized quality score \geq GCG specified "HIGH" value for that particular Prosite motif. Generally, score = 1.4-2.1.
Phred	A base-calling algorithm that examines automated sequencer traces with high sensitivity and probability.	Ewing, B. et al. (1998) Genome Res. 8:175-185; Ewing, B. and P. Green (1998) Genome Res. 8:186-194.	
Phrap	A Phils Revised Assembly Program including SWAT and CrossMatch, programs based on efficient implementation of the Smith-Waterman algorithm, useful in searching sequence homology and assembling DNA sequences.	Smith, T.F. and M.S. Waterman (1981) Adv. Appl. Math. 2:482-489; Smith, T.F. and M.S. Waterman (1981) J. Mol. Biol. 147:195-197; and Green, P., University of Washington, Seattle, WA.	Score = 120 or greater; Match length = 56 or greater
Consed	A graphical tool for viewing and editing Phrap assemblies.	Gordon, D. et al. (1998) Genome Res. 8:195-202.	
SPScan	A weight matrix analysis program that scans protein sequences for the presence of secretory signal peptides.	Nielson, H. et al. (1997) Protein Engineering 10:1-6; Claverie, J.M. and S. Audic (1997) CABIOS 12:431-439.	Score = 3.5 or greater
TMAP	A program that uses weight matrices to delineate transmembrane segments on protein sequences and determine orientation.	Persson, B. and P. Argos (1994) J. Mol. Biol. 237:182-192; Persson, B. and P. Argos (1996) Protein Sci. 5:363-371.	

Table 7

Program	Description	Reference	Parameter Threshold
TMHMMER	A program that uses a hidden Markov model (HMM) to delineate transmembrane segments on protein sequences and determine orientation.	Sonnhammer, E.L. et al. (1998) Proc. Sixth Intl. Conf. On Intelligent Systems for Mol. Biol., Glasgow et al., eds., The Am. Assoc. for Artificial Intelligence (AAAI) Press, Menlo Park, CA, and MIT Press, Cambridge, MA, pp. 175-182.	
Motifs	A program that searches amino acid sequences for patterns that matched those defined in Prosite.	Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221; Wisconsin Package Program Manual, version 9, page M51-59, Genetics Computer Group, Madison, WI.	

Table 8

SEQ ID NO:	PTD	EST ID	SNP ID	EST SNP	CB1 SNP	EST Allele	Allele 1	Allele 2	Amino Acid	Caucasian Allele 1 frequency	African Allele 1 frequency	Asian Allele 1 frequency	Hispanic Allele 1 frequency
60	7509332	1667982H1	SNP00071142	118	319	C	C	A	R28	1.00	n/a	n/a	n/a
62	7509132	7252817H2	SNP00120204	200	144	T	T	C	noncoding	n/a	n/a	n/a	n/a
62	7509132	7252817J2	SNP00131224	163	1787	T	T	C	noncoding	n/a	n/a	n/a	n/a
63	7509136	3000824H1	SNP00005163	185	1524	T	T	C	noncoding	0.82	0.81	0.76	0.83
63	7509136	3002289H1	SNP00005163	186	1523	T	T	C	noncoding	0.82	0.81	0.76	0.83
63	7509136	3506005H1	SNP00005163	67	1525	C	T	C	noncoding	0.82	0.81	0.76	0.83
65	7509214	1305469H1	SNP00057352	58	447	G	A	G	A119	n/a	n/a	n/a	n/a
65	7509214	1305469H1	SNP00136872	12	401	G	G	A	R104	n/a	n/a	n/a	n/a
65	7509214	1305469H1	SNP00136873	92	481	C	C	T	P131	n/a	n/a	n/a	n/a
65	7509214	1637908H1	SNP00136872	149	402	G	G	A	R104	n/a	n/a	n/a	n/a
65	7509214	2129306H1	SNP00047651	38	246	G	G	T	M52	n/d	n/a	n/a	n/a
65	7509214	2371557H1	SNP00136874	111	607	A	A	G	noncoding	n/a	n/a	n/a	n/a
65	7509214	2371557H1	SNP00004818	117	613	G	T	G	noncoding	n/a	n/a	n/a	n/a
65	7509214	2517189H2	SNP00136872	273	413	G	G	A	R108	n/a	n/a	n/a	n/a
65	7509214	2734103H1	SNP00057352	136	449	G	A	G	W120	n/a	n/a	n/a	n/a
65	7509214	2734103H1	SNP00136872	90	403	A	G	A	N105	n/a	n/a	n/a	n/a
65	7509214	2734103H1	SNP00136873	170	483	C	C	T	P131	n/a	n/a	n/a	n/a
65	7509214	3603012H1	SNP00136872	274	421	G	G	A	G111	n/a	n/a	n/a	n/a
65	7509214	3837531H1	SNP00136874	183	611	A	A	G	noncoding	n/a	n/a	n/a	n/a
65	7509214	3837531H1	SNP00057352	28	453	G	A	G	G121	n/a	n/a	n/a	n/a
65	7509214	3837531H1	SNP00136873	62	487	C	C	T	R133	n/a	n/a	n/a	n/a
65	7509214	3946173H1	SNP00136873	138	482	C	C	T	P131	n/a	n/a	n/a	n/a
65	7509214	4008514H1	SNP00047651	120	244	T	G	T	L52	n/d	n/a	n/a	n/a
65	7509214	4108144H1	SNP00047651	68	242	G	G	T	G51	n/d	n/a	n/a	n/a
65	7509214	4386522H1	SNP00057352	171	448	G	A	G	G120	n/a	n/a	n/a	n/a
65	7509214	5605610H1	SNP00004818	230	616	G	T	G	noncoding	n/a	n/a	n/a	n/a
65	7509214	5966775H1	SNP00136874	376	608	A	A	G	noncoding	n/a	n/a	n/a	n/a
65	7509214	5966775H1	SNP00004818	380	612	G	T	G	noncoding	n/a	n/a	n/a	n/a

Table 8

SEQ ID NO:	PID	EST ID	SNP ID	EST SNP	CB1 SNP	EST Allele	Allele 1.	Allele 2	Amino Acid	Caucasian Allele 1 frequency	African Allele 1 frequency	Asian Allele 1 frequency	Hispanic Allele 1 frequency
65	7509214	8611118H1	SNP00004818	178	609	G	T	G	noncoding	n/a	n/a	n/a	n/a
65	7509214	8611118H1	SNP00057352	343	444	G	A	G	L118	n/a	n/a	n/a	n/a
65	7509214	8611118H1	SNP00136872	389	398	G	G	A	R103	n/a	n/a	n/a	n/a
65	7509214	8611118H1	SNP00136873	309	478	C	C	T	R130	n/a	n/a	n/a	n/a
66	7509244	300824H1	SNP00005163	185	1491	T	T	C	noncoding	0.82	0.81	0.76	0.83
66	7509244	3002289H1	SNP00005163	186	1490	T	T	C	noncoding	0.82	0.81	0.76	0.83
66	7509244	3506005H1	SNP00005163	67	1492	C	T	C	noncoding	0.82	0.81	0.76	0.83
70	7503320	5681822H1	SNP00014931	23	552	C	C	T	noncoding	n/a	n/a	n/a	n/a
71	7503335	1454748H1	SNP00072734	211	1691	G	A	G	P536	0.43	0.45	0.14	0.22
71	7503335	1485166H1	SNP00069424	237	310	T	T	C	V76	0.93	n/d	0.96	0.96
71	7503335	2963710H1	SNP00069425	138	1432	C	A	C	A450	0.90	0.96	0.85	0.89
71	7503335	2963710H1	SNP00072733	73	1367	C	C	T	P428	n/a	n/a	n/a	n/a
71	7503335	4057086H1	SNP00069424	39	308	T	T	C	I75	0.93	n/d	0.96	0.96
71	7503335	4057086H1	SNP00120820	176	445	T	T	G	V121	n/a	n/a	n/a	n/a
71	7503335	4093467H1	SNP00072733	217	1366	C	C	T	P428	n/a	n/a	n/a	n/a
71	7503335	4295902H1	SNP00072733	243	1365	C	C	T	P428	n/a	n/a	n/a	n/a
71	7503335	6770662H1	SNP00120820	405	447	T	T	G	Y122	n/a	n/a	n/a	n/a
71	7503335	6867692H1	SNP00120821	515	546	C	C	T	H155	0.48	0.59	0.38	0.32
71	7503335	8084392H1	SNP00126828	93	987	G	A	G	A302	n/a	n/a	n/a	n/a
73	7504530	2639741H1	SNP00119886	47	90	A	A	C	noncoding	0.37	n/a	n/a	n/a
73	7504530	3601392H1	SNP00133389	204	824	G	A	G	G207	n/a	n/a	n/a	n/a
73	7504530	4080023H1	SNP00119886	18	87	C	A	C	noncoding	0.37	n/a	n/a	n/a
74	7509303	1546672H1	SNP00075644	35	1320	T	T	C	noncoding	n/a	n/a	n/a	n/a
74	7509303	4112747H1	SNP00005993	51	1818	G	G	A	noncoding	0.63	0.90	0.47	0.67
74	7509303	4897687H1	SNP00005993	103	1827	A	G	A	noncoding	0.63	0.90	0.47	0.67
74	7509303	5732638H1	SNP00005993	35	1828	A	G	A	noncoding	0.63	0.90	0.47	0.67
74	7509303	5955401H1	SNP00005993	35	1825	G	G	A	noncoding	0.63	0.90	0.47	0.67
74	7509303	6412945H1	SNP00005993	131	1810	G	G	A	noncoding	0.63	0.90	0.47	0.67

Table 8

SEQ ID NO:	PID	EST ID	SNP ID	EST SNP	CB1 SNP	EST Allele	Allele 1	Allele 2	Amino Acid	Caucasian Allele 1 frequency	African Allele 1 frequency	Asian Allele 1 frequency	Hispanic Allele 1 frequency
74	7509303	6937415H1	SNP00005993	388	1830	G	G	A	noncoding	0.63	0.90	0.47	0.67
75	7509910	1454748H1	SNP00072734	211	1913	G	A	G	noncoding	0.43	0.45	0.14	0.22
75	7509910	1485166H1	SNP00069424	237	310	T	T	C	V76	0.93	n/d	0.96	0.96
75	7509910	2963710H1	SNP00069425	138	1654	C	A	C	noncoding	0.90	0.96	0.85	0.89
75	7509910	2963710H1	SNP00072733	73	1589	C	C	T	noncoding	n/a	n/a	n/a	n/a
75	7509910	4057086H1	SNP00069424	39	308	T	T	C	I75	0.93	n/d	0.96	0.96
75	7509910	4057086H1	SNP00120820	176	445	T	T	G	V121	n/a	n/a	n/a	n/a
75	7509910	4093467H1	SNP00072733	217	1588	C	C	T	noncoding	n/a	n/a	n/a	n/a
75	7509910	4295902H1	SNP00072733	243	1587	C	C	T	noncoding	n/a	n/a	n/a	n/a
75	7509910	6770662H1	SNP00120820	405	447	T	T	G	Y122	n/a	n/a	n/a	n/a
75	7509910	6867692H1	SNP00120821	515	546	C	C	T	H155	0.48	0.59	0.38	0.32
75	7509910	7130883H1	SNP00126828	9	1209	A	A	G	noncoding	n/a	n/a	n/a	n/a
76	7509982	1307948H1	SNP00023319	77	4204	A	G	A	N1328	0.57	0.28	0.36	0.65
76	7509982	1307948H1	SNP00023320	201	4328	C	C	T	N1369	n/d	n/d	n/d	n/d
76	7509982	1307948H1	SNP00072137	91	4218	A	A	G	S1333	n/a	n/a	n/a	n/a
76	7509982	1965082H1	SNP00023319	146	4203	G	G	A	G1328	0.57	0.28	0.36	0.65
76	7509982	1965082H1	SNP00072137	160	4217	A	A	G	K1332	n/a	n/a	n/a	n/a
76	7509982	2764315H1	SNP00026116	169	4072	T	T	C	I1284	n/d	n/a	n/a	n/a
76	7509982	3781324H1	SNP00026116	174	4069	C	T	C	T1283	n/d	n/a	n/a	n/a
76	7509982	3781324H1	SNP00139248	272	4167	T	C	T	F1316	n/a	n/a	n/a	n/a
76	7509982	3948943H1	SNP00023320	89	4327	C	C	T	T1369	n/d	n/d	n/d	n/d
76	7509982	415352H1	SNP00058466	177	5510	C	C	G	noncoding	0.62	n/a	n/a	n/a
76	7509982	4776786H1	SNP00023319	67	4202	G	G	A	P1327	0.57	0.28	0.36	0.65
76	7509982	4776786H1	SNP00072137	81	4216	A	A	G	K1332	n/a	n/a	n/a	n/a
76	7509982	5704531H1	SNP00023320	113	4325	T	C	T	D1368	n/d	n/d	n/d	n/d
76	7509982	5704531H1	SNP00072137	3	4215	A	A	G	K1332	n/a	n/a	n/a	n/a
79	7510413	1667982H1	SNP00071142	118	319	C	C	A	R28	1.00	n/a	n/a	n/a
79	7510413	2240820H2	SNP00066386	8	358	A	A	G	K41	n/a	n/a	n/a	n/a

Table 8

SEQ ID NO:	PID	EST ID	SNP ID	EST SNP	CB1 SNP	EST Allele	Allele 1	Allele 2	Amino Acid	Caucasian Allele 1 frequency	African Allele 1 frequency	Asian Allele 1 frequency	Hispanic Allele 1 frequency
79	7510413	6844294H1	SNP00119027	246	280	A	A	G	M15	n/d	n/d	n/d	n/d
80	1721303	2905327H1	SNP00095824	93	94	T	T	C	P27	n/a	n/a	n/a	n/a
80	1721303	3881018H1	SNP00095824	62	96	T	T	C	I28	n/a	n/a	n/a	n/a
80	1721303	5765782H1	SNP00095824	98	98	C	T	C	R29	n/a	n/a	n/a	n/a
80	1721303	940621H1	SNP00016445	89	233	T	T	C	noncoding	n/a	n/a	n/a	n/a
81	7502007	3601392H1	SNP00133389	204	680	G	A	G	G206	n/a	n/a	n/a	n/a
82	7506439	7753512J1	SNP00039567	169	1803	C	C	T	noncoding	n/a	n/a	n/a	n/a
82	7506439	7753512J1	SNP00112674	25	1947	T	C	T	noncoding	0.97	n/a	n/a	n/a
85	7509439	015688H1	SNP00139297	11	279	C	C	T	A66	n/a	n/a	n/a	n/a
85	7509439	077004H1	SNP00139297	199	281	C	C	T	R67	n/a	n/a	n/a	n/a
85	7509439	1273186H1	SNP00139297	216	280	C	C	T	A66	n/a	n/a	n/a	n/a
85	7509439	1551917H1	SNP00139297	185	276	C	C	T	P65	n/a	n/a	n/a	n/a
85	7509439	167737H1	SNP00139297	206	277	C	C	T	P65	n/a	n/a	n/a	n/a
85	7509439	1844902H1	SNP00139297	62	278	C	C	T	P66	n/a	n/a	n/a	n/a
85	7509439	2866273H1	SNP00139297	159	229	C	C	T	N49	n/a	n/a	n/a	n/a
85	7509439	2960845H1	SNP00139297	49	275	C	C	T	P65	n/a	n/a	n/a	n/a
85	7509439	3026771H1	SNP00139297	210	274	C	C	T	N64	n/a	n/a	n/a	n/a
85	7509439	3080978H1	SNP00139297	198	264	C	C	T	T61	n/a	n/a	n/a	n/a
85	7509439	3115228H1	SNP00139297	265	272	C	C	T	Q64	n/a	n/a	n/a	n/a
85	7509439	3240634H1	SNP00139297	227	273	C	C	T	T64	n/a	n/a	n/a	n/a
85	7509439	4063887H1	SNP00139297	36	271	C	C	T	L63	n/a	n/a	n/a	n/a
85	7509439	6096843H1	SNP00139297	218	267	C	C	T	A62	n/a	n/a	n/a	n/a
85	7509439	6749571H1	SNP00124031	40	45	A	A	G	noncoding	n/d	n/a	n/a	n/a
86	7510202	1005109H1	SNP00004180	33	4131	G	C	G	P1377	n/a	n/a	n/a	n/a
86	7510202	2310340H1	SNP00004180	13	4124	G	C	G	R1375	n/a	n/a	n/a	n/a
86	7510202	2846425H1	SNP00049763	190	5108	C	C	T	noncoding	n/d	n/a	n/a	n/a
86	7510202	4619404H1	SNP00004180	230	4129	C	C	G	P1377	n/a	n/a	n/a	n/a
86	7510202	4619404H1	SNP00024790	104	4003	C	C	T	P1335	n/d	n/a	n/a	n/a

Table 8

SEQ ID NO:	PID	EST ID	SNP ID	EST SNP	CB1 SNP	EST Allele	Allele 1	Allele 2	Amino Acid	Caucasian Allele 1 frequency	African Allele 1 frequency	Asian Allele 1 frequency	Hispanic Allele 1 frequency
86	7510202	5195240H1	SNP00024790	123	4005	C	C	T	P1335	n/d	n/a	n/a	n/a
86	7510202	5699760H1	SNP00004180	24	4127	G	C	G	G1376	n/a	n/a	n/a	n/a
86	7510202	7659234H1	SNP00110738	261	4896	C	A	C	noncoding	n/d	n/a	n/a	n/a
87	7510203	5526052H2	SNP00109646	120	994	T	T	C	I54	0.74	0.66	0.87	0.83
87	7510203	6167684H1	SNP00052166	128	2921	T	C	T	noncoding	n/d	n/d	1.00	n/d
87	7510203	6438120H1	SNP00052167	442	3141	T	T	G	noncoding	n/a	n/a	n/a	n/a
87	7510203	6438174H1	SNP00052167	447	3144	T	T	G	noncoding	n/a	n/a	n/a	n/a
87	7510203	6811774J1	SNP00122473	96	562	T	T	C	noncoding	0.95	0.98	0.98	0.89
87	7510203	7604707H1	SNP00122473	422	556	T	T	C	noncoding	0.95	0.98	0.98	0.89
88	7510208	1223476H1	SNP00050176	208	7684	C	C	T	noncoding	n/d	0.87	n/d	0.98
88	7510208	1393432H1	SNP00151799	53	3654	C	C	T	noncoding	n/a	n/a	n/a	n/a
88	7510208	1421910H1	SNP00116827	34	6310	C	C	T	noncoding	n/a	n/a	n/a	n/a
88	7510208	1476551H1	SNP00036803	115	3317	T	T	C	noncoding	n/d	n/a	n/d	n/d
88	7510208	1476551H1	SNP00116828	89	3291	G	G	A	noncoding	n/a	n/a	n/a	n/a
88	7510208	1484827H1	SNP00036802	92	5946	T	T	C	noncoding	n/a	n/a	n/a	n/a
88	7510208	1831572H1	SNP00067230	96	7323	A	A	G	noncoding	n/d	n/d	n/d	n/d
88	7510208	1991459H1	SNP00055209	13	5677	T	T	C	noncoding	n/a	n/a	n/a	n/a
88	7510208	1993878H1	SNP00036803	23	6507	T	T	C	noncoding	n/d	n/a	n/d	n/d
88	7510208	23111751H1	SNP00036803	203	3316	T	T	C	noncoding	n/d	n/a	n/d	n/d
88	7510208	23111751H1	SNP00116828	177	3290	G	G	A	noncoding	n/a	n/a	n/a	n/a
88	7510208	2500080H1	SNP00055209	124	2642	T	T	C	A844	n/a	n/a	n/a	n/a
88	7510208	2572745H1	SNP00151799	219	3653	C	C	T	noncoding	n/a	n/a	n/a	n/a
88	7510208	2802374H1	SNP00050176	105	7685	C	C	T	noncoding	n/d	0.87	n/d	0.98
88	7510208	2846083H1	SNP00106013	228	328	C	C	T	S73	n/d	n/d	n/d	n/d
88	7510208	3087570H1	SNP00036803	181	3297	T	T	C	noncoding	n/d	n/a	n/d	n/d
88	7510208	3087570H1	SNP00116828	155	3271	G	G	A	noncoding	n/a	n/a	n/a	n/a
88	7510208	3398402H1	SNP00106329	137	1697	A	A	C	A529	n/a	n/a	n/a	n/a
88	7510208	3607395H1	SNP00036803	16	6506	T	T	C	noncoding	n/d	n/a	n/d	n/d

Table 8

SEQ ID NO:	PID	EST ID	SNP ID	EST SNP	CB1 SNP	EST Allele	Allele 1	Allele 2	Amino Acid	Caucasian Allele 1 frequency	African Allele 1 frequency	Asian Allele 1 frequency	Hispanic Allele 1 frequency
88	7510208	3744352H1	SNP00067230	59	7322	A	A	G	noncoding	n/d	n/d	n/d	n/d
88	7510208	3753638H1	SNP00116825	173	6859	C	C	T	noncoding	n/a	n/a	n/a	n/a
88	7510208	3753638H1	SNP00116826	270	6959	C	C	G	noncoding	n/d	n/d	n/d	n/d
88	7510208	3758446H1	SNP00121526	193	4177	G	G	T	noncoding	n/d	n/d	n/d	n/d
88	7510208	3758446H1	SNP00121527	89	4072	C	C	T	noncoding	n/a	n/a	n/a	n/a
88	7510208	3822281H1	SNP00151799	200	3652	C	C	T	noncoding	n/a	n/a	n/a	n/a
88	7510208	3824109H1	SNP00050176	146	7642	T	C	T	noncoding	n/d	0.87	n/d	0.98
88	7510208	3869114H1	SNP00116827	50	3124	C	C	T	noncoding	n/a	n/a	n/a	n/a
88	7510208	3941890H1	SNP00106328	73	1539	A	A	C	N477	n/a	n/a	n/a	n/a
88	7510208	3944290H1	SNP00106329	230	1696	A	A	C	E529	n/a	n/a	n/a	n/a
88	7510208	3950406H1	SNP00062364	71	6893	T	T	C	noncoding	0.35	0.33	0.26	0.52
88	7510208	4082010H1	SNP00050176	33	7683	C	C	T	noncoding	n/d	0.87	n/d	0.98
88	7510208	4093937H1	SNP00116827	148	6307	C	C	T	noncoding	n/a	n/a	n/a	n/a
88	7510208	4297233H1	SNP00151799	120	3648	C	C	T	noncoding	n/a	n/a	n/a	n/a
88	7510208	4342760H1	SNP00067230	210	7321	A	A	G	noncoding	n/d	n/d	n/d	n/d
88	7510208	4456967H1	SNP00055209	95	2643	C	T	C	R845	n/a	n/a	n/a	n/a
88	7510208	4745011H1	SNP00050176	193	7682	C	C	T	noncoding	n/d	0.87	n/d	0.98
88	7510208	4837070H1	SNP00067230	84	7320	A	A	G	noncoding	n/d	n/d	n/d	n/d
88	7510208	5024420H1	SNP00050176	201	7675	C	C	T	noncoding	n/d	0.87	n/d	0.98
88	7510208	5098681H2	SNP00067230	108	7260	A	A	G	noncoding	n/d	n/d	n/d	n/d
88	7510208	5840056H1	SNP00116825	179	3669	C	C	T	noncoding	n/a	n/a	n/a	n/a
88	7510208	5840056H1	SNP00116826	83	3765	C	C	G	noncoding	n/d	n/d	n/d	n/d
88	7510208	5971465H1	SNP00036802	105	5944	T	T	C	noncoding	n/a	n/a	n/a	n/a
88	7510208	5972928H1	SNP00050176	226	7681	C	C	T	noncoding	n/d	0.87	n/d	0.98
88	7510208	6253205H1	SNP00106330	504	1945	C	C	T	T612	n/a	n/a	n/a	n/a
88	7510208	6253205H1	SNP00106331	543	1984	A	A	G	K625	n/d	n/d	n/d	n/d
88	7510208	6436507H1	SNP00067230	181	7316	A	A	G	noncoding	n/d	n/d	n/d	n/d
88	7510208	6572414H1	SNP00106012	173	234	C	C	T	L42	n/a	n/a	n/a	n/a

Table 8

SEQ ID NO:	PID	EST ID	SNP ID	EST SNP	CB1 SNP	EST Allele	Allele 1	Allele 2	Amino Acid	Caucasian Allele 1 frequency	African Allele 1 frequency	Asian Allele 1 frequency	Hispanic Allele 1 frequency
88	7510208	6572451H1	SNP00106014	553	584	C	C	A	N158	n/d	n/d	n/d	n/d
88	7510208	6574888H1	SNP00060648	354	2717	T	T	C	G869	n/d	n/d	n/d	n/d
88	7510208	6618612H1	SNP00106015	279	790	A	A	G	E227	n/a	n/a	n/a	n/a
88	7510208	663140H1	SNP00036802	174	5947	T	T	C	noncoding	n/a	n/a	n/a	n/a
88	7510208	6757850J1	SNP00060647	263	5464	T	C	T	noncoding	n/a	n/a	n/a	n/a
88	7510208	6762912J1	SNP00093168	312	2382	C	C	T	R758	n/a	n/a	n/a	n/a
88	7510208	6763466J1	SNP00060647	263	2427	C	C	T	H773	n/a	n/a	n/a	n/a
88	7510208	6765168H1	SNP00106015	508	787	A	A	G	E226	n/a	n/a	n/a	n/a
88	7510208	6769705H1	SNP00116826	424	3766	C	C	G	noncoding	n/d	n/d	n/d	n/d
88	7510208	6814133H1	SNP00106013	22	327	C	C	T	P73	n/d	n/d	n/d	n/d
88	7510208	6814133H1	SNP00106014	282	583	C	C	A	T158	n/d	n/d	n/d	n/d
88	7510208	6872080H1	SNP00106329	180	1653	A	A	C	R515	n/a	n/a	n/a	n/a
88	7510208	6872080H1	SNP00106330	428	1904	C	C	T	Y598	n/a	n/a	n/a	n/a
88	7510208	6872080H1	SNP00106331	467	1942	A	A	G	Q611	n/d	n/d	n/d	n/d
88	7510208	6887907J1	SNP00106015	109	1085	G	A	G	G325	n/a	n/a	n/a	n/a
88	7510208	6893301J1	SNP00062364	361	6895	T	T	C	noncoding	0.35	0.33	0.26	0.52
88	7510208	6894642H1	SNP00062364	441	3704	T	T	C	noncoding	0.35	0.33	0.26	0.52
88	7510208	6949007H1	SNP00106015	524	999	T	T	C	S297	n/a	n/a	n/a	n/a
88	7510208	6975081H1	SNP00106012	152	233	C	C	T	G41	n/a	n/a	n/a	n/a
88	7510208	7071727H1	SNP00000461	353	7691	T	T	C	noncoding	0.47	n/a	n/a	n/a
88	7510208	7071727H1	SNP00050176	401	7643	C	C	T	noncoding	n/d	0.87	n/d	0.98
88	7510208	7071727H1	SNP00106015	307	788	A	A	G	E226	n/a	n/a	n/a	n/a
88	7510208	762966H2	SNP00036803	28	6464	A	A	G	noncoding	n/d	n/a	n/d	n/d
88	7510208	762966H2	SNP00036803	265	6462	A	A	G	noncoding	n/d	n/a	n/d	n/d
88	7505294	1597548H1	SNP00010943	166	419	G	G	A	G129	n/a	n/a	n/a	n/a
90	7505294	1915171H1	SNP00041595	37	1002	T	T	C	W324	n/d	n/a	n/a	n/a
90	7505294	2104778H1	SNP00115560	95	95	C	C	T	P21	n/d	n/d	n/a	n/a
90	7505294	2615711H1	SNP00041595	215	1003	T	T	C	L324	n/d	n/a	n/a	n/a

Table 8

SEQ ID NO:	PID	EST ID	SNP ID	EST SNP	CB1 SNP	EST Allele	Allele 1	Allele 2	Amino Acid	Caucasian Allele 1 frequency	African Allele 1 frequency	Asian Allele 1 frequency	Hispanic Allele 1 frequency
90	7505294	2679723H1	SNP00010943	24	418	G	G	A	G129	n/a	n/a	n/a	n/a
90	7505294	3763389H1	SNP00041595	6	1001	T	T	C	P323	n/d	n/a	n/a	n/a
90	7505294	3781729H1	SNP00010943	123	417	G	G	A	G129	n/a	n/a	n/a	n/a
90	7505294	3941309H1	SNP00041595	246	996	T	T	C	S322	n/d	n/a	n/a	n/a
90	7505294	5848280H1	SNP00041595	30	997	T	T	C	L322	n/d	n/a	n/a	n/a
90	7505294	6147146H1	SNP00010943	295	413	G	G	A	R127	n/a	n/a	n/a	n/a
91	7505631	1355009H1	SNP00025254	19	2357	C	C	T	noncoding	n/a	n/a	n/a	n/a
91	7505631	1355009H1	SNP00025255	95	2433	A	A	G	noncoding	n/a	n/a	n/a	n/a
91	7505631	1367924H1	SNP00004462	113	3354	A	A	G	noncoding	n/a	n/a	n/a	n/a
91	7505631	1644485H1	SNP00025253	32	1603	A	A	G	noncoding	n/a	n/a	n/a	n/a
91	7505631	2047058H1	SNP00025254	82	2356	C	C	T	noncoding	n/a	n/a	n/a	n/a
91	7505631	2047058H1	SNP00025255	6	2432	A	A	G	noncoding	n/a	n/a	n/a	n/a
91	7505631	2325919H1	SNP00004462	67	3351	A	A	G	noncoding	n/a	n/a	n/a	n/a
91	7505631	2824251H1	SNP00004462	114	3352	A	A	G	noncoding	n/a	n/a	n/a	n/a
91	7505631	3495656H1	SNP00025254	159	2354	C	C	T	noncoding	n/a	n/a	n/a	n/a
91	7505631	3495656H1	SNP00025255	235	2430	G	A	G	noncoding	n/a	n/a	n/a	n/a
91	7505631	4329080H1	SNP00025254	65	2355	C	C	T	noncoding	n/a	n/a	n/a	n/a
91	7505631	4329080H1	SNP00025255	141	2431	A	A	G	noncoding	n/a	n/a	n/a	n/a
91	7505631	4525326H1	SNP00025254	200	2352	C	C	T	noncoding	n/a	n/a	n/a	n/a
91	7505631	4647714H1	SNP00025253	196	1599	A	A	G	noncoding	n/a	n/a	n/a	n/a
91	7505631	4980914H1	SNP00025253	55	1601	A	A	G	noncoding	n/a	n/a	n/a	n/a
91	7505631	5681630H1	SNP00025253	198	1602	A	A	G	noncoding	n/a	n/a	n/a	n/a
92	7506561	1667982H1	SNP00071142	118	316	C	C	A	R26	1.00	n/a	n/a	n/a
93	7510733	1218582H1	SNP00052605	135	2689	C	C	T	noncoding	n/a	n/a	n/a	n/a
93	7510733	1222021H1	SNP00040592	51	2412	C	C	A	noncoding	n/a	n/a	n/a	n/a
93	7510733	1222329H1	SNP00040592	107	2419	A	C	A	noncoding	n/a	n/a	n/a	n/a
93	7510733	1559060H1	SNP00040591	61	2107	C	C	T	noncoding	n/a	n/a	n/a	n/a
93	7510733	1559060H1	SNP00047819	83	2129	G	C	G	noncoding	0.06	0.18	0.09	0.06

Table 8

SEQ ID NO:	PID	EST ID	SNP ID	EST SNP	CB1 SNP	EST Allele	Allele 1	Allele 2	Amino Acid	Caucasian Allele 1 frequency	African Allele 1 frequency	Asian Allele 1 frequency	Hispanic Allele 1 frequency
93	7510733	3693413H1	SNP00040592	227	2415	C	C	A	noncoding	n/a	n/a	n/a	n/a
93	7510733	3840578H1	SNP00040592	102	2416	C	C	A	noncoding	n/a	n/a	n/a	n/a
93	7510733	3840668H1	SNP00040591	125	2104	C	C	T	noncoding	n/a	n/a	n/a	n/a
93	7510733	3840668H1	SNP00047819	147	2126	G	C	G	noncoding	0.06	0.18	0.09	0.06
93	7510733	4410720H1	SNP00052604	19	903	G	G	A	A233	0.89	0.82	0.87	0.91
93	7510733	4414082H1	SNP00040591	59	2105	C	C	T	noncoding	n/a	n/a	n/a	n/a
93	7510733	4414082H1	SNP00047819	81	2127	G	C	G	noncoding	0.06	0.18	0.09	0.06
93	7510733	4414445H1	SNP00052605	163	2688	C	C	T	noncoding	n/a	n/a	n/a	n/a
93	7510733	478403H1	SNP00052605	87	2690	C	C	T	noncoding	n/a	n/a	n/a	n/a
93	7510733	557755H1	SNP00040592	133	2417	C	C	A	noncoding	n/a	n/a	n/a	n/a
93	7510733	559550H1	SNP00040591	60	2106	C	C	T	noncoding	n/a	n/a	n/a	n/a
93	7510733	559550H1	SNP00047819	82	2128	C	C	G	noncoding	0.06	0.18	0.09	0.06
93	7510733	5824493H1	SNP00052604	355	899	A	G	A	L231	0.89	0.82	0.87	0.91
93	7510733	6896821H1	SNP00052603	140	205	A	A	G	noncoding	0.95	n/d	n/d	0.97
94	7510734	1218582H1	SNP00052605	135	2774	C	C	T	noncoding	n/a	n/a	n/a	n/a
94	7510734	1222021H1	SNP00040592	51	2497	C	C	A	noncoding	n/a	n/a	n/a	n/a
94	7510734	1222329H1	SNP00040592	107	2504	A	C	A	noncoding	n/a	n/a	n/a	n/a
94	7510734	1559060H1	SNP00040591	61	2192	C	C	T	noncoding	n/a	n/a	n/a	n/a
94	7510734	1559060H1	SNP00047819	83	2214	G	C	G	noncoding	0.06	0.18	0.09	0.06
94	7510734	3693413H1	SNP00040592	227	2500	C	C	A	noncoding	n/a	n/a	n/a	n/a
94	7510734	3840578H1	SNP00040592	102	2501	C	C	A	noncoding	n/a	n/a	n/a	n/a
94	7510734	3840668H1	SNP00040591	125	2189	C	C	T	noncoding	n/a	n/a	n/a	n/a
94	7510734	3840668H1	SNP00047819	147	2211	G	C	G	noncoding	0.06	0.18	0.09	0.06
94	7510734	4410720H1	SNP00052604	19	988	G	G	A	noncoding	0.89	0.82	0.87	0.91
94	7510734	4414082H1	SNP00040591	59	2190	C	C	T	noncoding	n/a	n/a	n/a	n/a
94	7510734	4414082H1	SNP00047819	81	2212	G	C	G	noncoding	0.06	0.18	0.09	0.06
94	7510734	4414445H1	SNP00052605	163	2773	C	C	T	noncoding	n/a	n/a	n/a	n/a
94	7510734	478403H1	SNP00052605	87	2775	C	C	T	noncoding	n/a	n/a	n/a	n/a

Table 8

SEQ ID NO:	PID	EST ID	SNP ID	EST SNP	CB1 SNP	EST Allele	Allele 1	Allele 2	Amino Acid	Caucasian Allele 1 frequency	African Allele 1 frequency	Asian Allele 1 frequency	Hispanic Allele 1 frequency
94	7510734	557755H1	SNP00040592	133	2502	C	C	A	noncoding	n/a	n/a	n/a	n/a
94	7510734	559550H1	SNP00040591	60	2191	C	C	T	noncoding	n/a	n/a	n/a	n/a
94	7510734	559550H1	SNP00047819	82	2213	C	C	G	noncoding	0.06	0.18	0.09	0.06
94	7510734	5824493H1	SNP00052604	355	984	A	G	A	noncoding	0.89	0.82	0.87	0.91
94	7510734	6896821H1	SNP00052603	140	205	A	A	G	noncoding	0.95	n/d	n/d	0.97
95	7503977	1627645H1	SNP00033082	5	1937	C	C	T	noncoding	n/d	n/a	n/a	n/a
95	7503977	3027777F6	SNP00033081	49	1624	C	C	T	noncoding	n/a	n/a	n/a	n/a
95	7503977	6800356J1	SNP00107876	418	711	G	G	T	L173	n/d	n/a	n/a	n/a
96	7505084	2707270F6	SNP00152729	184	1603	A	A	G	noncoding	n/a	n/a	n/a	n/a
97	7506950	1412498H1	SNP00112954	200	439	G	G	A	K132	n/a	n/a	n/a	n/a
98	7506951	1412498H1	SNP00112954	200	439	G	G	A	K132	n/a	n/a	n/a	n/a
100	7506956	1412498H1	SNP00112954	200	439	G	G	A	K132	n/a	n/a	n/a	n/a
101	7506959	1412498H1	SNP00112954	200	439	G	G	A	K132	n/a	n/a	n/a	n/a
102	7506960	7233773H1	SNP00112954	137	448	A	A	C	noncoding	n/a	n/a	n/a	n/a
103	7510540	2923154F6	SNP00019786	209	1571	A	A	C	noncoding	0.07	n/a	n/a	n/a
103	7510540	6930765H1	SNP00098509	28	356	A	G	A	noncoding	n/a	n/a	n/a	n/a
104	7510545	1275854F6	SNP00124648	18	175	G	G	A	V39	n/d	n/d	n/d	n/d
104	7510545	2347746H1	SNP00041565	38	787	C	C	T	noncoding	n/a	n/a	n/a	n/a
104	7510545	2347746H1	SNP00041566	144	893	A	A	G	noncoding	n/a	n/a	n/a	n/a
104	7510545	7276247H2	SNP00124648	103	173	G	G	A	G38	n/d	n/d	n/d	n/d
104	7510545	7602268J1	SNP00124648	187	164	G	G	A	G35	n/d	n/d	n/d	n/d
104	7510545	7741944J1	SNP00124648	555	153	G	G	A	E31	n/d	n/d	n/d	n/d
105	7510654	1250172H1	SNP00098839	202	1274	G	G	A	noncoding	n/a	n/a	n/a	n/a
105	7510654	1416107F6	SNP00007052	479	1507	A	A	G	noncoding	n/a	n/a	n/a	n/a
105	7510654	1416107T6	SNP00007052	153	1582	A	A	G	noncoding	n/a	n/a	n/a	n/a
105	7510654	1416107T6	SNP00032083	118	1617	G	G	T	noncoding	n/a	n/a	n/a	n/a
105	7510654	1553708H1	SNP00007052	61	1506	A	A	G	noncoding	n/a	n/a	n/a	n/a
105	7510654	1553708H1	SNP00032083	26	1541	G	G	T	noncoding	n/a	n/a	n/a	n/a

Table 8

SEQ ID NO:	PID	EST ID	SNP ID	EST SNP	CB1 SNP	EST Allele	Allele 1	Allele 2	Amino Acid	Caucasian Allele 1 frequency	African Allele 1 frequency	Asian Allele 1 frequency	Hispanic Allele 1 frequency
105	7510634	1750720F6	SNP00001888	154	826	C	C	T	G260	n/a	n/a	n/a	n/a
105	7510634	1750720F6	SNP00074165	198	870	T	T	G	V275	n/a	n/a	n/a	n/a
105	7510634	2185847F6	SNP00001888	164	827	T	C	T	F261	n/a	n/a	n/a	n/a
105	7510634	2185847F6	SNP00074165	208	871	T	T	G	V275	n/a	n/a	n/a	n/a
106	7510660	1208437R1	SNP00076070	188	2807	C	C	T	S893	n/a	n/a	n/a	n/a
106	7510660	2723676F6	SNP00116349	246	1935	C	C	T	P603	n/a	n/a	n/a	n/a
106	7510660	3392285H1	SNP00116349	209	1932	C	C	T	L602	n/a	n/a	n/a	n/a
106	7510660	5401847F6	SNP00076069	316	1721	C	C	T	C531	n/d	n/a	n/a	n/a
107	7510661	1208437R1	SNP00076070	188	2737	C	C	T	noncoding	n/a	n/a	n/a	n/a
107	7510661	2723676F6	SNP00116349	246	1935	C	C	T	P603	n/a	n/a	n/a	n/a
107	7510661	3392285H1	SNP00116349	209	1932	C	C	T	L602	n/a	n/a	n/a	n/a
107	7510661	5401847F6	SNP00076069	316	1721	C	C	T	C531	n/d	n/a	n/a	n/a
108	7510680	1443748R1	SNP00149102	53	1909	G	G	A	noncoding	n/a	n/a	n/a	n/a
108	7510680	1443748T6	SNP00149102	5	1910	G	G	A	noncoding	n/a	n/a	n/a	n/a
109	7505145	1288322H1	SNP00020995	117	1419	C	C	A	noncoding	n/a	n/a	n/a	n/a
109	7505145	1307614H1	SNP00020993	11	466	C	C	T	T129	n/a	n/a	n/a	n/a
109	7505145	1954824H1	SNP00020995	3	1416	C	C	A	noncoding	n/a	n/a	n/a	n/a
109	7505145	2445108H1	SNP00020995	66	1415	C	C	A	noncoding	n/a	n/a	n/a	n/a
109	7505145	2701206H1	SNP00020995	48	1418	C	C	A	noncoding	n/a	n/a	n/a	n/a
109	7505145	2750471H1	SNP00020994	46	1358	G	G	A	noncoding	n/a	n/a	n/a	n/a
109	7505145	3508476H1	SNP00020992	20	110	C	G	C	T10	n/a	n/a	n/a	n/a
109	7505145	4375677H1	SNP00020993	76	465	C	C	T	P129	n/a	n/a	n/a	n/a
109	7505145	4595210H1	SNP00020993	108	464	C	C	T	A128	n/a	n/a	n/a	n/a
109	7505145	4649323H1	SNP00020993	247	467	C	C	T	T129	n/a	n/a	n/a	n/a
109	7505145	4764638H1	SNP00020994	210	1356	G	G	A	noncoding	n/a	n/a	n/a	n/a
109	7505145	5100029H1	SNP00020995	225	1421	C	C	A	noncoding	n/a	n/a	n/a	n/a
109	7505145	5951826H1	SNP00020995	214	1410	C	C	A	noncoding	n/a	n/a	n/a	n/a
109	7505145	6846420H1	SNP00020994	194	1361	G	G	A	noncoding	n/a	n/a	n/a	n/a

Table 8

SEQ ID NO:	PID	EST ID	SNP ID	EST SNP	CB1 SNP	EST Allele	Allele 1	Allele 2	Amino Acid	Caucasian Allele 1 frequency	African Allele 1 frequency	Asian Allele 1 frequency	Hispanic Allele 1 frequency
109	7505145	7344481H1	SNP00094043	138	1067	G	C	G	G329	n/d	n/a	n/a	n/a
110	7505162	139886H1	SNP00036849	97	1345	A	G	A	noncoding	0.77	n/a	n/a	n/a
110	7505162	1552730H1	SNP00075257	80	681	C	C	T	A156	n/a	n/a	n/a	n/a
110	7505162	1620127H1	SNP00009022	98	1542	G	G	C	noncoding	n/a	n/a	n/a	n/a
110	7505162	1620504H1	SNP00009022	99	1543	G	G	C	noncoding	n/a	n/a	n/a	n/a
110	7505162	2679787H1	SNP00036849	211	1349	G	G	A	noncoding	0.77	n/a	n/a	n/a
110	7505162	3556418H1	SNP00036849	174	1352	G	G	A	noncoding	0.77	n/a	n/a	n/a
110	7505162	3852765H1	SNP00009022	121	1541	G	G	C	noncoding	n/a	n/a	n/a	n/a
110	7505162	6746110H1	SNP00009022	554	1538	G	G	C	noncoding	n/a	n/a	n/a	n/a
111	7505469	217011H1	SNP00011018	91	2065	A	A	G	noncoding	n/a	n/a	n/a	n/a
111	7505469	2402129H1	SNP00011018	80	2066	G	A	G	noncoding	n/a	n/a	n/a	n/a
112	7505475	1307948H1	SNP00023319	77	4003	A	G	A	noncoding	0.57	0.28	0.36	0.65
112	7505475	1307948H1	SNP00023320	201	4127	C	C	T	noncoding	n/d	n/d	n/d	n/d
112	7505475	1307948H1	SNP00072137	91	4017	A	A	G	noncoding	n/a	n/a	n/a	n/a
112	7505475	1965082H1	SNP00023319	146	4002	G	G	A	noncoding	0.57	0.28	0.36	0.65
112	7505475	1965082H1	SNP00072137	160	4016	A	A	G	noncoding	n/a	n/a	n/a	n/a
112	7505475	2764315H1	SNP00026116	169	3871	T	T	C	noncoding	n/d	n/a	n/a	n/a
112	7505475	3781324H1	SNP00026116	174	3868	C	T	C	noncoding	n/d	n/a	n/a	n/a
112	7505475	3781324H1	SNP00139248	272	3966	T	C	T	noncoding	n/a	n/a	n/a	n/a
112	7505475	3948943H1	SNP00023320	89	4126	C	C	T	noncoding	n/d	n/d	n/d	n/d
112	7505475	5704531H1	SNP00023320	113	4124	T	C	T	noncoding	n/d	n/d	n/d	n/d
112	7505475	5704531H1	SNP00072137	3	4014	A	A	G	noncoding	n/a	n/a	n/a	n/a
113	7505568	2731808H1	SNP00035633	100	129	G	A	G	G25	0.73	0.30	0.74	0.73
113	7505568	4552729H1	SNP00035634	167	460	T	C	T	noncoding	n/a	n/a	n/a	n/a
116	7510541	2514486H1	SNP00142846	30	97	C	C	G	noncoding	n/a	n/a	n/a	n/a
116	7510541	574452H1	SNP00142846	60	96	C	C	G	noncoding	n/a	n/a	n/a	n/a
116	7510541	5758634H1	SNP00142846	45	94	C	C	G	noncoding	n/a	n/a	n/a	n/a
117	7510923	2514486H1	SNP00142846	30	97	C	C	G	noncoding	n/a	n/a	n/a	n/a

Table 8

SEQ ID NO.	PID	EST ID	SNP ID	EST SNP	CB1 SNP	EST Allele	Allele 1	Allele 2	Amino Acid	Caucasian Allele 1 frequency	African Allele 1 frequency	Asian Allele 1 frequency	Hispanic Allele 1 frequency
117	7510923	574452H1	SNP00142846	60	96	C	C	G	noncoding	n/a	n/a	n/a	n/a
117	7510923	5758634H1	SNP00142846	45	94	C	C	G	noncoding	n/a	n/a	n/a	n/a
118	7510984	1270543H1	SNP00121815	232	3202	G	G	A	R1049	n/a	n/a	n/a	n/a
118	7510984	2402461H1	SNP00051864	90	4465	C	C	T	noncoding	n/d	n/a	n/a	n/a
118	7510984	6559367H1	SNP00051863	151	3877	G	G	A	R1274	0.50	0.18	0.74	0.38
118	7510984	6908670H1	SNP00121813	251	262	C	C	T	P69	n/a	n/a	n/a	n/a
118	7510984	6908670H1	SNP00121814	374	385	C	C	T	A110	n/d	0.95	n/d	n/d

What is claimed is:

1. An isolated polypeptide selected from the group consisting of:
 - a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-59,
 - b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:10-11, SEQ ID NO:20-21, SEQ ID NO:23, SEQ ID NO:25-29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:38-40, SEQ ID NO:43-45, SEQ ID NO:49-51, and SEQ ID NO:56,
 - c) a polypeptide comprising a naturally occurring amino acid sequence at least 91% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:3 and SEQ ID NO:54,
 - d) a polypeptide comprising a naturally occurring amino acid sequence at least 92% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:19 and SEQ ID NO:22,
 - e) a polypeptide comprising a naturally occurring amino acid sequence at least 93% identical to the amino acid sequence of SEQ ID NO:46,
 - f) a polypeptide comprising a naturally occurring amino acid sequence at least 94% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:14-15,
 - g) a polypeptide comprising a naturally occurring amino acid sequence at least 95% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:13, SEQ ID NO:18, SEQ ID NO:36-37 and SEQ ID NO:52,
 - h) a polypeptide comprising a naturally occurring amino acid sequence at least 96% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:2 and SEQ ID NO:16,
 - i) a polypeptide comprising a naturally occurring amino acid sequence at least 97% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:30, SEQ ID NO:32 and SEQ ID NO:57-58,
 - j) a polypeptide comprising a naturally occurring amino acid sequence at least 98% identical to the amino acid sequence of SEQ ID NO:59,

- 5
- 10
- 15
- 20
- 25
- 30
- k) a polypeptide comprising a naturally occurring amino acid sequence at least 99% identical to the amino acid sequence of SEQ ID NO:12,
 - l) a polypeptide consisting essentially of a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:34, SEQ ID NO:41-42, SEQ ID NO:47, and SEQ ID NO:55.
 - m) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-59, and
 - n) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-59.
2. An isolated polypeptide of claim 1 comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-59.
3. An isolated polynucleotide encoding a polypeptide of claim 1.
4. An isolated polynucleotide encoding a polypeptide of claim 2.
5. An isolated polynucleotide of claim 4 comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:60-118.
6. A recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide of claim 3.
7. A cell transformed with a recombinant polynucleotide of claim 6.
8. A transgenic organism comprising a recombinant polynucleotide of claim 6.
9. A method of producing a polypeptide of claim 1, the method comprising:
- a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell is transformed with a recombinant polynucleotide, and said recombinant

polynucleotide comprises a promoter sequence operably linked to a polynucleotide encoding the polypeptide of claim 1, and

- b) recovering the polypeptide so expressed.

5 10. A method of claim 9, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NO:1-59.

11. An isolated antibody which specifically binds to a polypeptide of claim 1.

10 12. An isolated polynucleotide selected from the group consisting of:

- a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:60-118,
- b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ
15 ID NO:60, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:73, SEQ ID NO:76, SEQ ID NO:78-79, SEQ ID NO:81, SEQ ID NO:83-85, SEQ ID NO:90-92, SEQ ID NO:108 and SEQ ID NO:113,
- c) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 91% identical to the polynucleotide sequence of SEQ ID NO:70,
- 20 d) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 92% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:71 and SEQ ID NO:87,
- e) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 93% identical to the polynucleotide sequence of SEQ ID NO:115,
- 25 f) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 94% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:68 and SEQ ID NO:117,
- g) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 95% identical to a polynucleotide sequence selected from the group consisting of SEQ
30 ID NO:63, SEQ ID NO:66 and SEQ ID NO:118,

- h) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 96% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:64 and SEQ ID NO:75,
- 5 i) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 97% identical to the polynucleotide sequence of SEQ ID NO:106,
- j) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 98% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:80, SEQ ID NO:88, SEQ ID NO:95, SEQ ID NO:109 and SEQ ID NO:116,
- 10 k) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 99% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:62, SEQ ID NO:82, SEQ ID NO:86, SEQ ID NO:89, SEQ ID NO:96, SEQ ID NO:99 and SEQ ID NO:104,
- l) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:61, SEQ ID NO:69, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:93-94, SEQ ID NO:97-98, SEQ ID NO:100-103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:110-112 and SEQ ID NO:114,
- 15 m) a polynucleotide complementary to a polynucleotide of a),
- n) a polynucleotide complementary to a polynucleotide of b),
- 20 o) a polynucleotide complementary to a polynucleotide of c),
- p) a polynucleotide complementary to a polynucleotide of d),
- q) a polynucleotide complementary to a polynucleotide of e),
- r) a polynucleotide complementary to a polynucleotide of f),
- s) a polynucleotide complementary to a polynucleotide of g),
- 25 t) a polynucleotide complementary to a polynucleotide of h),
- u) a polynucleotide complementary to a polynucleotide of i),
- v) a polynucleotide complementary to a polynucleotide of j),
- w) a polynucleotide complementary to a polynucleotide of k),
- x) a polynucleotide complementary to a polynucleotide of l), and
- 30 y) an RNA equivalent of a)-x).

13. An isolated polynucleotide comprising at least 60 contiguous nucleotides of a polynucleotide of claim 12.

14. A method of detecting a target polynucleotide in a sample, said target polynucleotide
5 having a sequence of a polynucleotide of claim 12, the method comprising:
- a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target
10 polynucleotide or fragments thereof, and
 - b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof.

15. A method of claim 14, wherein the probe comprises at least 60 contiguous nucleotides.

16. A method of detecting a target polynucleotide in a sample, said target polynucleotide
having a sequence of a polynucleotide of claim 12, the method comprising:
- a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and
 - 20 b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

17. A composition comprising a polypeptide of claim 1 and a pharmaceutically acceptable excipient.

25 18. A composition of claim 17, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NO:1-59.

19. A method for treating a disease or condition associated with decreased expression of
30 functional TRICH, comprising administering to a patient in need of such treatment the composition of claim 17.

20. A method of screening a compound for effectiveness as an agonist of a polypeptide of claim 1, the method comprising:

- a) exposing a sample comprising a polypeptide of claim 1 to a compound, and
- b) detecting agonist activity in the sample.

5

21. A composition comprising an agonist compound identified by a method of claim 20 and a pharmaceutically acceptable excipient.

22. A method for treating a disease or condition associated with decreased expression of functional TRICH, comprising administering to a patient in need of such treatment a composition of claim 21.

23. A method of screening a compound for effectiveness as an antagonist of a polypeptide of claim 1, the method comprising:

- a) exposing a sample comprising a polypeptide of claim 1 to a compound, and
- b) detecting antagonist activity in the sample.

15

24. A composition comprising an antagonist compound identified by a method of claim 23 and a pharmaceutically acceptable excipient.

20

25. A method for treating a disease or condition associated with overexpression of functional TRICH, comprising administering to a patient in need of such treatment a composition of claim 24.

26. A method of screening for a compound that specifically binds to the polypeptide of claim 1, the method comprising:

25

- a) combining the polypeptide of claim 1 with at least one test compound under suitable conditions, and
- b) detecting binding of the polypeptide of claim 1 to the test compound, thereby identifying a compound that specifically binds to the polypeptide of claim 1.

30

27. A method of screening for a compound that modulates the activity of the polypeptide of claim 1, the method comprising:

- a) combining the polypeptide of claim 1 with at least one test compound under conditions permissive for the activity of the polypeptide of claim 1,
- b) assessing the activity of the polypeptide of claim 1 in the presence of the test compound, and
- 5 c) comparing the activity of the polypeptide of claim 1 in the presence of the test compound with the activity of the polypeptide of claim 1 in the absence of the test compound, wherein a change in the activity of the polypeptide of claim 1 in the presence of the test compound is indicative of a compound that modulates the activity of the polypeptide of claim 1.

10

28. A method of screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a sequence of claim 5, the method comprising:

- a) exposing a sample comprising the target polynucleotide to a compound, under
- 15 conditions suitable for the expression of the target polynucleotide,
- b) detecting altered expression of the target polynucleotide, and
- c) comparing the expression of the target polynucleotide in the presence of varying amounts of the compound and in the absence of the compound.

20

29. A method of assessing toxicity of a test compound; the method comprising:

- a) treating a biological sample containing nucleic acids with the test compound,
- b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide of claim 12 under conditions whereby a specific hybridization complex is formed between said probe and a target
- 25 polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide of claim 12 or fragment thereof,
- c) quantifying the amount of hybridization complex, and
- d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a
- 30 difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

30. A method for a diagnostic test for a condition or disease associated with the expression of TRICH in a biological sample, the method comprising:

- 5 a) combining the biological sample with an antibody of claim 11, under conditions suitable for the antibody to bind the polypeptide and form an antibody:polypeptide complex, and
- b) detecting the complex, wherein the presence of the complex correlates with the presence of the polypeptide in the biological sample.

31. The antibody of claim 11, wherein the antibody is:

- 10 a) a chimeric antibody,
- b) a single chain antibody,
- c) a Fab fragment,
- d) a F(ab')₂ fragment, or
- e) a humanized antibody.

15 32. A composition comprising an antibody of claim 11 and an acceptable excipient.

33. A method of diagnosing a condition or disease associated with the expression of TRICH in a subject, comprising administering to said subject an effective amount of the composition of claim

20 32.

34. A composition of claim 32, further comprising a label.

25 35. A method of diagnosing a condition or disease associated with the expression of TRICH in a subject, comprising administering to said subject an effective amount of the composition of claim 34.

36. A method of preparing a polyclonal antibody with the specificity of the antibody of claim 11, the method comprising:

- 30 a) immunizing an animal with a polypeptide consisting of an amino acid sequence selected from the group consisting of SEQ ID NO:1-59, or an immunogenic fragment thereof, under conditions to elicit an antibody response,
- b) isolating antibodies from the animal, and

- c) screening the isolated antibodies with the polypeptide, thereby identifying a polyclonal antibody which specifically binds to a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-59.

5 37. A polyclonal antibody produced by a method of claim 36.

38. A composition comprising the polyclonal antibody of claim 37 and a suitable carrier.

39. A method of making a monoclonal antibody with the specificity of the antibody of claim
10 11, the method comprising:

- a) immunizing an animal with a polypeptide consisting of an amino acid sequence selected from the group consisting of SEQ ID NO:1-59, or an immunogenic fragment thereof, under conditions to elicit an antibody response,
- b) isolating antibody producing cells from the animal,
- 15 c) fusing the antibody producing cells with immortalized cells to form monoclonal antibody-producing hybridoma cells,
- d) culturing the hybridoma cells, and
- e) isolating from the culture monoclonal antibody which specifically binds to a polypeptide comprising an amino acid sequence selected from the group consisting of
20 SEQ ID NO:1-59.

40. A monoclonal antibody produced by a method of claim 39.

41. A composition comprising the monoclonal antibody of claim 40 and a suitable carrier.

25

42. The antibody of claim 11, wherein the antibody is produced by screening a Fab expression library.

43. The antibody of claim 11, wherein the antibody is produced by screening a recombinant
30 immunoglobulin library.

44. A method of detecting a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-59 in a sample, the method comprising:

- 5
- a) incubating the antibody of claim 11 with the sample under conditions to allow specific binding of the antibody and the polypeptide, and
 - b) detecting specific binding, wherein specific binding indicates the presence of a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-59 in the sample.

45. A method of purifying a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-59 from a sample, the method comprising:

- 10
- a) incubating the antibody of claim 11 with the sample under conditions to allow specific binding of the antibody and the polypeptide, and
 - b) separating the antibody from the sample and obtaining the purified polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-59.

15 46. A microarray wherein at least one element of the microarray is a polynucleotide of claim 13.

47. A method of generating an expression profile of a sample which contains polynucleotides, the method comprising:

- 20
- a) labeling the polynucleotides of the sample,
 - b) contacting the elements of the microarray of claim 46 with the labeled polynucleotides of the sample under conditions suitable for the formation of a hybridization complex, and
 - c) quantifying the expression of the polynucleotides in the sample.

25

48. An array comprising different nucleotide molecules affixed in distinct physical locations on a solid substrate, wherein at least one of said nucleotide molecules comprises a first oligonucleotide or polynucleotide sequence specifically hybridizable with at least 30 contiguous nucleotides of a target polynucleotide, and wherein said target polynucleotide is a polynucleotide of claim 12.

30

49. An array of claim 48, wherein said first oligonucleotide or polynucleotide sequence is completely complementary to at least 30 contiguous nucleotides of said target polynucleotide.

50. An array of claim 48, wherein said first oligonucleotide or polynucleotide sequence is completely complementary to at least 60 contiguous nucleotides of said target polynucleotide.

51. An array of claim 48, wherein said first oligonucleotide or polynucleotide sequence is
5 completely complementary to said target polynucleotide.

52. An array of claim 48, which is a microarray.

53. An array of claim 48, further comprising said target polynucleotide hybridized to a
10 nucleotide molecule comprising said first oligonucleotide or polynucleotide sequence.

54. An array of claim 48, wherein a linker joins at least one of said nucleotide molecules to said solid substrate.

15 55. An array of claim 48, wherein each distinct physical location on the substrate contains multiple nucleotide molecules, and the multiple nucleotide molecules at any single distinct physical location have the same sequence, and each distinct physical location on the substrate contains nucleotide molecules having a sequence which differs from the sequence of nucleotide molecules at another distinct physical location on the substrate.

20

56. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:1.

57. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:2.

25 58. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:3.

59. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:4.

60. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:5.

30

61. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:6.

62. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:7.

63. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:8.
64. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:9.
- 5 65. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:10.
66. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:11.
67. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:12.
- 10 68. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:13.
69. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:14.
- 15 70. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:15.
71. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:16.
72. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:17.
- 20 73. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:18.
74. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:19.
- 25 75. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:20.
76. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:21.
77. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:22.
- 30 78. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:23.
79. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:24.

80. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:25.

81. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:26.

5 82. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:27.

83. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:28.

10 84. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:29.

85. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:30.

86. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:31.

15 87. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:32.

88. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:33.

20 89. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:34.

90. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:35.

91. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:36.

25 92. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:37.

93. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:38.

30 94. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:39.

95. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:40.

96. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:41.

97. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:42.
98. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:43.
- 5 99. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:44.
100. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:45.
101. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:46.
- 10 102. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:47.
103. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:48.
- 15 104. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:49.
105. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:50.
106. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:51.
- 20 107. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:52.
108. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:53.
- 25 109. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:54.
110. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:55.
111. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:56.
- 30 112. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:57.
113. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:58.

114. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:59.

115. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:60.

5

116. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:61.

117. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:62.

10

118. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:63.

15

119. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:64.

120. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:65.

20

121. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:66.

122. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:67.

25

123. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:68.

124. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:69.

30

125. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:70.

126. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID
5 NO:71.

127. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:72.

10 128. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:73.

129. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:74.

15 130. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:75.

131. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID
20 NO:76.

132. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:77.

25 133. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:78.

134. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:79.

30 135. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:80.

136. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:81.

137. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID
5 NO:82.

138. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:83.

10 139. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:84.

140. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:85.

15 141. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:86.

142. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID
20 NO:87.

143. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:88.

25 144. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:89.

145. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:90.

30 146. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:91.

147. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:92.
148. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:93.
149. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:94.
150. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:95.
151. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:96.
152. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:97.
153. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:98.
154. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:99.
155. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:100.
156. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:101.
157. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:102.

158. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID
NO:103.

159. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID
5 NO:104.

160. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID
NO:105.

10 161. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID
NO:106.

162. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID
NO:107.

15 163. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID
NO:108.

164. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID
20 NO:109.

165. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID
NO:110.

25 166. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID
NO:111.

167. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID
NO:112.

30 168. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID
NO:113.

169. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:114.

170. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID
5 NO:115.

171. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:116.

10 172. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:117.

173. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:118.

15

<110> INCYTE CORPORATION
 MARQUIS, Joseph P.
 LEE, Soo Y.
 EMERLING, Brooke M.
 HAFALLIA, April J.A.
 KHARE, Reena
 KABLE, Amy E.
 RICHARDSON, Thomas W.
 SWARNAKAR, Anita
 CHAWLA, Narinder K.
 BECHA, Shanya D.
 MASON, Patricia M.
 ELLIOTT, Vicki S.
 RAMKUMAR, Jayalaxmi
 GRIFFIN, Jennifer A.
 TRAN, Uyen K.
 ISON, Craig H.
 LINDQUIST, Erika A.
 JIANG, Xin
 JACKSON, Alan A.
 WILSON, Amy D.
 JIN, Pei
 CHANG, Hsin-Ru

<120> TRANSPORTERS AND ION CHANNELS

<130> PF-1397 PCT

<140> To Be Assigned

<141> Herewith

<150> US 60/368,840

<151> 2002-03-28

<150> US 60/375,637

<151> 2002-04-26

<160> 118

<170> PERL Program

<210> 1

<211> 195

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7509332CD1

<400> 1

Met	Asp	Met	Ala	Trp	Gln	Met	Met	Gln	Leu	Leu	Leu	Leu	Ala	Leu
1				5					10					15
Val	Thr	Ala	Ala	Gly	Ser	Ala	Gln	Pro	Arg	Ser	Ala	Arg	Ala	Arg
				20					25					30
Thr	Asp	Leu	Leu	Asn	Val	Cys	Met	Asn	Ala	Lys	His	His	Lys	Thr
				35					40					45

Gln	Pro	Ser	Pro	Glu	Asp	Glu	Leu	Tyr	Gly	Gln	Cys	Ser	Pro	Trp	
				50					55					60	
Lys	Lys	Asn	Ala	Cys	Cys	Thr	Ala	Ser	Thr	Ser	Gln	Glu	Leu	His	
				65					70					75	
Lys	Asp	Thr	Ser	Arg	Leu	Tyr	Asn	Phe	Asn	Trp	Asp	His	Cys	Glu	
				80					85					90	
Arg	Trp	Trp	Glu	Asp	Cys	Arg	Thr	Ser	Tyr	Thr	Cys	Lys	Ser	Asn	
				95					100					105	
Trp	His	Lys	Gly	Trp	Asn	Trp	Thr	Ser	Gly	Ile	Asn	Glu	Cys	Pro	
				110					115					120	
Ala	Gly	Ala	Leu	Cys	Ser	Thr	Phe	Glu	Ser	Tyr	Phe	Pro	Thr	Pro	
				125					130					135	
Ala	Ala	Leu	Cys	Glu	Gly	Leu	Trp	Ser	His	Ser	Phe	Lys	Val	Ser	
				140					145					150	
Asn	Tyr	Ser	Arg	Gly	Ser	Gly	Arg	Cys	Ile	Gln	Met	Trp	Phe	Asp	
				155					160					165	
Ser	Ala	Gln	Gly	Asn	Pro	Asn	Glu	Glu	Val	Ala	Lys	Phe	Tyr	Ala	
				170					175					180	
Ala	Ala	Met	Asn	Ala	Gly	Ala	Pro	Ser	Arg	Gly	Ile	Ile	Asp	Ser	
				185					190					195	

<210> 2

<211> 138

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7509102CD1

<400> 2

Met	Gly	Pro	Ser	Cys	Pro	Val	Phe	Leu	Ser	Phe	Thr	Lys	Leu	Gly	
1				5					10					15	
Leu	Trp	Trp	Leu	Leu	Leu	Thr	Pro	Ala	Gly	Gly	Glu	Glu	Ala	Lys	
				20					25					30	
Arg	Pro	Pro	Pro	Arg	Ala	Pro	Gly	Asp	Pro	Leu	Ser	Ser	Pro	Ser	
				35					40					45	
Pro	Thr	Ala	Leu	Pro	Gln	Gly	Gly	Ser	His	Thr	Glu	Thr	Glu	Asp	
				50					55					60	
Arg	Leu	Phe	Lys	His	Leu	Phe	Arg	Gly	Tyr	Asn	Arg	Trp	Ala	Arg	
				65					70					75	
Pro	Val	Pro	Asn	Thr	Ser	Asp	Val	Asp	Glu	Lys	Asn	Gln	Met	Met	
				80					85					90	
Thr	Thr	Asn	Val	Trp	Leu	Lys	Gln	Glu	Trp	Ser	Asp	Tyr	Lys	Leu	
				95					100					105	
Arg	Trp	Asn	Pro	Thr	Asp	Phe	Gly	Asn	Ile	Thr	Ser	Leu	Arg	Val	
				110					115					120	
Pro	Ser	Glu	Met	Ile	Trp	Ile	Pro	Asp	Ile	Val	Leu	Tyr	Asn	Lys	
				125					130					135	

Thr Ala Arg

<210> 3

<211> 355

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7509132CD1

<400> 3

Met	Ser	Trp	Arg	Cys	Trp	Gly	Ala	Ala	Ser	Trp	Ala	Trp	Pro	Met	1	5	10	15
Leu	Leu	Pro	Pro	Met	Lys	Cys	Ser	Ser	Leu	Asp	Asp	Ser	Ser	Leu	20	25	30	
Ala	Pro	Thr	Gln	Val	Leu	Gly	Leu	Glu	Ser	Leu	Leu	Gly	Thr	Ala	35	40	45	
Ser	Leu	Trp	Pro	Leu	Leu	Gly	Leu	Thr	Val	Leu	Pro	Ala	Leu		50	55	60	
Leu	Gln	Leu	Val	Leu	Leu	Pro	Phe	Cys	Pro	Glu	Ser	Pro	Arg	Tyr	65	70	75	
Leu	Tyr	Ile	Ile	Gln	Asn	Leu	Glu	Gly	Pro	Ala	Arg	Lys	Ser	Leu	80	85	90	
Lys	Arg	Leu	Thr	Gly	Trp	Ala	Asp	Val	Ser	Gly	Val	Leu	Ala	Glu	95	100	105	
Leu	Lys	Asp	Glu	Lys	Arg	Lys	Leu	Glu	Arg	Glu	Arg	Pro	Leu	Ser	110	115	120	
Leu	Leu	Gln	Leu	Leu	Gly	Ser	Arg	Thr	His	Arg	Gln	Pro	Leu	Ile	125	130	135	
Ile	Ala	Val	Val	Leu	Gln	Leu	Ser	Gln	Gln	Leu	Ser	Gly	Ile	Asn	140	145	150	
Ala	Val	Phe	Tyr	Tyr	Ser	Thr	Ser	Ile	Phe	Glu	Thr	Ala	Gly	Val	155	160	165	
Gly	Gln	Pro	Ala	Tyr	Ala	Thr	Ile	Gly	Ala	Gly	Val	Val	Asn	Thr	170	175	180	
Val	Phe	Thr	Leu	Val	Ser	Val	Leu	Leu	Val	Glu	Arg	Ala	Gly	Arg	185	190	195	
Arg	Thr	Leu	His	Leu	Leu	Gly	Leu	Ala	Gly	Met	Cys	Gly	Cys	Ala	200	205	210	
Ile	Leu	Met	Thr	Val	Ala	Leu	Leu	Leu	Leu	Glu	Arg	Val	Pro	Ala	215	220	225	
Met	Ser	Tyr	Val	Ser	Ile	Val	Ala	Ile	Phe	Gly	Phe	Val	Ala	Phe	230	235	240	
Phe	Glu	Ile	Gly	Pro	Gly	Pro	Ile	Pro	Trp	Phe	Ile	Val	Ala	Glu	245	250	255	
Leu	Phe	Ser	Gln	Gly	Pro	Arg	Pro	Ala	Ala	Met	Ala	Val	Ala	Gly	260	265	270	
Phe	Ser	Asn	Trp	Thr	Ser	Asn	Phe	Ile	Ile	Gly	Met	Gly	Phe	Gln	275	280	285	
Tyr	Val	Ala	Glu	Ala	Met	Gly	Pro	Tyr	Val	Phe	Leu	Leu	Phe	Ala	290	295	300	
Val	Leu	Leu	Leu	Gly	Phe	Phe	Ile	Phe	Thr	Phe	Leu	Arg	Val	Pro	305	310	315	
Glu	Thr	Arg	Gly	Arg	Thr	Phe	Asp	Gln	Ile	Ser	Ala	Ala	Phe	His	320	325	330	
Arg	Thr	Pro	Ser	Leu	Leu	Glu	Gln	Glu	Val	Lys	Pro	Ser	Thr	Glu	335	340	345	
Leu	Glu	Tyr	Leu	Gly	Pro	Asp	Glu	Asn	Asp						350	355		

<210> 4
 <211> 380
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 7509136CD1

<400> 4
 Met Ser Thr Lys Val Tyr Leu Asp Leu Glu Trp Thr Asp Tyr Arg
 1 5 10 15
 Leu Ser Trp Asp Pro Ala Glu His Asp Gly Ile Asp Ser Leu Arg
 20 25 30
 Ile Thr Ala Glu Ser Val Trp Leu Pro Asp Val Val Leu Leu Asn
 35 40 45
 Asn Asn Asp Gly Asn Phe Asp Val Ala Leu Asp Ile Ser Val Val
 50 55 60
 Val Ser Ser Asp Gly Ser Val Arg Trp Gln Pro Pro Gly Ile Tyr
 65 70 75
 Arg Ser Ser Cys Ser Ile Gln Val Thr Tyr Phe Pro Phe Asp Trp
 80 85 90
 Gln Asn Cys Thr Met Val Phe Ser Ser Tyr Ser Tyr Asp Ser Ser
 95 100 105
 Glu Val Ser Leu Gln Thr Gly Leu Gly Pro Asp Gly Gln Gly His
 110 115 120
 Gln Glu Ile His Ile His Glu Gly Thr Phe Ile Glu Asn Gly Gln
 125 130 135
 Trp Glu Ile Ile His Lys Pro Ser Arg Leu Ile Gln Pro Pro Gly
 140 145 150
 Asp Pro Arg Gly Gly Arg Glu Gly Gln Arg Gln Glu Val Ile Phe
 155 160 165
 Tyr Leu Ile Ile Arg Arg Lys Pro Leu Phe Tyr Leu Val Asn Val
 170 175 180
 Ile Ala Pro Cys Ile Leu Ile Thr Leu Leu Ala Ile Phe Val Phe
 185 190 195
 Tyr Leu Pro Pro Asp Ala Val Ile Leu Ser Val Val Val Leu Asn
 200 205 210
 Leu His His Arg Ser Pro His Thr His Gln Met Pro Leu Trp Val
 215 220 225
 Arg Gln Ile Phe Ile His Lys Leu Pro Leu Tyr Leu Arg Leu Lys
 230 235 240
 Arg Pro Lys Pro Glu Arg Asp Leu Met Pro Glu Pro Pro His Cys
 245 250 255
 Ser Ser Pro Gly Ser Gly Trp Gly Arg Gly Thr Asp Glu Tyr Phe
 260 265 270
 Ile Arg Lys Pro Pro Ser Asp Phe Leu Phe Pro Lys Pro Asn Arg
 275 280 285
 Phe Gln Pro Glu Leu Ser Ala Pro Asp Leu Arg Arg Phe Ile Asp
 290 295 300
 Gly Pro Asn Arg Ala Val Ala Leu Leu Pro Glu Leu Arg Glu Val
 305 310 315
 Val Ser Ser Ile Ser Tyr Ile Ala Arg Gln Leu Gln Glu Gln Glu
 320 325 330
 Asp His Asp Ala Leu Lys Glu Asp Trp Gln Phe Val Ala Met Val
 335 340 345

	290	295	300
His Ser Pro Leu	Ile Lys His Pro Glu	Val Lys Ser Ala Ile	Glu
	305	310	315
Gly Ile Lys Tyr	Ile Ala Glu Thr Met	Lys Ser Asp Gln Glu	Ser
	320	325	330
Asn Asn Ala Ala	Ala Glu Trp Lys Tyr	Val Ala Met Val Met	Asp
	335	340	345
His Ile Leu Leu	Gly Val Phe Met Leu	Val Cys Ile Ile Gly	Thr
	350	355	360
Leu Ala Val Phe	Ala Gly Arg Leu Ile	Glu Leu Asn Gln Gln	Gly
	365	370	375

<210> 6

<211> 153

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7509214CD1

<400> 6

Met Ala Pro Pro	Trp Val Pro Ala Met	Gly Phe Thr Leu Ala	Pro
1	5	10	15
Ser His Gly Val	Arg Leu Leu Pro Gly	Leu Glu Arg Ala Gly	Arg
	20	25	30
Leu His Arg Glu	Gly Cys Gly Ser Pro	Gly Pro Leu His Trp	Ala
	35	40	45
Ala Gly Pro Glu	Leu Gly Met Ala Pro	His Leu Leu Trp Cys	Pro
	50	55	60
Thr Asn Gly Leu	Gly Leu Gly Gly Ser	Pro Ala Gly Gln Trp	Gly
	65	70	75
Gly Gly Ser His	Tyr Arg Gly Leu Val	Pro Gly Glu Pro Ala	Gly
	80	85	90
Arg Pro Pro Ala	Leu Pro Leu Pro Gly	Leu Ala Gly Leu Arg	Asp
	95	100	105
His Thr Gln Leu	Leu Arg Met Ala Gly	Gln Pro Trp Leu Ala	Trp
	110	115	120
Gly Thr Ala Ala	Ala Arg Val Ser Ala	Arg Pro Thr Arg Asp	Cys
	125	130	135
Ser Cys Thr Ser	Arg Cys His His Ala	Cys Asp Val Val Ala	Val
	140	145	150
Thr Leu Ser			

<210> 7

<211> 369

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7509244CD1

<400> 7

Met	Ser	Thr	Lys	Val	Tyr	Leu	Asp	Leu	Glu	Trp	Thr	Asp	Tyr	Arg	1	5	10	15
Leu	Ser	Trp	Asp	Pro	Ala	Glu	His	Asp	Gly	Ile	Asp	Ser	Leu	Arg	20	25	30	
Ile	Thr	Ala	Glu	Ser	Val	Trp	Leu	Pro	Asp	Val	Val	Leu	Leu	Asn	35	40	45	
Asn	Asn	Asp	Gly	Asn	Phe	Asp	Val	Ala	Leu	Asp	Ile	Ser	Val	Val	50	55	60	
Val	Ser	Ser	Asp	Gly	Ser	Val	Arg	Trp	Gln	Pro	Pro	Gly	Ile	Tyr	65	70	75	
Arg	Ser	Ser	Cys	Ser	Ile	Gln	Val	Thr	Tyr	Phe	Pro	Phe	Asp	Trp	80	85	90	
Gln	Asn	Cys	Thr	Met	Val	Phe	Ser	Ser	Tyr	Ser	Tyr	Asp	Ser	Ser	95	100	105	
Glu	Val	Ser	Leu	Gln	Thr	Gly	Leu	Gly	Pro	Asp	Gly	Gln	Gly	His	110	115	120	
Gln	Glu	Ile	His	Ile	His	Glu	Gly	Thr	Phe	Ile	Glu	Asn	Gly	Gln	125	130	135	
Trp	Glu	Ile	Ile	His	Lys	Pro	Ser	Arg	Leu	Ile	Gln	Pro	Pro	Gly	140	145	150	
Asp	Pro	Arg	Gly	Gly	Arg	Glu	Gly	Gln	Arg	Gln	Glu	Val	Ile	Phe	155	160	165	
Tyr	Leu	Ile	Ile	Arg	Arg	Lys	Pro	Leu	Phe	Tyr	Leu	Val	Asn	Val	170	175	180	
Ile	Ala	Pro	Cys	Ile	Leu	Ile	Thr	Leu	Leu	Ala	Ile	Phe	Val	Phe	185	190	195	
Tyr	Leu	Pro	Pro	Asp	Ala	Gly	Glu	Lys	Met	Gly	Leu	Ser	Ile	Phe	200	205	210	
Ala	Leu	Leu	Thr	Leu	Thr	Val	Phe	Leu	Leu	Leu	Leu	Ala	Asp	Lys	215	220	225	
Val	Pro	Glu	Thr	Ser	Leu	Ser	Val	Pro	Ile	Ile	Ile	Lys	Tyr	Leu	230	235	240	
Met	Phe	Thr	Met	Val	Leu	Val	Thr	Phe	Ser	Val	Ile	Leu	Ser	Val	245	250	255	
Val	Val	Leu	Asn	Leu	His	His	Arg	Ser	Pro	His	Thr	His	Gln	Met	260	265	270	
Pro	Leu	Trp	Val	Arg	Gln	Ile	Phe	Ile	His	Lys	Leu	Pro	Leu	Tyr	275	280	285	
Leu	Arg	Leu	Lys	Arg	Pro	Lys	Pro	Glu	Arg	Asp	Leu	Met	Pro	Glu	290	295	300	
Leu	Arg	Glu	Val	Val	Ser	Ser	Ile	Ser	Tyr	Ile	Ala	Arg	Gln	Leu	305	310	315	
Gln	Glu	Gln	Glu	Asp	His	Asp	Ala	Leu	Lys	Glu	Asp	Trp	Gln	Phe	320	325	330	
Val	Ala	Met	Val	Val	Asp	Arg	Leu	Phe	Leu	Trp	Thr	Phe	Ile	Ile	335	340	345	
Phe	Thr	Ser	Val	Gly	Thr	Leu	Val	Ile	Phe	Leu	Asp	Ala	Thr	Tyr	350	355	360	
His	Leu	Pro	Pro	Pro	Asp	Pro	Phe	Pro							365			

<210> 8

<211> 303

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7509256CD1

<400> 8

```

Met Lys Phe Leu Leu Thr Thr Ala Phe Leu Ile Leu Ile Ser Leu
 1          5          10          15
Trp Val Glu Glu Ala Tyr Ser Lys Glu Lys Ser Ser Lys Lys Gly
          20          25          30
Lys Gly Lys Lys Lys Gln Tyr Leu Cys Pro Ser Gln Gln Ser Ala
          35          40          45
Glu Asp Leu Ala Arg Val Pro Ala Asn Ser Thr Ser Asn Ile Leu
          50          55          60
Asn Arg Leu Leu Val Ser Tyr Asp Pro Arg Ile Arg Pro Asn Phe
          65          70          75
Lys Gly Ile Pro Val Asp Val Val Val Asn Ile Phe Ile Asn Ser
          80          85          90
Phe Gly Ser Ile Gln Glu Thr Thr Met Asp Tyr Arg Val Asn Ile
          95          100          105
Phe Leu Arg Gln Lys Trp Asn Asp Pro Arg Leu Lys Leu Pro Ser
          110          115          120
Asp Phe Arg Gly Ser Asp Ala Leu Thr Val Asp Pro Thr Met Tyr
          125          130          135
Lys Cys Leu Trp Lys Pro Asp Leu Phe Phe Ala Asn Glu Lys Ser
          140          145          150
Ala Asn Phe His Asp Val Thr Gln Glu Asn Ile Leu Leu Phe Ile
          155          160          165
Phe Arg Asp Gly Asp Val Leu Val Ser Met Arg Leu Ser Ile Thr
          170          175          180
Leu Ser Cys Pro Leu Asp Leu Thr Leu Phe Pro Met Asp Thr Gln
          185          190          195
Arg Cys Lys Met Gln Leu Glu Ser Phe Gly Tyr Thr Thr Asp Asp
          200          205          210
Leu Arg Phe Ile Trp Gln Ser Gly Asp Pro Val Gln Leu Glu Lys
          215          220          225
Ile Ala Leu Pro Gln Phe Asp Ile Lys Lys Glu Asp Ile Glu Tyr
          230          235          240
Gly Asn Cys Thr Lys Tyr Tyr Lys Gly Thr Gly Tyr Tyr Thr Cys
          245          250          255
Val Glu Val Ile Phe Thr Leu Arg Arg Gln Val Gly Phe Tyr Met
          260          265          270
Met Gly Val Tyr Ala Pro Thr Leu Leu Ile Val Val Leu Ser Trp
          275          280          285
Leu Ser Phe Trp Ile Asn Pro Asp Ala Ser Ala Ala Arg Val Pro
          290          295          300
Leu Gly Trp

```

<210> 9

<211> 370

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7509395CD1

<400> 9

```

Met Glu Pro Trp Pro Leu Leu Leu Leu Phe Ser Leu Cys Ser Ala
 1          5          10          15
Gly Leu Val Leu Gly Ser Glu His Glu Thr Arg Leu Val Ala Lys
          20          25          30
Leu Phe Lys Asp Tyr Ser Ser Val Val Arg Pro Val Glu Asp His
          35          40          45
Arg Gln Val Val Glu Val Thr Val Gly Leu Gln Leu Ile Gln Leu
          50          55          60
Ile Asn Val Asp Glu Val Asn Gln Ile Val Thr Thr Asn Asn Cys
          65          70          75
Ser Met Lys Leu Gly Thr Trp Thr Tyr Asp Gly Ser Val Val Ala
          80          85          90
Ile Asn Pro Glu Ser Asp Gln Pro Asp Leu Ser Asn Phe Met Glu
          95          100          105
Ser Gly Glu Trp Val Ile Lys Glu Ser Arg Gly Trp Lys His Ser
          110          115          120
Val Thr Tyr Ser Cys Cys Pro Asp Thr Pro Tyr Leu Asp Ile Thr
          125          130          135
Tyr His Phe Val Met Gln Arg Leu Pro Leu Tyr Phe Ile Val Asn
          140          145          150
Val Ile Ile Pro Cys Leu Leu Phe Ser Phe Leu Thr Gly Leu Val
          155          160          165
Phe Tyr Leu Pro Thr Asp Ser Gly Glu Lys Met Thr Leu Ser Ile
          170          175          180
Ser Val Leu Leu Ser Leu Thr Val Phe Leu Leu Val Ile Val Glu
          185          190          195
Leu Ile Pro Ser Thr Ser Ser Ala Val Pro Leu Ile Gly Lys Tyr
          200          205          210
Met Leu Phe Thr Met Val Phe Val Ile Ala Ser Ile Ile Ile Thr
          215          220          225
Val Ile Val Ile Asn Thr His His Arg Ser Pro Ser Thr His Val
          230          235          240
Met Pro Asn Trp Val Arg Lys Val Phe Ile Asp Thr Ile Pro Asn
          245          250          255
Ile Met Phe Phe Ser Thr Met Lys Arg Pro Ser Arg Glu Lys Gln
          260          265          270
Asp Lys Lys Ile Phe Thr Glu Asp Ile Asp Ile Ser Asp Ile Ser
          275          280          285
Gly Lys Pro Gly Pro Pro Pro Met Gly Phe His Ser Pro Leu Ile
          290          295          300
Lys His Pro Glu Val Lys Ser Ala Ile Glu Gly Ile Lys Tyr Ile
          305          310          315
Ala Glu Thr Met Lys Ser Asp Gln Glu Ser Asn Asn Ala Ala Ala
          320          325          330
Glu Trp Lys Tyr Val Ala Met Val Met Asp His Ile Leu Leu Gly
          335          340          345
Val Phe Met Leu Val Cys Ile Ile Gly Thr Leu Ala Val Phe Ala
          350          355          360
Gly Arg Leu Ile Glu Leu Asn Gln Gln Gly
          365          370

```

<210> 10

<211> 283

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7503287CD1

<400> 10

```

Met Glu Leu Lys Ala Glu Glu Glu Glu Val Gly Gly Val Gln Pro
 1          5          10          15
Val Ser Ile Gln Ala Phe Ala Ser Ser Ser Thr Leu His Gly Leu
          20          25          30
Ala His Ile Phe Ser Tyr Glu Arg Leu Ser Leu Lys Arg Ala Leu
          35          40          45
Trp Ala Leu Cys Phe Leu Gly Ser Leu Ala Val Leu Leu Cys Val
          50          55          60
Cys Thr Glu Arg Val Gln Tyr Tyr Phe His Tyr His His Val Thr
          65          70          75
Lys Leu Asp Glu Val Ala Ala Ser Gln Leu Thr Phe Pro Ala Val
          80          85          90
Thr Leu Cys Asn Leu Asn Glu Phe Arg Phe Ser Gln Val Ser Lys
          95          100          105
Asn Asp Leu Tyr His Ala Gly Glu Leu Leu Ala Leu Leu Asn Asn
          110          115          120
Arg Tyr Glu Ile Pro Asp Thr Gln Met Ala Asp Glu Lys Gln Leu
          125          130          135
Glu Ile Leu Gln Asp Lys Ala Asn Phe Arg Ser Phe Lys Pro Lys
          140          145          150
Pro Phe Asn Met Arg Glu Phe Tyr Asp Arg Ala Gly His Asp Ile
          155          160          165
Arg Asp Met Leu Leu Ser Cys His Phe Arg Gly Glu Val Cys Ser
          170          175          180
Ala Glu Asp Phe Lys Val Val Phe Thr Arg Tyr Gly Lys Cys Tyr
          185          190          195
Thr Phe Asn Ser Gly Arg Asp Gly Arg Pro Arg Leu Lys Thr Met
          200          205          210
Lys Gly Gly Thr Gly Asn Gly Leu Glu Ile Met Leu Asp Ile Gln
          215          220          225
Gln Asp Glu Tyr Leu Pro Val Trp Gly Glu Thr Asp Glu Thr Ser
          230          235          240
Phe Glu Ala Gly Ile Lys Val Gln Ile Phe Pro Leu Val Cys Gly
          245          250          255
Lys Glu Gly Val Leu Thr Ile Glu Ser Ser Leu Cys Leu Tyr Pro
          260          265          270
Ile Leu Phe Thr Phe Asn Lys Thr Asn Leu Lys Lys Asn
          275          280

```

<210> 11

<211> 90

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7503320CD1

<400> 11

```

Met Arg Cys Ser Pro Gly Gly Val Trp Leu Ala Leu Ala Ala Ser
 1          5          10          15

```


Leu	Leu	His	Val	Ser	Leu	Gln	Gly	Glu	Phe	Gln	Arg	Lys	Leu	Tyr
				20					25					30
Lys	Glu	Leu	Val	Lys	Asn	Tyr	Asn	Pro	Leu	Glu	Arg	Pro	Val	Ala
				35					40					45
Asn	Asp	Ser	Gln	Pro	Leu	Thr	Val	Tyr	Phe	Ser	Leu	Ser	Leu	Leu
				50					55					60
Gln	Ile	Met	Asp	Val	Asp	Glu	Lys	Asn	Gln	Val	Leu	Thr	Thr	Thr
				65					70					75
Thr	Pro	Thr	Gly	Ala	Arg	Cys	Pro	Ser	Gly	Pro	Glu	Ser	Ser	Phe
				80					85					90

<210> 12

<211> 549

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7503335CD1

<400> 12

Met	Pro	Ala	Cys	Cys	Ser	Cys	Ser	Asp	Val	Phe	Gln	Tyr	Glu	Thr
1				5					10					15
Asn	Lys	Val	Thr	Arg	Ile	Gln	Ser	Met	Asn	Tyr	Gly	Thr	Ile	Lys
				20					25					30
Trp	Phe	Phe	His	Val	Ile	Ile	Phe	Ser	Tyr	Val	Cys	Phe	Ala	Leu
				35					40					45
Val	Ser	Asp	Lys	Leu	Tyr	Gln	Arg	Lys	Glu	Pro	Val	Ile	Ser	Ser
				50					55					60
Val	His	Thr	Lys	Val	Lys	Gly	Ile	Ala	Glu	Val	Lys	Glu	Glu	Ile
				65					70					75
Val	Glu	Asn	Gly	Val	Lys	Lys	Leu	Val	His	Ser	Val	Phe	Asp	Thr
				80					85					90
Ala	Asp	Tyr	Thr	Phe	Pro	Leu	Gln	Gly	Asn	Ser	Phe	Phe	Val	Met
				95					100					105
Thr	Asn	Phe	Leu	Lys	Thr	Glu	Gly	Gln	Glu	Gln	Arg	Leu	Cys	Pro
				110					115					120
Glu	Tyr	Pro	Thr	Arg	Arg	Thr	Leu	Cys	Ser	Ser	Asp	Arg	Gly	Cys
				125					130					135
Lys	Lys	Gly	Trp	Met	Asp	Pro	Gln	Ser	Lys	Gly	Ile	Gln	Thr	Gly
				140					145					150
Arg	Cys	Val	Val	His	Glu	Gly	Asn	Gln	Lys	Thr	Cys	Glu	Val	Ser
				155					160					165
Ala	Trp	Cys	Pro	Ile	Glu	Ala	Val	Glu	Glu	Ala	Pro	Arg	Pro	Ala
				170					175					180
Leu	Leu	Asn	Ser	Ala	Glu	Asn	Phe	Thr	Val	Leu	Ile	Lys	Asn	Asn
				185					190					195
Ile	Asp	Phe	Pro	Gly	His	Asn	Tyr	Thr	Thr	Arg	Asn	Ile	Leu	Pro
				200					205					210
Gly	Leu	Asn	Ile	Thr	Cys	Thr	Phe	His	Lys	Thr	Gln	Asn	Pro	Gln
				215					220					225
Cys	Pro	Ile	Phe	Arg	Leu	Gly	Asp	Ile	Phe	Arg	Glu	Gln	Ala	Ile
				230					235					240
Ile	Phe	Gln	Met	Trp	Gln	Phe	Arg	Tyr	Ala	Lys	Tyr	Tyr	Lys	Glu
				245					250					255

```

Asn Asn Val Glu Lys Arg Thr Leu Ile Lys Val Phe Gly Ile Arg
260                               265                               270
Phe Asp Ile Leu Val Phe Gly Thr Gly Gly Lys Phe Asp Ile Ile
275                               280                               285
Gln Leu Val Val Tyr Ile Gly Ser Thr Leu Ser Tyr Phe Gly Leu
290                               295                               300
Ala Ala Val Phe Ile Asp Phe Leu Ile Asp Thr Tyr Ser Ser Asn
305                               310                               315
Cys Cys Arg Ser His Ile Tyr Pro Trp Cys Lys Cys Cys Gln Pro
320                               325                               330
Cys Val Val Asn Glu Tyr Tyr Tyr Arg Lys Lys Cys Glu Ser Ile
335                               340                               345
Val Glu Pro Lys Pro Thr Leu Lys Tyr Val Ser Phe Val Asp Glu
350                               355                               360
Ser His Ile Arg Met Val Asn Gln Gln Leu Leu Gly Arg Ser Leu
365                               370                               375
Gln Asp Val Lys Gly Gln Glu Val Pro Arg Pro Ala Met Asp Phe
380                               385                               390
Thr Asp Leu Ser Arg Leu Pro Leu Ala Leu His Asp Thr Pro Pro
395                               400                               405
Ile Pro Gly Gln Pro Glu Glu Ile Gln Leu Leu Arg Lys Glu Ala
410                               415                               420
Thr Pro Arg Ser Arg Asp Ser Pro Val Trp Cys Gln Cys Gly Ser
425                               430                               435
Cys Leu Pro Ser Gln Leu Pro Glu Ser His Arg Cys Leu Glu Glu
440                               445                               450
Leu Cys Cys Arg Lys Lys Pro Gly Ala Cys Ile Thr Thr Ser Glu
455                               460                               465
Leu Phe Arg Lys Leu Val Leu Ser Arg His Val Leu Gln Phe Leu
470                               475                               480
Leu Leu Tyr Gln Glu Pro Leu Leu Ala Leu Asp Val Asp Ser Thr
485                               490                               495
Asn Ser Arg Leu Arg His Cys Ala Tyr Arg Cys Tyr Ala Thr Trp
500                               505                               510
Arg Phe Gly Ser Gln Asp Met Ala Asp Phe Ala Ile Leu Pro Ser
515                               520                               525
Cys Cys Arg Trp Arg Ile Arg Lys Glu Phe Pro Lys Ser Glu Gly
530                               535                               540
Gln Tyr Ser Gly Phe Lys Ser Pro Tyr
545

```

<210> 13

<211> 246

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7503952CD1

<400> 13

```

Met Leu Ser Ser Val Met Ala Pro Leu Trp Ala Cys Ile Leu Val
1           5           10           15
Ala Ala Gly Ile Leu Ala Thr Asp Thr His His Pro Gln Asp Ser
20           25           30
Ala Leu Tyr His Leu Ser Lys Gln Leu Leu Gln Lys Tyr His Lys

```

```

          35          40          45
Glu Val Arg Pro Val Tyr Asn Trp Thr Lys Ala Thr Thr Val Tyr
          50          55          60
Leu Asp Leu Phe Val His Ala Ile Leu Asp Val Asp Ala Glu Asn
          65          70          75
Gln Ile Leu Lys Thr Ser Val Trp Tyr Gln Glu Val Trp Asn Asp
          80          85          90
Glu Phe Leu Ser Trp Asn Ser Ser Met Phe Asp Glu Ile Arg Glu
          95         100         105
Ile Ser Leu Pro Leu Ser Ala Ile Trp Ala Pro Asp Ile Ile Ile
         110         115         120
Asn Glu Phe Val Asp Ile Glu Arg Tyr Pro Asp Leu Pro Tyr Val
         125         130         135
Tyr Val Asn Ser Ser Gly Thr Ile Glu Asn Tyr Lys Pro Ile Gln
         140         145         150
Val Val Ser Ala Cys Ser Leu Glu Thr Tyr Ala Phe Pro Phe Asp
         155         160         165
Val Gln Asn Cys Ser Leu Thr Phe Lys Ser Ile Leu His Thr Val
         170         175         180
Glu Asp Val Asp Leu Ala Phe Leu Arg Ser Pro Glu Asp Ile Gln
         185         190         195
His Asp Lys Lys Ala Phe Leu Asn Asp Ser Glu Trp Glu Leu Leu
         200         205         210
Ser Val Ser Ser Thr Tyr Ser Ile Leu Gln Ser Ser Ala Gly Gly
         215         220         225
Phe Ala Gln Ile Gln Phe Asn Gly Thr Ser Ser Pro Ser Ala Trp
         230         235         240
Pro Ser Trp Phe Ser Ala
         245

```

<210> 14

<211> 273

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7504530CD1

<400> 14

```

Met Val Gln Ala Ser Gly His Arg Arg Ser Thr Arg Gly Ser Lys
  1          5          10          15
Met Val Ser Trp Ser Val Ile Ala Lys Ile Gln Glu Ile Leu Gln
         20          25          30
Arg Lys Met Val Arg Glu Phe Leu Ala Glu Phe Met Ser Thr Tyr
         35          40          45
Val Met Met Val Phe Gly Leu Gly Ser Val Ala His Met Val Leu
         50          55          60
Asn Lys Lys Tyr Gly Ser Tyr Leu Gly Val Asn Leu Gly Phe Gly
         65          70          75
Phe Gly Val Thr Met Gly Val His Val Ala Gly Arg Ile Ser Gly
         80          85          90
Ala His Met Asn Ala Ala Val Thr Phe Ala Asn Cys Ala Leu Gly
         95         100         105
Arg Val Pro Trp Arg Lys Phe Pro Val Tyr Val Leu Gly Gln Phe
        110        115        120

```

```

Leu Gly Ser Phe Leu Ala Ala Ala Thr Ile Tyr Ser Leu Phe Tyr
125 130 135
Thr Ala Ile Leu His Phe Ser Gly Gly Gln Leu Met Val Thr Gly
140 145 150
Pro Val Ala Thr Ala Gly Ile Phe Ala Thr Tyr Leu Pro Asp His
155 160 165
Met Thr Leu Trp Arg Gly Phe Leu Asn Glu Ala Trp Leu Thr Gly
170 175 180
Met Leu Gln Leu Cys Leu Phe Ala Ile Thr Asp Gln Glu Asn Asn
185 190 195
Pro Ala Leu Pro Gly Thr Glu Ala Leu Val Ile Gly Ile Leu Val
200 205 210
Val Ile Ile Gly Val Ser Leu Gly Met Asn Thr Gly Tyr Ala Ile
215 220 225
Asn Pro Ser Arg Asp Leu Pro Pro Arg Ile Phe Thr Phe Ile Ala
230 235 240
Gly Trp Gly Lys Gln Val Phe Arg Trp His His Leu Pro Gly Leu
245 250 255
His Trp Leu His His Pro Thr Gly Ala Pro Glu Ile Gly Gly Phe
260 265 270
Cys Gly Val

```

<210> 15

<211> 245

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7509303CD1

<400> 15

```

Met Glu Gly Asn Lys Leu Glu Glu Gln Asp Ser Ser Pro Pro Gln
1 5 10 15
Ser Thr Pro Gly Leu Met Lys Gly Asn Lys Arg Glu Glu Gln Gly
20 25 30
Leu Gly Pro Glu Pro Ala Ala Pro Gln Gln Pro Thr Ala Glu Glu
35 40 45
Glu Ala Leu Ile Glu Phe His Arg Ser Tyr Arg Glu Leu Phe Glu
50 55 60
Phe Phe Cys Asn Asn Thr Thr Ile His Gly Ala Ile Arg Leu Val
65 70 75
Cys Ser Gln His Asn Arg Met Lys Thr Ala Phe Trp Ala Val Leu
80 85 90
Trp Leu Cys Thr Phe Gly Met Met Tyr Trp Gln Phe Gly Leu Leu
95 100 105
Phe Gly Glu Tyr Phe Ser Tyr Pro Val Ser Leu Asn Ile Asn Leu
110 115 120
Asn Ser Asp Lys Leu Val Phe Pro Ala Val Thr Ile Cys Thr Leu
125 130 135
Asn Pro Tyr Arg Tyr Pro Glu Ile Lys Glu Glu Leu Glu Glu Leu
140 145 150
Asp Arg Ile Thr Glu Gln Thr Leu Phe Asp Leu Tyr Lys Tyr Ser
155 160 165
Ser Phe Thr Thr Leu Val Ala Gly Ser Arg Ser Arg Arg Asp Leu

```

	170		175		180
Arg Gly Thr Leu	Pro His Pro Leu Gln	Arg Leu Arg Val Pro	Pro		
	185		190		195
Pro Pro His Gly	Ala Arg Arg Ala Arg	Ser Val Ala Ser Ser	Leu		
	200		205		210
Arg Asp Asn Asn	Pro Gln Val Asp Trp	Lys Asp Trp Lys Ile	Gly		
	215		220		225
Phe Gln Leu Glu	Leu Leu Ser Leu Pro	Pro Pro Asp Val Trp	Lys		
	230		235		240
Leu Leu Tyr Phe	Gln				
	245				

<210> 16

<211> 364

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7509910CD1

<400> 16

Met Pro Ala Cys Cys	Ser Cys Ser Asp Val	Phe Gln Tyr Glu Thr
1	5	10 15
Asn Lys Val Thr Arg	Ile Gln Ser Met Asn	Tyr Gly Thr Ile Lys
	20	25 30
Trp Phe Phe His Val	Ile Ile Phe Ser Tyr	Val Cys Phe Ala Leu
	35	40 45
Val Ser Asp Lys Leu	Tyr Gln Arg Lys Glu	Pro Val Ile Ser Ser
	50	55 60
Val His Thr Lys Val	Lys Gly Ile Ala Glu	Val Lys Glu Glu Ile
	65	70 75
Val Glu Asn Gly Val	Lys Lys Leu Val His	Ser Val Phe Asp Thr
	80	85 90
Ala Asp Tyr Thr Phe	Pro Leu Gln Gly Asn	Ser Phe Phe Val Met
	95	100 105
Thr Asn Phe Leu Lys	Thr Glu Gly Gln Glu	Gln Arg Leu Cys Pro
	110	115 120
Glu Tyr Pro Thr Arg	Arg Thr Leu Cys Ser	Ser Asp Arg Gly Cys
	125	130 135
Lys Lys Gly Trp Met	Asp Pro Gln Ser Lys	Gly Ile Gln Thr Gly
	140	145 150
Arg Cys Val Val His	Glu Gly Asn Gln Lys	Thr Cys Glu Val Ser
	155	160 165
Ala Trp Cys Pro Ile	Glu Ala Val Glu Glu	Ala Pro Arg Pro Ala
	170	175 180
Leu Leu Asn Ser Ala	Glu Asn Phe Thr Val	Leu Ile Lys Asn Asn
	185	190 195
Ile Asp Phe Pro Gly	His Asn Tyr Thr Thr	Arg Asn Ile Leu Pro
	200	205 210
Gly Leu Asn Ile Thr	Cys Thr Phe His Lys	Thr Gln Asn Pro Gln
	215	220 225
Cys Pro Ile Phe Arg	Leu Gly Asp Ile Phe	Arg Glu Thr Gly Asp
	230	235 240
Asn Phe Ser Asp Val	Ala Ile Gln Gly Gly	Ile Met Gly Ile Glu
	245	250 255

```

Ile Tyr Trp Asp Cys Asn Leu Asp Arg Trp Phe His His Cys Arg
      260                      265                      270
Pro Lys Tyr Ser Phe Arg Arg Leu Asp Asp Lys Thr Thr Asn Val
      275                      280                      285
Ser Leu Tyr Pro Gly Tyr Asn Phe Arg Tyr Ala Lys Tyr Tyr Lys
      290                      295                      300
Glu Asn Asn Val Glu Lys Arg Thr Leu Ile Lys Val Phe Gly Ile
      305                      310                      315
Arg Phe Asp Ile Leu Val Phe Gly Thr Gly Gly Lys Phe Asp Ile
      320                      325                      330
Ile Gln Leu Val Val Tyr Ile Gly Ser Thr Leu Ser Tyr Phe Gly
      335                      340                      345
Leu Val Arg Asp Ser Leu Phe His Ala Leu Gly Lys Trp Phe Gly
      350                      355                      360
Glu Gly Ser Asp

```

```

<210> 17
<211> 1623
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<223> Incyte ID No: 7509982CD1

```

```

<400> 17
Met Asn Met Lys Gln Lys Ser Val Tyr Gln Gln Thr Lys Ala Leu
  1                      5                      10                      15
Leu Cys Lys Asn Phe Leu Lys Lys Trp Arg Met Lys Arg Glu Ser
      20                      25                      30
Leu Leu Glu Trp Gly Leu Ser Ile Leu Leu Gly Leu Cys Ile Ala
      35                      40                      45
Leu Phe Ser Ser Ser Met Arg Asn Val Gln Phe Pro Gly Met Ala
      50                      55                      60
Pro Gln Asn Leu Gly Arg Val Asp Lys Phe Asn Ser Ser Ser Leu
      65                      70                      75
Met Val Val Tyr Thr Pro Ile Ser Asn Leu Thr Gln Gln Ile Met
      80                      85                      90
Asn Lys Thr Ala Leu Ala Pro Leu Leu Lys Gly Thr Ser Val Ile
      95                      100                     105
Gly Ala Pro Asn Lys Thr His Met Asp Glu Ile Leu Leu Glu Asn
     110                      115                     120
Leu Pro Tyr Ala Met Gly Ile Ile Phe Asn Glu Thr Phe Ser Tyr
     125                      130                     135
Lys Leu Ile Phe Phe Gln Gly Tyr Asn Ser Pro Leu Trp Lys Glu
     140                      145                     150
Asp Phe Ser Ala His Cys Trp Asp Gly Tyr Gly Glu Phe Ser Cys
     155                      160                     165
Thr Leu Thr Lys Tyr Trp Asn Arg Gly Phe Val Ala Leu Gln Thr
     170                      175                     180
Ala Ile Asn Thr Ala Ile Ile Glu Ile Thr Thr Asn His Pro Val
     185                      190                     195
Met Glu Glu Leu Met Ser Val Thr Ala Ile Thr Met Lys Thr Leu
     200                      205                     210
Pro Phe Ile Thr Lys Asn Leu Leu His Asn Glu Met Phe Ile Leu

```

	215		220		225
Phe Phe Leu Leu	His Phe Ser Pro Leu	Val Tyr Phe Ile Ser	Leu		
	230		235		240
Asn Val Thr Lys	Glu Arg Lys Lys Ser	Lys Asn Leu Met Lys	Met		
	245		250		255
Met Gly Leu Gln	Asp Ser Ala Phe Trp	Leu Ser Trp Gly Leu	Ile		
	260		265		270
Tyr Ala Gly Phe	Ile Phe Ile Ile Ser	Ile Phe Ile Thr Ile	Ile		
	275		280		285
Ile Thr Phe Thr	Gln Ile Ile Val Met	Thr Gly Phe Met Val	Ile		
	290		295		300
Phe Ile Pro Phe	Phe Leu Tyr Gly Leu	Ser Leu Val Ala Leu	Val		
	305		310		315
Phe Leu Leu Ser	Val Leu Leu Lys Lys	Ala Val Leu Thr Asn	Leu		
	320		325		330
Val Val Phe Leu	Leu Thr Leu Phe Trp	Gly Cys Leu Gly Phe	Thr		
	335		340		345
Val Phe Tyr Glu	Gln Leu Pro Ser Ser	Leu Glu Trp Ile Leu	Asn		
	350		355		360
Ile Cys Ser Pro	Phe Ala Phe Thr Thr	Gly Met Ile Gln Ile	Ile		
	365		370		375
Lys Leu Asp Tyr	Asn Leu Asn Gly Val	Ile Phe Pro Asp Pro	Ser		
	380		385		390
Gly Asp Ser Tyr	Thr Met Ile Ala Thr	Phe Ser Met Leu Leu	Leu		
	395		400		405
Asp Gly Leu Ile	Tyr Leu Leu Leu Ala	Leu Tyr Phe Asp Lys	Ile		
	410		415		420
Leu Pro Tyr Gly	Asp Glu Arg His Tyr	Ser Pro Leu Phe Phe	Leu		
	425		430		435
Asn Ser Ser Ser	Cys Phe Gln His Gln	Arg Thr Asn Ala Lys	Val		
	440		445		450
Ile Glu Lys Glu	Ile Asp Ala Glu His	Pro Ser Asp Asp Tyr	Phe		
	455		460		465
Glu Pro Val Ala	Pro Glu Phe Gln Gly	Lys Glu Ala Ile Arg	Ile		
	470		475		480
Arg Asn Val Lys	Lys Glu Tyr Lys Gly	Lys Ser Gly Lys Val	Glu		
	485		490		495
Ala Leu Lys Gly	Leu Leu Phe Asp Ile	Tyr Glu Gly Gln Ile	Thr		
	500		505		510
Ala Ile Leu Gly	His Ser Gly Ala Gly	Lys Ser Ser Leu Leu	Asn		
	515		520		525
Ile Leu Asn Gly	Leu Ser Val Pro Thr	Glu Gly Ser Val Thr	Ile		
	530		535		540
Tyr Asn Lys Asn	Leu Ser Glu Met Gln	Asp Leu Glu Glu Ile	Arg		
	545		550		555
Lys Ile Thr Gly	Val Cys Pro Gln Phe	Asn Val Gln Phe Asp	Ile		
	560		565		570
Leu Thr Val Lys	Glu Asn Leu Ser Leu	Phe Ala Lys Ile Lys	Gly		
	575		580		585
Ile His Leu Lys	Glu Val Glu Gln Glu	Val Gln Arg Ile Leu	Leu		
	590		595		600
Glu Leu Asp Met	Gln Asn Ile Gln Asp	Asn Leu Ala Lys His	Leu		
	605		610		615
Ser Glu Gly Gln	Lys Arg Lys Leu Thr	Phe Gly Ile Thr Ile	Leu		
	620		625		630
Gly Asp Pro Gln	Ile Leu Leu Leu Asp	Glu Pro Thr Thr Gly	Leu		

	635		640		645
Asp Pro Phe Ser Arg Asp Gln Val Trp Ser Leu Leu Arg Glu Arg					
	650		655		660
Arg Ala Asp His Val Ile Leu Phe Ser Thr Gln Ser Met Asp Glu					
	665		670		675
Ala Asp Ile Leu Ala Asp Arg Lys Val Ile Met Ser Asn Gly Arg					
	680		685		690
Leu Lys Cys Ala Gly Ser Ser Met Phe Leu Lys Arg Arg Trp Gly					
	695		700		705
Leu Gly Tyr His Leu Ser Leu His Arg Asn Glu Ile Cys Asn Pro					
	710		715		720
Glu Gln Ile Thr Ser Phe Ile Thr His His Ile Pro Asp Ala Lys					
	725		730		735
Leu Lys Thr Glu Asn Lys Glu Lys Leu Val Tyr Thr Leu Pro Leu					
	740		745		750
Glu Arg Thr Asn Thr Phe Pro Asp Leu Phe Ser Asp Leu Asp Lys					
	755		760		765
Cys Ser Asp Gln Gly Val Thr Gly Tyr Asp Ile Ser Met Ser Thr					
	770		775		780
Leu Asn Glu Val Phe Met Lys Leu Glu Gly Gln Ser Thr Ile Glu					
	785		790		795
Gln Gly Lys Ala Ile Cys Ile Asn Phe Glu Gln Val Glu Met Ile					
	800		805		810
Arg Asp Ser Glu Ser Leu Asn Glu Met Glu Leu Ala His Ser Ser					
	815		820		825
Phe Ser Glu Met Gln Thr Ala Val Ser Asp Met Gly Leu Trp Arg					
	830		835		840
Met Gln Val Phe Ala Met Ala Arg Leu Arg Phe Leu Lys Leu Lys					
	845		850		855
Arg Gln Thr Lys Val Leu Leu Thr Leu Leu Leu Val Phe Gly Ile					
	860		865		870
Ala Ile Phe Pro Leu Ile Val Glu Asn Ile Ile Tyr Ala Met Leu					
	875		880		885
Asn Glu Lys Ile Asp Trp Glu Phe Lys Asn Glu Leu Tyr Phe Leu					
	890		895		900
Ser Pro Gly Gln Leu Pro Gln Glu Pro Arg Thr Ser Leu Leu Ile					
	905		910		915
Ile Asn Asn Thr Glu Ser Asn Ile Glu Asp Phe Ile Lys Ser Leu					
	920		925		930
Lys His Gln Asn Ile Leu Leu Glu Val Asp Asp Phe Glu Asn Arg					
	935		940		945
Asn Gly Thr Asp Gly Leu Ser Tyr Asn Gly Ala Ile Ile Val Ser					
	950		955		960
Gly Lys Gln Lys Asp Tyr Arg Phe Ser Val Val Cys Asn Thr Lys					
	965		970		975
Arg Leu His Cys Phe Pro Ile Leu Met Asn Ile Ile Ser Asn Gly					
	980		985		990
Leu Leu Gln Met Phe Asn His Thr Gln His Ile Arg Ile Glu Ser					
	995		1000		1005
Ser Pro Phe Pro Leu Ser His Ile Gly Leu Trp Thr Gly Leu Pro					
	1010		1015		1020
Asp Gly Ser Phe Phe Leu Phe Leu Val Leu Cys Ser Ile Ser Pro					
	1025		1030		1035
Tyr Ile Thr Met Gly Ser Ile Ser Asp Tyr Lys Lys Asn Ala Lys					
	1040		1045		1050
Ser Gln Leu Trp Ile Ser Gly Leu Tyr Thr Ser Ala Tyr Trp Cys					

1055	1060	1065
Gly Gln Ala Leu Val Asp Val Ser Phe Phe Ile Leu Ile Leu Leu		
1070	1075	1080
Leu Met Tyr Leu Ile Phe Tyr Ile Glu Asn Met Gln Tyr Leu Leu		
1085	1090	1095
Ile Thr Ser Gln Ile Val Phe Ala Leu Val Ile Val Thr Pro Gly		
1100	1105	1110
Tyr Ala Ala Ser Leu Val Phe Phe Ile Tyr Met Ile Ser Phe Ile		
1115	1120	1125
Phe Arg Lys Arg Arg Lys Asn Ser Gly Leu Trp Ser Phe Tyr Phe		
1130	1135	1140
Phe Phe Ala Ser Thr Ile Met Phe Ser Ile Thr Leu Ile Asn His		
1145	1150	1155
Phe Asp Leu Ser Ile Leu Ile Thr Thr Met Val Leu Val Pro Ser		
1160	1165	1170
Tyr Thr Leu Leu Gly Phe Lys Thr Phe Leu Glu Val Arg Asp Gln		
1175	1180	1185
Glu His Tyr Arg Glu Phe Pro Glu Ala Asn Phe Glu Leu Ser Ala		
1190	1195	1200
Thr Asp Phe Leu Val Cys Phe Ile Pro Tyr Phe Gln Thr Leu Leu		
1205	1210	1215
Phe Val Phe Val Leu Arg Tyr Met Glu Leu Lys Cys Gly Lys Lys		
1220	1225	1230
Arg Met Arg Lys Asp Pro Val Phe Arg Ile Ser Pro Gln Ser Arg		
1235	1240	1245
Asp Ala Lys Pro Asn Pro Glu Glu Pro Ile Asp Glu Asp Glu Asp		
1250	1255	1260
Ile Gln Thr Glu Arg Ile Arg Thr Val Thr Ala Leu Thr Thr Ser		
1265	1270	1275
Ile Leu Asp Glu Lys Pro Val Ile Ile Ala Ser Cys Leu His Lys		
1280	1285	1290
Glu Tyr Ala Gly Gln Lys Lys Ser Cys Phe Ser Lys Arg Lys Lys		
1295	1300	1305
Lys Ile Ala Ala Arg Asn Ile Ser Phe Cys Val Gln Glu Gly Glu		
1310	1315	1320
Ile Leu Gly Leu Leu Gly Pro Ser Gly Ala Gly Lys Ser Ser Ser		
1325	1330	1335
Ile Arg Met Ile Ser Gly Ile Thr Lys Pro Thr Ala Gly Glu Val		
1340	1345	1350
Glu Leu Lys Gly Cys Ser Ser Val Leu Gly His Leu Gly Tyr Cys		
1355	1360	1365
Pro Gln Glu Asn Val Leu Trp Pro Met Leu Thr Leu Arg Glu His		
1370	1375	1380
Leu Glu Val Tyr Ala Ala Val Lys Gly Leu Arg Glu Ala Asp Ala		
1385	1390	1395
Arg Leu Ala Ile Ala Arg Leu Val Ser Ala Phe Lys Leu His Glu		
1400	1405	1410
Gln Leu Asn Val Pro Val Gln Lys Leu Thr Ala Gly Ile Thr Arg		
1415	1420	1425
Lys Leu Cys Phe Val Leu Ser Leu Leu Gly Asn Ser Pro Val Leu		
1430	1435	1440
Leu Leu Asp Glu Pro Ser Thr Gly Ile Asp Pro Thr Gly Gln Gln		
1445	1450	1455
Gln Met Trp Gln Ala Ile Gln Ala Val Val Lys Asn Thr Glu Arg		
1460	1465	1470
Gly Val Leu Leu Thr Thr His Asn Leu Ala Glu Ala Glu Ala Leu		

	1475	1480	1485
Cys Asp Arg Val Ala Ile Met Val Ser Gly Arg Leu Arg Cys Ile			
	1490	1495	1500
Gly Ser Ile Gln His Leu Lys Asn Lys Leu Gly Lys Asp Tyr Ile			
	1505	1510	1515
Leu Glu Leu Lys Val Lys Glu Thr Ser Gln Val Thr Leu Val His			
	1520	1525	1530
Thr Glu Ile Leu Lys Leu Phe Pro Gln Ala Ala Gly Gln Glu Arg			
	1535	1540	1545
Tyr Ser Ser Leu Leu Thr Tyr Lys Leu Pro Val Ala Asp Val Tyr			
	1550	1555	1560
Pro Leu Ser Gln Thr Phe His Lys Leu Glu Ala Val Lys His Asn			
	1565	1570	1575
Phe Asn Leu Glu Glu Tyr Ser Leu Ser Gln Cys Thr Leu Glu Lys			
	1580	1585	1590
Val Phe Leu Glu Leu Ser Lys Glu Gln Glu Val Gly Asn Phe Asp			
	1595	1600	1605
Glu Glu Ile Asp Thr Thr Met Arg Trp Lys Leu Leu Pro His Ser			
	1610	1615	1620
Asp Glu Pro			

<210> 18

<211> 611

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7510082CD1

<400> 18

Met Pro Ala Pro Arg Ala Arg Glu Gln Pro Arg Val Pro Gly Glu		
1	5	10
Arg Gln Pro Leu Leu Pro Arg Gly Ala Arg Gly Pro Arg Arg Trp		
	20	25
Arg Arg Ala Ala Gly Ala Ala Val Leu Leu Val Glu Met Leu Glu		
	35	40
Arg Ala Ala Phe Phe Gly Val Thr Ala Asn Leu Val Leu Tyr Leu		
	50	55
Asn Ser Thr Asn Phe Asn Trp Thr Gly Glu Gln Ala Thr Arg Ala		
	65	70
Ala Leu Val Phe Leu Gly Ala Ser Tyr Leu Leu Ala Pro Val Gly		
	80	85
Gly Trp Leu Ala Asp Val Tyr Leu Gly Arg Tyr Arg Ala Val Ala		
	95	100
Leu Ser Leu Leu Leu Tyr Leu Ala Ala Ser Gly Leu Leu Pro Ala		
	110	115
Thr Ala Phe Pro Asp Gly Arg Ser Ser Phe Cys Gly Glu Met Pro		
	125	130
Ala Ser Pro Leu Gly Pro Ala Cys Pro Ser Ala Gly Cys Pro Arg		
	140	145
Ser Ser Pro Ser Pro Tyr Cys Ala Pro Val Leu Tyr Ala Gly Leu		
	155	160
Leu Leu Leu Gly Leu Ala Ala Ser Ser Val Arg Ser Asn Leu Thr		
	170	175
		180

Ser Phe Gly Ala Asp Gln Val Met Asp Leu Gly Arg Asp Ala Thr	185	190	195
Arg Arg Phe Phe Asn Trp Phe Tyr Trp Ser Ile Asn Leu Gly Ala	200	205	210
Val Leu Ser Leu Leu Val Val Ala Phe Ile Gln Gln Asn Ile Ser	215	220	225
Phe Leu Leu Gly Tyr Ser Ile Pro Val Gly Cys Val Gly Leu Ala	230	235	240
Phe Phe Ile Phe Leu Phe Ala Thr Pro Val Phe Ile Thr Lys Pro	245	250	255
Pro Met Gly Ser Gln Val Ser Ser Met Leu Lys Leu Ala Leu Gln	260	265	270
Asn Cys Cys Pro Gln Leu Trp Gln Arg His Ser Ala Arg Asp Arg	275	280	285
Gln Cys Ala Arg Val Leu Ala Asp Glu Arg Ser Pro Gln Pro Gly	290	295	300
Ala Ser Pro Gln Glu Asp Ile Ala Asn Phe Gln Val Leu Val Lys	305	310	315
Ile Leu Pro Val Met Val Thr Leu Val Pro Tyr Trp Met Val Tyr	320	325	330
Phe Gln Met Gln Ser Thr Tyr Val Leu Gln Gly Leu His Leu His	335	340	345
Ile Pro Asn Ile Phe Pro Ala Asn Pro Ala Asn Ile Ser Val Ala	350	355	360
Leu Arg Ala Gln Gly Ser Ser Tyr Thr Ile Pro Glu Ala Trp Leu	365	370	375
Leu Leu Ala Asn Val Val Val Val Leu Ile Leu Val Pro Leu Lys	380	385	390
Asp Arg Leu Ile Asp Pro Leu Leu Leu Arg Cys Lys Leu Leu Pro	395	400	405
Ser Ala Leu Gln Lys Met Ala Leu Gly Met Phe Phe Gly Phe Thr	410	415	420
Ser Val Ile Val Ala Gly Val Leu Glu Met Glu Arg Leu His Tyr	425	430	435
Ile His His Asn Glu Thr Val Ser Gln Gln Ile Gly Glu Val Leu	440	445	450
Tyr Asn Ala Ala Pro Leu Ser Ile Trp Trp Gln Ile Pro Gln Tyr	455	460	465
Leu Leu Ile Gly Ile Ser Glu Ile Phe Ala Ser Ile Pro Gly Leu	470	475	480
Glu Phe Ala Tyr Ser Glu Ala Pro Arg Ser Met Gln Gly Ala Ile	485	490	495
Met Gly Ile Phe Phe Cys Leu Ser Gly Val Gly Ser Leu Leu Gly	500	505	510
Ser Ser Leu Val Ala Leu Leu Ser Leu Pro Gly Gly Trp Leu His	515	520	525
Cys Pro Lys Asp Phe Gly Asn Ile Asn Asn Cys Arg Met Asp Leu	530	535	540
Tyr Phe Phe Leu Leu Ala Gly Ile Gln Ala Val Thr Ala Leu Leu	545	550	555
Phe Val Trp Ile Ala Gly Arg Tyr Glu Arg Ala Ser Gln Gly Pro	560	565	570
Ala Ser His Arg Pro Phe Gln His Gly Gln Gly Leu Asp Arg Pro	575	580	585
Tyr Pro Gly Pro Leu Val Tyr Ser Thr Gly Lys Asn Gly Ser Ser	590	595	600

Pro Ser Ser Gly Phe Leu Leu Gly Leu Phe Cys
 605 610

<210> 19
 <211> 55
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 7510367CD1

<400> 19
 Met Thr Gly Gln Gly Gln Ser Ala Ser Gly Ser Ser Ala Trp Ser
 1 5 10 15
 Thr Val Phe Arg His Val Arg Tyr Glu Asn Leu Ile Ala Gly Val
 20 25 30
 Ser Gly Gly Val Leu Ser Asn Leu Ala Leu His Pro Leu Asp Leu
 35 40 45
 Val Lys Ile Arg Phe Ala Gly Thr Ile Leu
 50 55

<210> 20
 <211> 287
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 7510413CD1

<400> 20
 Met Asp Met Ala Trp Gln Met Met Gln Leu Leu Leu Leu Ala Leu
 1 5 10 15
 Val Thr Ala Ala Gly Ser Ala Gln Pro Arg Ser Ala Arg Ala Arg
 20 25 30
 Thr Asp Leu Leu Asn Val Cys Met Asn Ala Lys His His Lys Thr
 35 40 45
 Gln Pro Ser Pro Glu Asp Glu Leu Tyr Gly Gln Val Gly Ala Pro
 50 55 60
 Gln Gly Pro Ser Pro Gly Ser Val Pro Leu Asp Asp Leu Pro Gly
 65 70 75
 Ala Glu Glu Pro Glu Tyr Gly Gly Asp Gly Cys Gly Gly Glu Arg
 80 85 90
 Leu Ser Pro Val Ser Ser Pro Pro Ser Ala Val Pro Gly Arg Arg
 95 100 105
 Met Pro Ala Ala Arg Pro Ala Pro Ala Arg Ser Cys Thr Arg Thr
 110 115 120
 Pro Pro Ala Cys Thr Thr Leu Thr Gly Ile Thr Val Val Arg Trp
 125 130 135
 Asn Pro Pro Ala Ser Ala Thr Leu Ser Arg Thr Ala Val Ser Glu
 140 145 150
 Cys Ser Pro Asn Leu Gly Pro Trp Ile Arg Gln Val Asn Gln Ser
 155 160 165
 Trp Arg Lys Glu Arg Ile Leu Asn Val Pro Leu Cys Lys Glu Asp
 170 175 180

Cys	Glu	Arg	Trp	Trp	Glu	Asp	Cys	Arg	Thr	Ser	Tyr	Thr	Cys	Lys
				185					190					195
Ser	Asn	Trp	His	Lys	Gly	Trp	Asn	Trp	Thr	Ser	Gly	Ile	Asn	Glu
				200					205					210
Cys	Pro	Ala	Gly	Ala	Leu	Cys	Ser	Thr	Phe	Glu	Ser	Tyr	Phe	Pro
				215					220					225
Thr	Pro	Ala	Ala	Leu	Cys	Glu	Gly	Leu	Trp	Ser	His	Ser	Phe	Lys
				230					235					240
Val	Ser	Asn	Tyr	Ser	Arg	Gly	Ser	Gly	Arg	Cys	Ile	Gln	Met	Trp
				245					250					255
Phe	Asp	Ser	Ala	Gln	Gly	Asn	Pro	Asn	Glu	Glu	Val	Ala	Lys	Phe
				260					265					270
Tyr	Ala	Ala	Ala	Met	Asn	Ala	Gly	Ala	Pro	Ser	Arg	Gly	Ile	Ile
				275					280					285

Asp Ser

<210> 21
 <211> 55
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 1721303CD1

<400> 21

Met	Ala	Ser	Val	Gly	Glu	Cys	Pro	Ala	Pro	Val	Pro	Val	Lys	Asp
1				5					10					15
Lys	Lys	Leu	Leu	Glu	Val	Lys	Leu	Gly	Glu	Leu	Pro	Ser	Trp	Ile
				20					25					30
Leu	Met	Arg	Asp	Phe	Ser	Pro	Ser	Gly	Ile	Phe	Gly	Ala	Phe	Gln
				35					40					45
Arg	Glu	His	Glu	Arg	Leu	Arg	Lys	Tyr	His					
				50					55					

<210> 22
 <211> 272
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 7502007CD1

<400> 22

Met	Gly	Ser	Gly	His	Cys	Leu	Arg	Ser	Thr	Arg	Gly	Ser	Lys	Met
1				5					10					15
Val	Ser	Trp	Ser	Val	Ile	Ala	Lys	Ile	Gln	Glu	Ile	Leu	Gln	Arg
				20					25					30
Lys	Met	Val	Arg	Glu	Phe	Leu	Ala	Glu	Phe	Met	Ser	Thr	Tyr	Val
				35					40					45
Met	Met	Val	Phe	Gly	Leu	Gly	Ser	Val	Ala	His	Met	Val	Leu	Asn
				50					55					60
Lys	Lys	Tyr	Gly	Ser	Tyr	Leu	Gly	Val	Asn	Leu	Gly	Phe	Gly	Phe
				65					70					75

Gly Val Thr Met Gly Val His Val Ala Gly Arg Ile Ser Gly Ala		
	80	85 90
His Met Asn Ala Ala Val Thr Phe Ala Asn Cys Ala Leu Gly Arg		
	95	100 105
Val Pro Trp Arg Lys Phe Pro Val Tyr Val Leu Gly Gln Phe Leu		
	110	115 120
Gly Ser Phe Leu Ala Ala Ala Thr Ile Tyr Ser Leu Phe Tyr Thr		
	125	130 135
Ala Ile Leu His Phe Ser Gly Gly Gln Leu Met Val Thr Gly Pro		
	140	145 150
Val Ala Thr Ala Gly Ile Phe Ala Thr Tyr Leu Pro Asp His Met		
	155	160 165
Thr Leu Trp Arg Gly Phe Leu Asn Glu Ala Trp Leu Thr Gly Met		
	170	175 180
Leu Gln Leu Cys Leu Phe Ala Ile Thr Asp Gln Glu Asn Asn Pro		
	185	190 195
Ala Leu Pro Gly Thr Glu Ala Leu Val Ile Gly Ile Leu Val Val		
	200	205 210
Ile Ile Gly Val Ser Leu Gly Met Asn Thr Gly Tyr Ala Ile Asn		
	215	220 225
Pro Ser Arg Asp Leu Pro Pro Arg Ile Phe Thr Phe Ile Ala Gly		
	230	235 240
Trp Gly Lys Gln Val Phe Arg Trp His His Leu Pro Gly Leu His		
	245	250 255
Trp Leu His His Pro Thr Gly Ala Pro Glu Ile Gly Gly Phe Cys		
	260	265 270
Gly Val		

<210> 23

<211> 188

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7506439CD1

<400> 23

Met Leu Gly Lys Leu Ala Met Leu Leu Trp Val Gln Gln Ala Leu		
1	5	10 15
Leu Ala Leu Leu Leu Pro Thr Leu Leu Ala Gln Gly Glu Ala Arg		
	20	25 30
Arg Ser Arg Asn Thr Thr Arg Pro Ala Leu Leu Arg Leu Ser Asp		
	35	40 45
Tyr Leu Leu Thr Asn Tyr Arg Lys Gly Val Arg Pro Val Arg Asp		
	50	55 60
Trp Arg Lys Pro Thr Thr Val Ser Ile Asp Val Ile Val Tyr Ala		
	65	70 75
Ile Leu Asn Val Asp Glu Lys Asn Gln Val Leu Thr Thr Tyr Ile		
	80	85 90
Trp Tyr Arg Gln Tyr Trp Thr Asp Glu Phe Leu Gln Trp Asn Pro		
	95	100 105
Glu Asp Phe Asp Asn Ile Thr Lys Leu Ser Ile Pro Thr Asp Ser		
	110	115 120
Ile Trp Val Pro Asp Ile Leu Ile Asn Glu Phe Val Asp Val Gly		

	125		130		135
Lys Ser Pro Asn Ile Pro Tyr Val Tyr Ile Arg His Gln His Leu					
	140		145		150
Phe Val Ala Leu Ala Arg Lys Gly Glu Ile Arg Gln Glu Cys Leu					
	155		160		165
His Glu Pro Gly Arg Val Gly Val Ala Gly Gly Ala Ala Leu Leu					
	170		175		180
Ser Gly Val Gln His Gly Lys Gln					
	185				

<210> 24

<211> 111

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7509243CD1

<400> 24

Met Pro Ser Ala Gly Leu Cys Ser Cys Trp Gly Gly Arg Val Leu		
1	5	10
Pro Leu Leu Leu Ala Tyr Val Cys Tyr Leu Leu Gly Ala Thr		
	20	25
Ile Phe Gln Leu Leu Glu Arg Gln Ala Glu Ala Gln Ser Arg Asp		
	35	40
Gln Phe Gln Leu Glu Lys Leu Arg Phe Leu Glu Asn Tyr Thr Cys		
	50	55
Leu Asp Gln Trp Ala Met Glu Gln Phe Val Gln Val Ile Met Glu		
	65	70
Ala Trp Val Lys Gly Val Asn Pro Lys Gly Asn Ser Thr Asn Pro		
	80	85
Ser Asn Trp Asp Phe Gly Ser Ser Phe Phe Phe Ala Gly Thr Val		
	95	100
Val Thr Thr Ile Gly His		
	110	

<210> 25

<211> 46

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7509404CD1

<400> 25

Met Lys Phe Leu Leu Thr Thr Ala Phe Leu Ile Leu Ile Ser Leu		
1	5	10
Trp Val Glu Glu Ala Tyr Ser Lys Glu Lys Ser Ser Lys Lys Gly		
	20	25
Lys Gly Lys Lys Lys Gln Tyr Leu Cys Pro Ser Glu Arg Leu Tyr		
	35	40
His		

<210> 26
 <211> 204
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 7509439CD1

<400> 26
 Met Phe Ser Arg Ala Gly Val Ala Gly Leu Ser Ala Trp Thr Leu
 1 5 10 15
 Gln Pro Gln Trp Ile Gln Val Arg Asn Met Ala Thr Leu Lys Asp
 20 25 30
 Ile Thr Arg Arg Leu Lys Ser Ile Lys Asn Ile Gln Lys Ile Thr
 35 40 45
 Lys Ser Met Lys Met Val Ala Ala Ala Lys Tyr Ala Arg Ala Glu
 50 55 60
 Arg Glu Leu Lys Pro Ala Arg Ile Tyr Gly Leu Gly Ser Leu Ala
 65 70 75
 Leu Tyr Glu Lys Ala Asp Ile Lys Gly Pro Glu Asp Lys Lys Lys
 80 85 90
 His Leu Leu Ile Gly Val Ser Ser Asp Arg Gly Leu Cys Gly Ala
 95 100 105
 Ile His Ser Ser Ile Ala Lys Gln Met Lys Ser Glu Val Ala Thr
 110 115 120
 Leu Thr Ala Ala Gly Lys Glu Val Met Leu Val Gly Ile Gly Asp
 125 130 135
 Lys Ile Arg Gly Ile Leu Tyr Ser Ser Leu Gln Val Leu Lys Glu
 140 145 150
 Arg Asn Asp Asp Ser Val Trp Asn Asn Ser Gly Asn His His His
 155 160 165
 Pro Tyr Pro Lys Asp Leu Ile His Gly Leu Ile Leu Thr Ser Phe
 170 175 180
 Trp Trp His Ser Lys Lys Trp Glu Glu Ser Pro Pro Leu Leu Glu
 185 190 195
 Met Arg Gln Ser Leu Pro Leu Asn Tyr
 200

<210> 27
 <211> 1400
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 7510202CD1

<400> 27
 Met Ser Lys Arg Arg Met Ser Val Gly Gln Gln Thr Trp Ala Leu
 1 5 10 15
 Leu Cys Lys Asn Cys Leu Lys Lys Trp Arg Met Lys Arg Gln Thr
 20 25 30
 Leu Leu Glu Trp Leu Phe Ser Phe Leu Leu Val Leu Phe Leu Tyr
 35 40 45
 Leu Phe Phe Ser Asn Leu His Gln Val His Asp Thr Pro Gln Met

	50		55		60
Ser Ser Met Asp Leu Gly Arg Val Asp Ser Phe Asn Asp Thr Asn					
	65		70		75
Tyr Val Ile Ala Phe Ala Pro Glu Ser Lys Thr Thr Gln Glu Ile					
	80		85		90
Met Asn Lys Val Ala Ser Ala Pro Phe Leu Lys Gly Arg Thr Ile					
	95		100		105
Met Gly Trp Pro Asp Glu Lys Ser Met Asp Glu Leu Asp Leu Asn					
	110		115		120
Tyr Ser Ile Asp Ala Val Arg Val Ile Phe Thr Asp Thr Phe Ser					
	125		130		135
Tyr His Leu Lys Phe Ser Trp Gly His Arg Ile Pro Met Met Lys					
	140		145		150
Glu His Arg Asp His Ser Ala His Cys Gln Ala Val Asn Glu Lys					
	155		160		165
Met Lys Cys Glu Gly Ser Glu Phe Trp Glu Lys Gly Phe Val Ala					
	170		175		180
Phe Gln Ala Ala Ile Asn Ala Ala Ile Ile Glu Ile Ala Thr Asn					
	185		190		195
His Ser Val Met Glu Gln Leu Met Ser Val Thr Gly Val His Met					
	200		205		210
Lys Ile Leu Pro Phe Val Ala Gln Gly Gly Val Ala Thr Asp Phe					
	215		220		225
Phe Ile Phe Phe Cys Ile Ile Ser Phe Ser Thr Phe Ile Tyr Tyr					
	230		235		240
Val Ser Val Asn Val Thr Gln Glu Arg Gln Tyr Ile Thr Ser Leu					
	245		250		255
Met Thr Met Met Gly Leu Arg Glu Ser Ala Phe Trp Leu Ser Trp					
	260		265		270
Gly Leu Met Tyr Ala Gly Phe Ile Leu Ile Met Ala Thr Leu Met					
	275		280		285
Ala Leu Ile Val Lys Ser Ala Gln Ile Val Val Leu Thr Gly Phe					
	290		295		300
Val Met Val Phe Thr Leu Phe Leu Leu Tyr Gly Leu Ser Leu Ile					
	305		310		315
Thr Leu Ala Phe Leu Met Ser Val Leu Ile Lys Lys Pro Phe Leu					
	320		325		330
Thr Gly Leu Val Val Phe Leu Leu Ile Val Phe Trp Gly Ile Leu					
	335		340		345
Gly Phe Pro Ala Leu Tyr Thr His Leu Pro Ala Phe Leu Glu Trp					
	350		355		360
Thr Leu Cys Leu Leu Ser Pro Phe Ala Phe Thr Val Gly Met Ala					
	365		370		375
Gln Leu Ile His Leu Asp Tyr Asp Val Asn Ser Asn Ala His Leu					
	380		385		390
Asp Ser Ser Gln Asn Pro Tyr Leu Ile Ile Ala Thr Leu Phe Met					
	395		400		405
Leu Val Phe Asp Thr Leu Leu Tyr Leu Val Leu Thr Leu Tyr Phe					
	410		415		420
Asp Lys Ile Leu Pro Ala Glu Tyr Gly His Arg Cys Ser Pro Leu					
	425		430		435
Phe Phe Leu Lys Ser Cys Phe Trp Phe Gln His Gly Arg Ala Asn					
	440		445		450
His Val Val Leu Glu Asn Glu Thr Asp Ser Asp Pro Thr Pro Asn					
	455		460		465
Asp Cys Phe Glu Pro Val Ser Pro Glu Phe Cys Gly Lys Glu Ala					

	470		475		480
Ile Arg Ile Lys	Asn Leu Lys Lys Glu Tyr Ala Gly Lys Cys Glu				
	485		490		495
Arg Val Glu Ala	Leu Lys Gly Val Val Phe Asp Ile Tyr Glu Gly				
	500		505		510
Gln Ile Thr Ala	Leu Leu Gly His Ser Gly Ala Gly Lys Thr Thr				
	515		520		525
Leu Leu Asn Ile	Leu Ser Gly Leu Ser Val Pro Thr Ser Gly Ser				
	530		535		540
Val Thr Val Tyr	Asn His Thr Leu Ser Arg Met Ala Asp Ile Glu				
	545		550		555
Asn Ile Ser Lys	Phe Thr Gly Phe Cys Pro Gln Ser Asn Val Gln				
	560		565		570
Phe Gly Phe Leu	Thr Val Lys Glu Asn Leu Arg Leu Phe Ala Lys				
	575		580		585
Ile Lys Gly Ile	Leu Pro His Glu Val Glu Lys Glu Val Leu Leu				
	590		595		600
Leu Asp Glu Pro	Thr Ala Gly Leu Asp Pro Leu Ser Arg His Arg				
	605		610		615
Ile Trp Asn Leu	Leu Lys Glu Gly Lys Ser Asp Arg Val Ile Leu				
	620		625		630
Phe Ser Thr Gln	Phe Ile Asp Glu Ala Asp Ile Leu Ala Asp Arg				
	635		640		645
Lys Val Phe Ile	Ser Asn Gly Lys Leu Lys Cys Ala Gly Ser Ser				
	650		655		660
Leu Phe Leu Lys	Lys Lys Trp Gly Ile Gly Tyr His Leu Ser Leu				
	665		670		675
His Leu Asn Glu	Arg Cys Asp Pro Glu Ser Ile Thr Ser Leu Val				
	680		685		690
Lys Gln His Ile	Ser Asp Ala Lys Leu Thr Ala Gln Ser Glu Glu				
	695		700		705
Lys Leu Val Tyr	Ile Leu Pro Leu Glu Arg Thr Asn Lys Phe Pro				
	710		715		720
Glu Leu Tyr Arg	Asp Leu Asp Arg Cys Ser Asn Gln Gly Ile Glu				
	725		730		735
Asp Tyr Gly Val	Ser Ile Thr Thr Leu Asn Glu Val Phe Leu Lys				
	740		745		750
Leu Glu Gly Lys	Ser Thr Ile Asp Glu Ser Asp Ile Gly Ile Trp				
	755		760		765
Gly Gln Leu Gln	Thr Asp Gly Ala Lys Asp Ile Gly Ser Leu Val				
	770		775		780
Glu Leu Glu Gln	Val Leu Ser Ser Phe His Glu Thr Arg Lys Thr				
	785		790		795
Ile Ser Gly Val	Ala Leu Trp Arg Gln Gln Val Cys Ala Ile Ala				
	800		805		810
Lys Val Arg Phe	Leu Lys Leu Lys Lys Glu Arg Lys Ser Leu Trp				
	815		820		825
Thr Ile Leu Leu	Leu Phe Gly Ile Ser Phe Ile Pro Gln Leu Leu				
	830		835		840
Glu His Leu Phe	Tyr Glu Ser Tyr Gln Lys Ser Tyr Pro Trp Glu				
	845		850		855
Leu Ser Pro Asn	Thr Tyr Phe Leu Ser Pro Gly Gln Gln Pro Gln				
	860		865		870
Asp Pro Leu Thr	His Leu Leu Val Ile Asn Lys Thr Gly Ser Thr				
	875		880		885
Ile Asp Asn Phe	Leu His Ser Leu Arg Arg Gln Asn Ile Ala Ile				

	890		895		900
Glu Val Asp Ala Phe Gly Thr Arg Asn Gly Thr Asp Asp Pro Ser					
	905		910		915
Tyr Asn Gly Ala Ile Ile Val Ser Gly Asp Glu Lys Asp His Arg					
	920		925		930
Phe Ser Ile Ala Cys Asn Thr Lys Arg Leu Asn Cys Phe Pro Val					
	935		940		945
Leu Leu Asp Val Ile Ser Asn Gly Leu Leu Gly Ile Phe Asn Ser					
	950		955		960
Ser Glu His Ile Gln Thr Asp Arg Ser Thr Phe Phe Glu Glu His					
	965		970		975
Met Asp Tyr Glu Tyr Gly Tyr Arg Ser Asn Thr Phe Phe Trp Ile					
	980		985		990
Pro Met Ala Ala Ser Phe Thr Pro Tyr Ile Ala Met Ser Ser Ile					
	995		1000		1005
Gly Asp Tyr Lys Lys Lys Ala His Ser Gln Leu Arg Ile Ser Gly					
	1010		1015		1020
Leu Tyr Pro Ser Ala Tyr Trp Phe Gly Gln Ala Leu Val Asp Val					
	1025		1030		1035
Ser Leu Tyr Phe Leu Ile Leu Leu Leu Met Gln Ile Met Asp Tyr					
	1040		1045		1050
Ile Phe Ser Pro Glu Glu Ile Ile Phe Ile Ile Gln Asn Leu Leu					
	1055		1060		1065
Ile Gln Ile Leu Cys Ser Ile Gly Tyr Val Ser Ser Pro Val Phe					
	1070		1075		1080
Leu Thr Tyr Val Ile Ser Phe Ile Phe Arg Asn Gly Arg Lys Asn					
	1085		1090		1095
Ser Gly Ile Trp Ser Phe Phe Phe Leu Ile Val Val Ile Phe Ser					
	1100		1105		1110
Ile Val Ala Thr Asp Leu Asn Glu Tyr Gly Phe Leu Gly Leu Phe					
	1115		1120		1125
Phe Gly Thr Met Leu Ile Pro Pro Phe Thr Leu Ile Gly Ser Leu					
	1130		1135		1140
Phe Ile Phe Ser Glu Ile Ser Pro Asp Ser Met Asp Tyr Leu Gly					
	1145		1150		1155
Ala Ser Glu Ser Glu Ile Val Tyr Leu Ala Leu Leu Ile Pro Tyr					
	1160		1165		1170
Leu His Phe Leu Ile Phe Leu Phe Ile Leu Arg Cys Leu Glu Met					
	1175		1180		1185
Asn Cys Arg Lys Lys Leu Met Arg Lys Asp Pro Val Phe Arg Ile					
	1190		1195		1200
Ser Pro Arg Ser Asn Ala Ile Phe Pro Asn Pro Glu Glu Pro Glu					
	1205		1210		1215
Gly Glu Glu Glu Asp Ile Gln Met Glu Arg Met Arg Thr Val Asn					
	1220		1225		1230
Ala Met Ala Val Arg Asp Phe Asp Glu Thr Pro Val Ile Ile Ala					
	1235		1240		1245
Ser Cys Leu Arg Lys Glu Tyr Ala Gly Lys Lys Lys Asn Cys Phe					
	1250		1255		1260
Ser Lys Arg Lys Lys Thr Ile Ala Thr Arg Asn Val Ser Phe Cys					
	1265		1270		1275
Val Lys Lys Gly Glu Val Ile Gly Leu Leu Gly His Asn Gly Ala					
	1280		1285		1290
Gly Lys Ser Thr Thr Ile Lys Met Ile Thr Gly Asp Thr Lys Pro					
	1295		1300		1305
Thr Ala Gly Gln Val Ile Leu Lys Gly Ser Gly Gly Gly Glu Pro					

1310	1315	1320
Leu Gly Phe Leu Gly Tyr Cys Pro Gln Glu Asn Ala Leu Trp Pro		
1325	1330	1335
Asn Leu Thr Val Arg Gln His Leu Glu Val Tyr Ala Ala Val Lys		
1340	1345	1350
Gly Leu Arg Lys Gly Asp Ala Met Ile Ala Ile Thr Arg Leu Val		
1355	1360	1365
Asp Ala Leu Lys Leu Gln Asp Gln Leu Lys Ala Pro Val Lys Thr		
1370	1375	1380
Leu Ser Glu Gly Ile Lys Arg Lys Val Arg Ala Gly Leu Val Val		
1385	1390	1395
Ala Leu Gln Val Pro		
1400		

<210> 28

<211> 438

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7510203CD1

<400> 28

Met Gln Ala Thr Arg Asn Ala Ala Asp Trp Trp Leu Ser His Trp		
1	5	10
Ile Ser Gln Leu Lys Ala Glu Asn Ser Ser Gln Glu Ala Gln Pro		
20	25	30
Ser Thr Ser Pro Ala Ser Met Gly Leu Phe Ser Pro Gln Leu Leu		
35	40	45
Leu Phe Ser Pro Gly Asn Leu Tyr Ile Pro Val Phe Pro Leu Pro		
50	55	60
Lys Ala Ala Pro Asn Gly Ser Ser Asp Ile Arg Phe Tyr Leu Thr		
65	70	75
Val Tyr Ala Thr Ile Ala Gly Val Asn Ser Leu Cys Thr Leu Leu		
80	85	90
Arg Ala Val Leu Phe Ala Ala Gly Thr Leu Gln Ala Ala Ala Thr		
95	100	105
Leu His Arg Arg Leu Leu His Arg Val Leu Met Ala Pro Val Thr		
110	115	120
Phe Phe Asn Ala Thr Pro Thr Gly Arg Ile Leu Asn Arg Phe Ser		
125	130	135
Ser Asp Val Ala Cys Ala Asp Asp Ser Leu Pro Phe Ile Leu Asn		
140	145	150
Ile Leu Leu Ala Asn Ala Ala Gly Leu Leu Gly Leu Leu Ala Val		
155	160	165
Leu Gly Ser Gly Leu Pro Trp Leu Leu Leu Leu Pro Pro Leu		
170	175	180
Ser Ile Met Tyr Tyr His Val Gln Arg His Tyr Arg Ala Ser Ser		
185	190	195
Arg Glu Leu Arg Arg Leu Gly Ser Leu Thr Leu Ser Pro Leu Tyr		
200	205	210
Ser His Leu Ala Asp Thr Leu Ala Gly Leu Ser Val Leu Arg Ala		
215	220	225
Thr Gly Ala Thr Tyr Arg Phe Glu Glu Glu Asn Leu Arg Leu Leu		
230	235	240

Glu Leu Asn Gln Arg Cys Gln Phe Ala Thr Ser Ala Thr Met Gln
 245 250 255
 Trp Leu Asp Ile Arg Leu Gln Leu Met Gly Ala Ala Val Val Ser
 260 265 270
 Ala Ile Ala Gly Ile Ala Leu Val Gln His Gln Gln Gly Leu Ala
 275 280 285
 Asn Pro Gly Leu Val Gly Leu Ser Leu Ser Tyr Ala Leu Ser Leu
 290 295 300
 Thr Gly Leu Leu Ser Gly Leu Val Ser Ser Phe Thr Gln Thr Glu
 305 310 315
 Ala Met Leu Val Ser Val Glu Arg Leu Glu Glu Tyr Thr Cys Asp
 320 325 330
 Leu Pro Gln Glu Pro Gln Gly Gln Pro Leu Gln Val Gly Leu Tyr
 335 340 345
 Pro His Pro Arg Pro Lys Leu Trp Asn Pro Glu Gly Pro Ser Leu
 350 355 360
 Pro His Asn Ser Phe Leu Phe Ala His Pro Ser Phe Ser Ala Pro
 365 370 375
 Ile Thr Ser Leu His Asp Asp His Asn Ser Ser Pro Cys Pro Phe
 380 385 390
 Phe Pro Ile Ser His Ser Leu Ile Pro Leu Thr Leu Ser Ile Ser
 395 400 405
 His Tyr Ser Pro Leu Leu Thr Ile Ala Pro His Leu Pro Tyr Leu
 410 415 420
 Pro Phe Pro Val Cys Leu Pro Pro Met Asp Pro Thr Ser Trp Ala
 425 430 435
 Pro Ala Gly

<210> 29

<211> 871

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7510208CD1

<400> 29

Met Gly Phe Leu His Gln Leu Gln Leu Leu Leu Trp Lys Asn Val
 1 5 10 15
 Thr Leu Lys Arg Arg Ser Pro Trp Val Leu Ala Phe Glu Ile Phe
 20 25 30
 Ile Pro Leu Val Leu Phe Phe Ile Leu Leu Gly Leu Arg Gln Lys
 35 40 45
 Lys Pro Thr Ile Ser Val Lys Glu Val Ser Phe Tyr Thr Ala Ala
 50 55 60
 Pro Leu Thr Ser Ala Gly Ile Leu Pro Val Met Gln Ser Leu Cys
 65 70 75
 Pro Asp Gly Gln Arg Asp Glu Phe Gly Phe Leu Gln Tyr Ala Asn
 80 85 90
 Ser Thr Val Thr Gln Leu Leu Glu Arg Leu Asp Arg Val Val Glu
 95 100 105
 Glu Gly Asn Leu Phe Asp Pro Ala Arg Pro Ser Leu Gly Ser Glu
 110 115 120
 Leu Glu Ala Leu Arg Gln His Leu Glu Ala Leu Ser Ala Gly Pro

	125	130	135
Gly Thr Ser Gly Ser His Leu Asp Arg Ser Thr Val Ser Ser Phe			
	140	145	150
Ser Leu Asp Ser Val Ala Arg Asn Pro Gln Glu Leu Trp Arg Phe			
	155	160	165
Leu Thr Gln Asn Leu Ser Leu Pro Asn Ser Thr Ala Gln Ala Leu			
	170	175	180
Leu Ala Ala Arg Val Asp Pro Pro Glu Val Tyr His Leu Leu Phe			
	185	190	195
Gly Pro Ser Ser Ala Leu Asp Ser Gln Ser Gly Leu His Lys Gly			
	200	205	210
Gln Glu Pro Trp Ser Arg Leu Gly Gly Asn Pro Leu Phe Arg Met			
	215	220	225
Glu Glu Leu Leu Leu Ala Pro Ala Leu Leu Glu Gln Leu Thr Cys			
	230	235	240
Thr Pro Gly Ser Gly Glu Leu Gly Arg Ile Leu Thr Val Pro Glu			
	245	250	255
Ser Gln Lys Gly Ala Leu Gln Gly Tyr Arg Asp Ala Val Cys Ser			
	260	265	270
Gly Gln Ala Ala Ala Arg Ala Arg Arg Phe Ser Gly Leu Ser Ala			
	275	280	285
Glu Leu Arg Asn Gln Leu Asp Val Ala Lys Val Ser Gln Gln Leu			
	290	295	300
Gly Leu Asp Ala Pro Asn Gly Ser Asp Ser Ser Pro Gln Ala Pro			
	305	310	315
Pro Pro Arg Arg Leu Gln Ala Leu Leu Gly Asp Leu Leu Asp Ala			
	320	325	330
Gln Lys Val Leu Gln Asp Val Asp Val Leu Ser Ala Leu Ala Leu			
	335	340	345
Leu Leu Pro Gln Gly Ala Cys Thr Gly Arg Thr Pro Gly Pro Pro			
	350	355	360
Ala Ser Gly Ala Gly Gly Ala Ala Asn Gly Thr Gly Ala Gly Ala			
	365	370	375
Val Met Gly Pro Asn Ala Thr Ala Glu Glu Gly Ala Pro Ser Ala			
	380	385	390
Ala Ala Leu Ala Thr Pro Asp Thr Leu Gln Gly Gln Cys Ser Ala			
	395	400	405
Phe Val Gln Leu Trp Ala Gly Leu Gln Pro Ile Leu Cys Gly Asn			
	410	415	420
Asn Arg Thr Ile Glu Pro Glu Ala Leu Arg Arg Gly Asn Met Ser			
	425	430	435
Ser Leu Gly Phe Thr Ser Lys Glu Gln Arg Asn Leu Gly Leu Leu			
	440	445	450
Val His Leu Met Thr Ser Asn Pro Lys Ile Leu Tyr Ala Pro Ala			
	455	460	465
Gly Ser Glu Val Asp Arg Val Ile Leu Lys Ala Asn Glu Thr Phe			
	470	475	480
Ala Phe Val Gly Asn Val Thr His Tyr Ala Gln Val Trp Leu Asn			
	485	490	495
Ile Ser Ala Glu Ile Arg Ser Phe Leu Glu Gln Gly Arg Leu Gln			
	500	505	510
Gln His Leu Arg Trp Leu Gln Gln Tyr Val Ala Glu Leu Arg Leu			
	515	520	525
His Pro Glu Ala Leu Asn Leu Ser Leu Asp Glu Leu Pro Pro Ala			
	530	535	540
Leu Arg Gln Asp Asn Phe Ser Leu Pro Ser Gly Met Ala Leu Leu			

	545	550	555
Gln Gln Leu Asp Thr Ile Asp Asn Ala	Ala Cys Gly Trp Ile Gln		
560	565	570	
Phe Met Ser Lys Val Ser Val Asp Ile	Phe Lys Gly Phe Pro Asp		
575	580	585	
Glu Glu Ser Ile Val Asn Tyr Thr Leu	Asn Gln Ala Tyr Gln Asp		
590	595	600	
Asn Val Thr Val Phe Ala Ser Val Ile	Phe Gln Thr Arg Lys Asp		
605	610	615	
Gly Ser Leu Pro Pro His Val His Tyr	Lys Ile Arg Gln Asn Ser		
620	625	630	
Ser Phe Thr Glu Lys Thr Asn Glu Ile	Arg Arg Ala Tyr Trp Arg		
635	640	645	
Pro Gly Pro Asn Thr Gly Gly Arg Phe	Tyr Phe Leu Tyr Gly Phe		
650	655	660	
Val Trp Ile Gln Asp Met Met Glu Arg	Ala Ile Ile Asp Thr Phe		
665	670	675	
Val Gly His Asp Val Val Glu Pro Gly	Ser Tyr Val Gln Met Phe		
680	685	690	
Pro Tyr Pro Cys Tyr Thr Arg Asp Asp	Phe Leu Phe Val Ile Glu		
695	700	705	
His Met Met Pro Leu Cys Met Val Ile	Ser Trp Val Tyr Ser Val		
710	715	720	
Ala Met Thr Ile Gln His Ile Val Ala	Glu Lys Glu His Arg Leu		
725	730	735	
Lys Glu Val Arg Gly Pro Gly Leu Ser	Leu Glu Ala Arg Ala Gly		
740	745	750	
Arg Glu Gly Arg Arg Pro Pro Arg Gly	Leu Pro Gln Ala Pro Gly		
755	760	765	
Pro Pro Ala Gly Asp Glu Asp His Gly	Pro Glu Gln Arg Gly Ala		
770	775	780	
Leu Gly Gly Leu Val His His Arg Leu	Cys Ala Ala Val His Leu		
785	790	795	
Arg Asp Ser Thr His Arg His Pro Glu	Val Arg Pro Gly Ala Tyr		
800	805	810	
Ala Gln Pro Arg Gly His His Leu Ala	Leu Pro Gly Ser Leu Arg		
815	820	825	
Gly Gly His His Val Leu Leu Pro Gly	Val Cys Ala Val Leu		
830	835	840	
Gln Gly Gln Ala Gly Leu Gly Leu Arg	Trp His His Leu Leu Pro		
845	850	855	
Glu Leu Arg Ala Leu His Val Arg Gly	Asp Pro Arg Gly Gly Gly		
860	865	870	
Ala			

<210> 30

<211> 104

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7510446CD1

<400> 30

```

Met Glu Gln Ser Arg Ser Gln Gln Arg Gly Gly Glu Gln Ser Trp
 1          5          10          15
Trp Gly Ser Asp Pro Gln Tyr Gln Tyr Met Pro Phe Glu His Cys
          20          25          30
Thr Ser Tyr Gly Leu Pro Ser Glu Asn Gly Gly Leu Gln His Arg
          35          40          45
Leu Arg Lys Asp Ala Gly Pro Arg His Asn Val His Pro Thr Gln
          50          55          60
Ile Tyr Gly His His Lys Glu Gln Phe Ser Asp Arg Glu Gln Asp
          65          70          75
Ile Gly Met Pro Lys Lys Thr Gly Ser Ser Ser Thr Val Asp Ser
          80          85          90
Lys Asp Glu Asp His Tyr Ser Lys Cys Gln Gly Asp Gly Asp
          95          100

```

<210> 31

<211> 336

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7505294CD1

<400> 31

```

Met Ala Ser Asp Pro Ile Phe Thr Leu Ala Pro Pro Leu His Cys
 1          5          10          15
His Tyr Gly Ala Phe Pro Pro Asn Ala Ser Gly Trp Glu Gln Pro
          20          25          30
Pro Asn Ala Ser Gly Val Ser Val Ala Ser Ala Ala Leu Ala Ala
          35          40          45
Ser Ala Ala Ser Arg Val Ala Thr Ser Thr Asp Pro Ser Cys Ser
          50          55          60
Gly Phe Ala Pro Pro Asp Phe Asn His Cys Leu Lys Asp Trp Asp
          65          70          75
Tyr Asn Gly Leu Pro Val Leu Thr Thr Asn Ala Ile Gly Gln Trp
          80          85          90
Asp Leu Val Cys Asp Leu Gly Trp Gln Val Ile Leu Glu Gln Ile
          95          100          105
Leu Phe Ile Leu Gly Phe Ala Ser Gly Tyr Leu Phe Leu Gly Tyr
          110          115          120
Pro Ala Asp Arg Phe Gly Arg Arg Gly Ile Val Leu Leu Thr Leu
          125          130          135
Gly Leu Val Gly Pro Cys Gly Val Gly Gly Ala Ala Ala Gly Ser
          140          145          150
Ser Thr Gly Val Met Ala Leu Arg Phe Leu Leu Gly Phe Leu Leu
          155          160          165
Ala Gly Val Asp Leu Gly Val Tyr Leu Met Arg Leu Glu Leu Cys
          170          175          180
Asp Pro Thr Gln Arg Leu Arg Val Ala Leu Ala Gly Glu Leu Val
          185          190          195
Gly Val Gly Gly His Phe Leu Phe Leu Gly Leu Ala Leu Val Ser
          200          205          210
Lys Asp Trp Arg Phe Leu Gln Arg Met Ile Thr Ala Pro Cys Ile
          215          220          225
Leu Phe Leu Phe Tyr Gly Trp Pro Gly Leu Phe Leu Glu Ser Ala

```


	230		235		240
Arg Trp Leu Ile	Val Lys Arg Gln Ile	Glu Glu Ala Gln Ser	Val		
	245		250		255
Leu Arg Ile Leu	Ala Glu Arg Asn Arg	Pro His Gly Gln Met	Leu		
	260		265		270
Gly Glu Glu Ala	Gln Glu Ala Leu Gln	Ala Ser Leu Pro Met	Pro		
	275		280		285
Phe Ala Thr Ala	Thr Ser Leu Trp Glu	Glu Glu Gly Ala His	Arg		
	290		295		300
Thr Ser Thr Cys	Ala Leu Cys Trp Pro	Ala Ala Pro Gln Pro	Trp		
	305		310		315
Pro Val Ser Ser	Trp Gly Ser Pro Trp	Thr Asp Leu Ala Ala	Gly		
	320		325		330
Ala Ser Phe Phe	Ser Pro				
	335				

<210> 32

<211> 271

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7505631CD1

<400> 32

Met Asp Asp Phe Ile	Ser Ile Ser Leu Leu	Ser Leu Ala Met Leu		
1	5	10	15	
Val Gly Cys Tyr Val	Ala Gly Ile Ile	Pro Leu Ala Val Asn Phe		
	20	25	30	
Ser Glu Glu Arg Leu	Lys Leu Val Thr	Val Leu Gly Ala Gly Leu		
	35	40	45	
Leu Cys Gly Thr Ala	Leu Ala Val Ile	Val Pro Glu Gly Val His		
	50	55	60	
Ala Leu Tyr Glu Asp	Ile Leu Glu Gly Lys	His His Gln Ala Ser		
	65	70	75	
Glu Thr His Asn Val	Ile Ala Ser Asp	Lys Ala Ala Glu Lys Ser		
	80	85	90	
Val Val His Glu His	Glu His Ser His	Asp His Thr Gln Leu His		
	95	100	105	
Ala Tyr Ile Gly Val	Ser Leu Val Leu	Gly Phe Val Phe Met Leu		
	110	115	120	
Leu Val Asp Gln Ile	Gly Asn Ser His	Val His Ser Thr Asp Asp		
	125	130	135	
Pro Glu Ala Ala Arg	Ser Ser Asn Ser	Lys Ile Thr Thr Thr Leu		
	140	145	150	
Gly Leu Val Val His	Ala Ala Ala Asp	Gly Val Ala Leu Gly Ala		
	155	160	165	
Ala Ala Ser Thr Ser	Gln Thr Ser Val	Gln Leu Ile Val Phe Val		
	170	175	180	
Ala Ile Met Leu His	Lys Ala Pro Ala	Ala Phe Gly Leu Val Ser		
	185	190	195	
Phe Leu Met His Ala	Gly Leu Glu Arg	Asn Arg Ile Arg Lys His		
	200	205	210	
Leu Leu Val Phe Ala	Leu Ala Ala Pro	Val Met Ser Met Val Thr		
	215	220	225	

Tyr Leu Gly Leu Ser Lys Ser Ser Lys Glu Ala Leu Ser Glu Val
 230 235 240
 Asn Ala Thr Gly Val Ala Met Leu Phe Ser Ala Gly Thr Phe Leu
 245 250 255
 Tyr Val Ala Thr Val Arg Lys Val Ala Gln Ile Gly Tyr Ser Cys
 260 265 270
 Met

<210> 33

<211> 107

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7506561CD1

<400> 33

Met Ala Trp Gln Met Met Gln Leu Leu Leu Leu Ala Leu Val Thr
 1 5 10 15
 Ala Ala Gly Ser Ala Gln Pro Arg Ser Ala Arg Ala Arg Thr Asp
 20 25 30
 Leu Leu Asn Val Cys Met Asn Ala Lys His His Lys Thr Gln Pro
 35 40 45
 Ser Pro Glu Asp Glu Leu Tyr Gly Gln Cys Ser Pro Trp Lys Lys
 50 55 60
 Asn Ala Cys Cys Thr Ala Ser Thr Ser Gln Glu Leu His Lys Asp
 65 70 75
 Thr Ser Arg Leu Tyr Asn Phe Asn Trp Asp His Cys Gly Gln Pro
 80 85 90
 Glu Leu Ala Gln Arg Ala His Ser Glu Arg Ala Pro Val Gln Arg
 95 100 105
 Gly Leu

<210> 34

<211> 249

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7510733CD1

<400> 34

Met Gln Pro Glu Gly Ala Glu Lys Gly Lys Ser Phe Lys Gln Arg
 1 5 10 15
 Leu Val Leu Lys Ser Ser Leu Ala Lys Glu Thr Leu Ser Glu Phe
 20 25 30
 Leu Gly Thr Phe Ile Leu Ile Val Leu Gly Cys Gly Cys Val Ala
 35 40 45
 Gln Ala Ile Leu Ser Arg Gly Arg Phe Gly Gly Val Ile Thr Ile
 50 55 60
 Asn Val Gly Phe Ser Met Ala Val Ala Met Ala Ile Tyr Val Ala
 65 70 75

Gly	Gly	Val	Ser	Asp	Gly	Leu	Met	Ser	Phe	Ala	Gly	Gly	Lys	Leu	
				80					85					90	
Leu	Ile	Val	Gly	Glu	Asn	Ala	Thr	Ala	His	Ile	Phe	Ala	Thr	Tyr	
				95					100					105	
Pro	Ala	Pro	Tyr	Leu	Ser	Leu	Ala	Asn	Ala	Phe	Ala	Asp	Gln	Val	
				110					115					120	
Val	Ala	Thr	Met	Ile	Leu	Leu	Ile	Ile	Val	Phe	Ala	Ile	Phe	Asp	
				125					130					135	
Ser	Arg	Asn	Leu	Gly	Ala	Pro	Arg	Gly	Leu	Glu	Pro	Ile	Ala	Ile	
				140					145					150	
Gly	Leu	Leu	Ile	Ile	Val	Ile	Ala	Ser	Ser	Leu	Gly	Leu	Asn	Ser	
				155					160					165	
Gly	Cys	Ala	Met	Asn	Pro	Ala	Arg	Asp	Leu	Ser	Pro	Arg	Leu	Phe	
				170					175					180	
Thr	Ala	Leu	Ala	Gly	Trp	Gly	Phe	Glu	Val	Phe	Arg	Ala	Gly	Asn	
				185					190					195	
Asn	Phe	Trp	Trp	Ile	Pro	Val	Val	Gly	Pro	Leu	Val	Gly	Ala	Val	
				200					205					210	
Ile	Gly	Gly	Leu	Ile	Tyr	Val	Leu	Val	Ile	Glu	Ile	His	His	Pro	
				215					220					225	
Glu	Pro	Asp	Ser	Val	Phe	Lys	Ala	Glu	Gln	Ser	Glu	Asp	Lys	Pro	
				230					235					240	
Glu	Lys	Tyr	Glu	Leu	Ser	Val	Ile	Met							
				245											

<210> 35

<211> 216

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7510734CD1

<400> 35

Met	Gln	Pro	Glu	Gly	Ala	Glu	Lys	Gly	Lys	Ser	Phe	Lys	Gln	Arg	
1				5					10					15	
Leu	Val	Leu	Lys	Ser	Ser	Leu	Ala	Lys	Glu	Thr	Leu	Ser	Glu	Phe	
				20					25					30	
Leu	Gly	Thr	Phe	Ile	Leu	Ile	Val	Leu	Gly	Cys	Gly	Cys	Val	Ala	
				35					40					45	
Gln	Ala	Ile	Leu	Ser	Arg	Gly	Arg	Phe	Gly	Gly	Val	Ile	Thr	Ile	
				50					55					60	
Asn	Val	Gly	Phe	Ser	Met	Ala	Val	Ala	Met	Ala	Ile	Tyr	Val	Ala	
				65					70					75	
Gly	Gly	Val	Ser	Gly	Gly	His	Ile	Asn	Pro	Ala	Val	Ser	Leu	Ala	
				80					85					90	
Met	Cys	Leu	Phe	Gly	Arg	Met	Lys	Trp	Phe	Lys	Leu	Pro	Phe	Tyr	
				95					100					105	
Val	Gly	Ala	Gln	Phe	Leu	Gly	Ala	Phe	Val	Gly	Ala	Ala	Thr	Val	
				110					115					120	
Phe	Gly	Ile	Tyr	Tyr	Asp	Gly	Leu	Met	Ser	Phe	Ala	Gly	Gly	Lys	
				125					130					135	
Leu	Leu	Ile	Val	Gly	Glu	Asn	Ala	Thr	Ala	His	Ile	Phe	Ala	Thr	
				140					145					150	
Tyr	Pro	Ala	Pro	Tyr	Leu	Ser	Leu	Ala	Asn	Ala	Phe	Ala	Asp	Gln	

	155		160		165
Lys Leu Gly Ser Pro Gln Arg Pro Arg Ala His Cys His Arg Pro					
	170		175		180
Pro Asp Tyr Cys His Cys Phe Leu Pro Gly Thr Glu Gln Trp Leu					
	185		190		195
Cys His Glu Pro Ser Ser Arg Pro Glu Ser Gln Thr Phe His Cys					
	200		205		210
Leu Gly Arg Leu Gly Val					
	215				

<210> 36

<211> 223

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7503977CD1

<400> 36

Met Ala Ser Thr Gly Gly Thr Lys Val Val Ala Met Gly Val Ala		
1	5	10
Pro Trp Gly Val Val Arg Asn Arg Asp Thr Leu Ile Asn Pro Lys		
	20	25
Gly Ser Phe Pro Ala Arg Tyr Arg Trp Arg Gly Asp Pro Glu Asp		
	35	40
Gly Val Gln Phe Pro Leu Asp Tyr Asn Tyr Ser Ala Phe Phe Leu		
	50	55
Val Asp Asp Gly Thr His Gly Cys Leu Gly Gly Glu Asn Arg Phe		
	65	70
Arg Leu Arg Leu Glu Ser Tyr Ile Ser Gln Gln Lys Thr Gly Val		
	80	85
Gly Gly Thr Gly Ile Asp Ile Pro Val Leu Leu Leu Leu Ile Asp		
	95	100
Gly Asp Glu Lys Met Leu Thr Arg Ile Glu Asn Ala Thr Gln Ala		
	110	115
Gln Leu Pro Cys Leu Leu Val Ala Gly Ser Gly Gly Ala Ala Asp		
	125	130
Cys Leu Ala Glu Thr Leu Glu Asp Thr Leu Ala Pro Gly Ser Gly		
	140	145
Gly Ala Arg Gln Gly Glu Ala Arg Asp Arg Ile Arg Arg Phe Phe		
	155	160
Pro Lys Gly Asp Leu Glu Val Leu Gln Ala Gln Val Glu Arg Ile		
	170	175
Met Thr Arg Lys Glu Leu Leu Thr Val Tyr Ser Ser Glu Asp Gly		
	185	190
Ser Glu Glu Phe Glu Thr Ile Val Leu Lys Ala Leu Val Lys Val		
	200	205
Leu Pro Ser Arg Ser Phe Pro His Gly Arg Pro Ala Glu		
	215	220

<210> 37

<211> 394

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7505084CD1

<400> 37

```

Met Glu Ser Gly Thr Ser Ser Pro Gln Pro Pro Gln Leu Asp Pro
 1          5          10          15
Leu Asp Ala Phe Pro Gln Lys Gly Leu Glu Pro Gly Asp Ile Ala
          20          25          30
Val Leu Val Leu Tyr Phe Leu Phe Val Leu Ala Val Gly Leu Trp
          35          40          45
Ser Thr Val Lys Thr Lys Arg Asp Thr Val Lys Gly Tyr Phe Leu
          50          55          60
Ala Gly Gly Asp Met Val Trp Trp Pro Val Gly Ala Ser Leu Phe
          65          70          75
Ala Ser Asn Val Gly Ser Gly His Phe Ile Gly Leu Ala Gly Ser
          80          85          90
Gly Ala Ala Thr Gly Ile Ser Val Ser Ala Tyr Glu Leu Asn Gly
          95          100          105
Leu Phe Ser Val Leu Met Leu Ala Trp Ile Phe Leu Pro Ile Tyr
          110          115          120
Ile Ala Gly Gln Val Thr Thr Met Pro Glu Tyr Leu Arg Lys Arg
          125          130          135
Phe Gly Gly Ile Arg Ile Pro Ile Ile Leu Ala Val Leu Tyr Leu
          140          145          150
Phe Ile Tyr Ile Phe Thr Lys Ile Ser Val Asp Met Tyr Ala Gly
          155          160          165
Ala Ile Phe Ile Gln Gln Ser Leu His Leu Asp Leu Tyr Leu Ala
          170          175          180
Ile Val Gly Leu Leu Ala Ile Thr Ala Val Tyr Thr Val Ala Gly
          185          190          195
Gly Leu Ala Ala Val Ile Tyr Thr Asp Ala Leu Gln Thr Leu Ile
          200          205          210
Met Leu Ile Gly Ala Leu Thr Leu Met Gly Tyr Ser Phe Ala Ala
          215          220          225
Val Gly Gly Met Glu Gly Leu Lys Glu Lys Tyr Phe Leu Ala Leu
          230          235          240
Ala Ser Asn Arg Ser Glu Asn Ser Ser Cys Gly Leu Pro Arg Glu
          245          250          255
Asp Ala Phe His Ile Phe Arg Asp Pro Leu Thr Ser Asp Leu Pro
          260          265          270
Trp Pro Gly Val Leu Phe Gly Met Ser Ile Pro Ser Leu Trp Tyr
          275          280          285
Trp Cys Thr Asp Gln Val Ile Val Gln Arg Thr Leu Ala Ala Lys
          290          295          300
Asn Leu Ser His Ala Lys Gly Gly Ala Leu Met Ala Ala Tyr Leu
          305          310          315
Lys Val Leu Pro Leu Phe Ile Met Val Phe Pro Gly Met Val Ser
          320          325          330
Arg Ile Leu Phe Pro Asp Gln Val Ala Cys Ala Asp Pro Glu Ile
          335          340          345
Cys Gln Lys Ile Cys Ser Asn Pro Ser Gly Cys Ser Asp Ile Ala
          350          355          360
Tyr Pro Lys Leu Val Leu Glu Leu Leu Pro Thr Val Pro Ala Pro
          365          370          375
Ser Ser Pro Trp Thr Ser Gly Ile Thr Ser Gly Leu Gly His Leu

```

380
Arg Arg Ser Ser

385

390

<210> 38
<211> 202
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 7506950CD1

<400> 38
Met Lys Thr Lys Leu Asn Ile Tyr Asn Met Gln Phe Leu Leu Phe
1 5 10 15
Val Phe Leu Val Trp Asp Pro Ala Arg Leu Val Leu Ala Asn Ile
20 25 30
Gln Glu Asp Glu Ala Lys Asn Asn Ile Thr Ile Phe Thr Arg Ile
35 40 45
Leu Asp Arg Leu Leu Asp Gly Tyr Asp Asn Arg Leu Arg Pro Gly
50 55 60
Leu Gly Asp Ser Ile Thr Glu Val Phe Thr Asn Ile Tyr Val Thr
65 70 75
Ser Phe Gly Pro Val Ser Asp Thr Asp Met Glu Tyr Thr Ile Asp
80 85 90
Val Phe Phe Arg Gln Lys Trp Lys Asp Glu Arg Leu Lys Phe Lys
95 100 105
Gly Pro Met Asn Ile Leu Arg Leu Asn Asn Leu Met Ala Ser Lys
110 115 120
Ile Trp Thr Pro Asp Thr Phe Phe His Asn Gly Lys Lys Ser Val
125 130 135
Ala His Asn Met Thr Met Pro Asn Lys Leu Leu Arg Ile Gln Asp
140 145 150
Asp Gly Thr Leu Leu Tyr Thr Met Arg Ser Asn Asn Cys Pro Asn
155 160 165
Asn Asp Asn Ser Lys His Gln Cys Ser Glu Phe Ser Pro Gln Ser
170 175 180
Gly Leu Cys Asn Cys His Gly Leu Val Tyr Cys Cys Leu Leu Cys
185 190 195
Ile Cys Val Leu Cys Pro Asn
200

<210> 39
<211> 337
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 7506951CD1

<400> 39
Met Lys Thr Lys Leu Asn Ile Tyr Asn Met Gln Phe Leu Leu Phe
1 5 10 15
Val Phe Leu Val Trp Asp Pro Ala Arg Leu Val Leu Ala Asn Ile

	20		25		30
Gln Glu Asp Glu	Ala Lys Asn Asn Ile Thr Ile Phe Thr Arg Ile				
	35		40		45
Leu Asp Arg Leu	Leu Asp Gly Tyr Asp Asn Arg Leu Arg Pro Gly				
	50		55		60
Leu Gly Asp Ser	Ile Thr Glu Val Phe Thr Asn Ile Tyr Val Thr				
	65		70		75
Ser Phe Gly Pro	Val Ser Asp Thr Asp Met Glu Tyr Thr Ile Asp				
	80		85		90
Val Phe Phe Arg	Gln Lys Trp Lys Asp Glu Arg Leu Lys Phe Lys				
	95		100		105
Gly Pro Met Asn	Ile Leu Arg Leu Asn Asn Leu Met Ala Ser Lys				
	110		115		120
Ile Trp Thr Pro	Asp Thr Phe Phe His Asn Gly Lys Lys Ser Val				
	125		130		135
Ala His Asn Met	Thr Met Pro Asn Lys Leu Leu Arg Ile Gln Asp				
	140		145		150
Asp Gly Thr Leu	Leu Tyr Thr Met Arg Leu Thr Val Gln Ala Glu				
	155		160		165
Cys Pro Met His	Leu Glu Asp Phe Pro Met Asp Ala His Ser Cys				
	170		175		180
Pro Leu Lys Phe	Gly Ser Tyr Ala Tyr Thr Thr Ser Glu Val Thr				
	185		190		195
Tyr Ile Trp Thr	Tyr Asn Ala Ser Asp Ser Val Gln Val Ala Pro				
	200		205		210
Asp Gly Ser Arg	Leu Asn Gln Tyr Asp Leu Leu Gly Gln Ser Ile				
	215		220		225
Gly Lys Glu Thr	Ile Lys Ser Ser Thr Gly Glu Tyr Thr Val Met				
	230		235		240
Thr Ala His Phe	His Leu Lys Arg Lys Ile Gly Tyr Phe Val Ile				
	245		250		255
Gln Thr Tyr Leu	Pro Cys Ile Met Thr Val Ile Leu Ser Gln Val				
	260		265		270
Ser Phe Trp Leu	Asn Arg Glu Ser Val Pro Ala Arg Thr Val Phe				
	275		280		285
Glu Lys Arg Lys	Gly Phe Arg Tyr Asp Thr Glu Gln Arg Leu Cys				
	290		295		300
Ser Gly Cys Cys	Gln Leu Cys Pro Glu Ser Phe Lys Arg Ser Ser				
	305		310		315
Ser Leu His His	Leu Gln Glu Cys Asn His Ala Arg Thr Gln Gln				
	320		325		330
Glu Ala Arg Lys	Gln Ala Ser				
	335				

<210> 40

<211> 114

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7506954CD1

<400> 40

Met Lys Thr Lys Leu Asn Ile Tyr Asn Met Gln Phe Leu Leu Phe
1 5 10 15

```

Val Phe Leu Val Trp Asp Pro Ala Arg Leu Val Leu Ala Asn Ile
      20                      25                      30
Gln Glu Asp Glu Ala Lys Asn Asn Ile Thr Ile Phe Thr Arg Ile
      35                      40                      45
Leu Asp Arg Leu Leu Asp Gly Tyr Asp Asn Arg Leu Arg Pro Gly
      50                      55                      60
Leu Gly Glu Lys Arg Lys Gly Phe Arg Tyr Asp Thr Glu Gln Arg
      65                      70                      75
Leu Cys Ser Gly Cys Cys Gln Leu Cys Pro Glu Ser Phe Lys Arg
      80                      85                      90
Ser Ser Ser Leu His His Leu Gln Glu Cys Asn His Ala Arg Thr
      95                      100                     105
Gln Gln Glu Ala Arg Lys Gln Ala Ser
      110

```

<210> 41

<211> 400

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7506956CD1

<400> 41

```

Met Lys Thr Lys Leu Asn Ile Tyr Asn Met Gln Phe Leu Leu Phe
  1          5          10          15
Val Phe Leu Val Trp Asp Pro Ala Arg Leu Val Leu Ala Asn Ile
      20                      25                      30
Gln Glu Asp Glu Ala Lys Asn Asn Ile Thr Ile Phe Thr Arg Ile
      35                      40                      45
Leu Asp Arg Leu Leu Asp Gly Tyr Asp Asn Arg Leu Arg Pro Gly
      50                      55                      60
Leu Gly Asp Ser Ile Thr Glu Val Phe Thr Asn Ile Tyr Val Thr
      65                      70                      75
Ser Phe Gly Pro Val Ser Asp Thr Asp Met Glu Tyr Thr Ile Asp
      80                      85                      90
Val Phe Phe Arg Gln Lys Trp Lys Asp Glu Arg Leu Lys Phe Lys
      95                      100                     105
Gly Pro Met Asn Ile Leu Arg Leu Asn Asn Leu Met Ala Ser Lys
      110                     115                     120
Ile Trp Thr Pro Asp Thr Phe Phe His Asn Gly Lys Lys Ser Val
      125                     130                     135
Ala His Asn Met Thr Met Pro Asn Lys Leu Leu Arg Ile Gln Asp
      140                     145                     150
Asp Gly Thr Leu Leu Tyr Thr Met Arg Leu Thr Val Gln Ala Glu
      155                     160                     165
Cys Pro Met His Leu Glu Asp Phe Pro Met Asp Ala His Ser Cys
      170                     175                     180
Pro Leu Lys Phe Gly Ser Tyr Ala Tyr Thr Thr Ser Glu Val Thr
      185                     190                     195
Tyr Ile Trp Thr Tyr Asn Ala Ser Asp Ser Val Gln Val Ala Pro
      200                     205                     210
Asp Gly Ser Arg Leu Asn Gln Tyr Asp Leu Leu Gly Gln Ser Ile
      215                     220                     225
Gly Lys Glu Thr Ile Lys Ser Ser Thr Gly Val Thr Thr Val Leu

```


	230	235	240
Thr Met Thr Thr	Leu Ser Ile Ser Ala Arg Asn Ser Leu Pro Lys		
	245	250	255
Val Ala Tyr Ala	Thr Ala Met Asp Trp Phe Ile Ala Val Cys Tyr		
	260	265	270
Ala Phe Val Phe	Ser Ala Leu Ile Glu Phe Ala Thr Val Asn Tyr		
	275	280	285
Phe Thr Lys Arg	Gly Trp Ala Trp Asp Gly Lys Ser Val Val Asn		
	290	295	300
Asp Lys Lys Lys	Glu Lys Ala Ser Val Met Ile Gln Asn Asn Ala		
	305	310	315
Tyr Ala Val Ala	Val Ala Asn Tyr Ala Pro Asn Leu Ser Lys Asp		
	320	325	330
Pro Val Leu Ser	Thr Ile Ser Lys Ser Ala Thr Thr Pro Glu Pro		
	335	340	345
Asn Lys Lys Pro	Glu Asn Lys Pro Ala Glu Ala Lys Lys Thr Phe		
	350	355	360
Asn Ser Val Ser	Lys Ile Asp Arg Met Ser Arg Ile Val Phe Pro		
	365	370	375
Val Leu Phe Gly	Thr Phe Asn Leu Val Tyr Trp Ala Thr Tyr Leu		
	380	385	390
Asn Arg Glu Pro	Val Leu Gly Val Ser Pro		
	395	400	

<210> 42

<211> 403

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7506959CD1

<400> 42

Met Lys Thr Lys	Leu Asn Ile Tyr Asn Met Gln Phe Leu Leu Phe	
1	5	10 15
Val Phe Leu Val	Trp Asp Pro Ala Arg Leu Val Leu Ala Asn Ile	
	20	25 30
Gln Glu Asp Glu	Ala Lys Asn Asn Ile Thr Ile Phe Thr Arg Ile	
	35	40 45
Leu Asp Arg Leu	Leu Asp Gly Tyr Asp Asn Arg Leu Arg Pro Gly	
	50	55 60
Leu Gly Asp Ser	Ile Thr Glu Val Phe Thr Asn Ile Tyr Val Thr	
	65	70 75
Ser Phe Gly Pro	Val Ser Asp Thr Asp Met Glu Tyr Thr Ile Asp	
	80	85 90
Val Phe Phe Arg	Gln Lys Trp Lys Asp Glu Arg Leu Lys Phe Lys	
	95	100 105
Gly Pro Met Asn	Ile Leu Arg Leu Asn Asn Leu Met Ala Ser Lys	
	110	115 120
Ile Trp Thr Pro	Asp Thr Phe Phe His Asn Gly Lys Lys Ser Val	
	125	130 135
Ala His Asn Met	Thr Met Pro Asn Lys Leu Leu Arg Ile Gln Asp	
	140	145 150
Asp Gly Thr Leu	Leu Tyr Thr Met Arg Leu Thr Val Gln Ala Glu	
	155	160 165

Cys	Pro	Met	His	Leu	Glu	Asp	Phe	Pro	Met	Asp	Ala	His	Ser	Cys	
				170					175					180	
Pro	Leu	Lys	Phe	Gly	Ser	Cys	Glu	Tyr	Thr	Val	Met	Thr	Ala	His	
				185					190					195	
Phe	His	Leu	Lys	Arg	Lys	Ile	Gly	Tyr	Phe	Val	Ile	Gln	Thr	Tyr	
				200					205					210	
Leu	Pro	Cys	Ile	Met	Thr	Val	Ile	Leu	Ser	Gln	Val	Ser	Phe	Trp	
				215					220					225	
Leu	Asn	Arg	Glu	Ser	Val	Pro	Ala	Arg	Thr	Val	Phe	Gly	Val	Thr	
				230					235					240	
Thr	Val	Leu	Thr	Met	Thr	Thr	Leu	Ser	Ile	Ser	Ala	Arg	Asn	Ser	
				245					250					255	
Leu	Pro	Lys	Val	Ala	Tyr	Ala	Thr	Ala	Met	Asp	Trp	Phe	Ile	Ala	
				260					265					270	
Val	Cys	Tyr	Ala	Phe	Val	Phe	Ser	Ala	Leu	Ile	Glu	Phe	Ala	Thr	
				275					280					285	
Val	Asn	Tyr	Phe	Thr	Lys	Arg	Gly	Trp	Ala	Trp	Asp	Gly	Lys	Ser	
				290					295					300	
Val	Val	Asn	Asp	Lys	Lys	Lys	Glu	Lys	Ala	Ser	Val	Met	Ile	Gln	
				305					310					315	
Asn	Asn	Ala	Tyr	Ala	Val	Ala	Val	Ala	Asn	Tyr	Ala	Pro	Asn	Leu	
				320					325					330	
Ser	Lys	Asp	Pro	Val	Leu	Ser	Thr	Ile	Ser	Lys	Ser	Ala	Thr	Thr	
				335					340					345	
Pro	Glu	Pro	Asn	Lys	Lys	Pro	Glu	Asn	Lys	Pro	Ala	Glu	Ala	Lys	
				350					355					360	
Lys	Thr	Phe	Asn	Ser	Val	Ser	Lys	Ile	Asp	Arg	Met	Ser	Arg	Ile	
				365					370					375	
Val	Phe	Pro	Val	Leu	Phe	Gly	Thr	Phe	Asn	Leu	Val	Tyr	Trp	Ala	
				380					385					390	
Thr	Tyr	Leu	Asn	Arg	Glu	Pro	Val	Leu	Gly	Val	Ser	Pro			
				395					400						

<210> 43

<211> 66

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7506960CD1

<400> 43

Met	Lys	Thr	Lys	Leu	Asn	Ile	Tyr	Asn	Met	Gln	Phe	Leu	Leu	Phe	
1				5					10					15	
Val	Phe	Leu	Val	Trp	Asp	Pro	Ala	Arg	Leu	Val	Leu	Ala	Asn	Ile	
				20					25					30	
Gln	Glu	Asp	Glu	Ala	Lys	Asn	Asn	Ile	Thr	Ile	Phe	Thr	Arg	Ile	
				35					40					45	
Leu	Asp	Arg	Leu	Leu	Asp	Gly	Tyr	Asp	Asn	Arg	Leu	Arg	Pro	Gly	
				50					55					60	
Leu	Gly	Gly	Ile	Tyr	Asn										
				65											

<210> 44

<211> 89

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7510540CD1

<400> 44

Met	Thr	Glu	Asp	Lys	Val	Thr	Gly	Thr	Leu	Val	Phe	Thr	Val	Ile
1				5					10					15
Thr	Ala	Val	Leu	Gly	Ser	Phe	Gln	Phe	Gly	Tyr	Asp	Ile	Gly	Val
			20						25					30
Ile	Asn	Ala	Pro	Gln	Asn	Gln	Ser	His	Val	Ser	Ser	Lys	His	
			35						40					45
Ser	Val	Ile	Ser	Trp	Ser	Ser	Leu	Asp	Gly	Val	Phe	Lys	Ile	Gly
			50						55					60
Thr	Ile	Ser	Tyr	Thr	Tyr	Asn	Cys	Trp	Lys	Lys	His	Ile	Arg	Thr
			65						70					75
Ile	Leu	Trp	Ala	Asn	Phe	Arg	Pro	Gly	Ser	Tyr	Val	Tyr	Arg	
			80						85					

<210> 45

<211> 146

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7510545CD1

<400> 45

Met	Glu	Asn	Ala	His	Thr	Lys	Thr	Val	Glu	Glu	Val	Leu	Gly	His
1				5					10					15
Phe	Gly	Val	Asn	Glu	Ser	Glu	Ser	Val	Ser	Val	Ile	Lys	His	Thr
			20						25					30
Asp	Pro	Val	Pro	Asp	Pro	Arg	Ala	Val	Asn	Gln	Asp	Lys	Lys	Asn
			35						40					45
Met	Leu	Phe	Ser	Val	Ala	Leu	Ala	Val	Ala	Ala	Ile	Pro	Glu	Gly
			50						55					60
Leu	Pro	Ala	Val	Ile	Thr	Thr	Cys	Leu	Ala	Leu	Gly	Thr	Arg	Arg
			65						70					75
Met	Ala	Lys	Lys	Asn	Ala	Ile	Val	Arg	Ser	Leu	Pro	Ser	Val	Glu
			80						85					90
Thr	Leu	Gly	Cys	Thr	Ser	Val	Ile	Cys	Ser	Asp	Lys	Thr	Gly	Thr
			95						100					105
Leu	Thr	Thr	Asn	Gln	Met	Ser	Val	Cys	Arg	Met	Phe	Ile	Leu	Asp
			110						115					120
Arg	Val	Glu	Asp	His	Thr	Ala	Glu	Arg	Asp	Pro	Val	Ala	Asp	Gly
			125						130					135
Ala	Glu	Asn	Leu	Leu	Ala	Arg	Asp	Ser	His	Gly				
			140						145					

<210> 46

<211> 353

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7510654CD1

<400> 46

Met	Thr	Pro	Glu	Asp	Pro	Glu	Glu	Thr	Gln	Pro	Leu	Leu	Gly	Pro
1				5					10					15
Pro	Gly	Gly	Ser	Ala	Pro	Arg	Gly	Arg	Arg	Val	Phe	Leu	Ala	Ala
				20					25					30
Phe	Ala	Ala	Ala	Leu	Gly	Pro	Leu	Ser	Phe	Gly	Phe	Ala	Leu	Gly
				35					40					45
Tyr	Ser	Ser	Pro	Ala	Ile	Pro	Ser	Leu	Gln	Arg	Ala	Ala	Pro	Pro
				50					55					60
Ala	Pro	Arg	Leu	Asp	Asp	Ala	Ala	Ala	Ser	Trp	Phe	Gly	Ala	Val
				65					70					75
Val	Thr	Leu	Gly	Ala	Ala	Ala	Gly	Gly	Val	Leu	Gly	Gly	Trp	Leu
				80					85					90
Val	Asp	Arg	Ala	Gly	Arg	Lys	Leu	Ser	Leu	Leu	Leu	Cys	Ser	Val
				95					100					105
Pro	Phe	Val	Ala	Gly	Phe	Ala	Val	Ile	Thr	Ala	Ala	Gln	Asp	Val
				110					115					120
Trp	Met	Leu	Leu	Gly	Gly	Arg	Leu	Leu	Thr	Gly	Leu	Ala	Cys	Gly
				125					130					135
Val	Ala	Ser	Leu	Val	Ala	Pro	Val	Tyr	Ile	Ser	Glu	Ile	Ala	Tyr
				140					145					150
Pro	Ala	Val	Arg	Gly	Leu	Leu	Gly	Ser	Cys	Val	Gln	Leu	Met	Val
				155					160					165
Val	Val	Gly	Ile	Leu	Leu	Ala	Tyr	Leu	Ala	Gly	Trp	Val	Leu	Glu
				170					175					180
Trp	Arg	Trp	Leu	Ala	Val	Leu	Gly	Cys	Val	Pro	Pro	Ser	Leu	Met
				185					190					195
Leu	Leu	Leu	Met	Cys	Phe	Met	Pro	Glu	Thr	Pro	Arg	Phe	Leu	Leu
				200					205					210
Thr	Gln	His	Arg	Arg	Gln	Glu	Ala	Met	Ala	Ala	Leu	Arg	Phe	Leu
				215					220					225
Trp	Gly	Ser	Glu	Gln	Gly	Trp	Glu	Asp	Pro	Pro	Ile	Gly	Ala	Glu
				230					235					240
Gln	Ser	Phe	His	Leu	Ala	Leu	Leu	Arg	Gln	Pro	Gly	Ile	Tyr	Lys
				245					250					255
Pro	Phe	Ile	Ile	Gly	Val	Ser	Leu	Met	Ala	Phe	Gln	Gln	Leu	Ser
				260					265					270
Gly	Val	Asn	Ala	Val	Met	Phe	Tyr	Ala	Glu	Thr	Ile	Phe	Glu	Glu
				275					280					285
Ala	Lys	Phe	Lys	Asp	Ser	Ser	Leu	Ala	Ser	Val	Val	Val	Gly	Val
				290					295					300
Ile	Gln	Val	Leu	Phe	Thr	Ala	Val	Ala	Ala	Leu	Ile	Met	Asp	Arg
				305					310					315
Ala	Gly	Arg	Arg	Leu	Leu	Leu	Val	Leu	Ser	Gly	Gly	Pro	Gln	Ala
				320					325					330
Leu	Trp	Ser	Leu	Leu	Ala	Cys	Leu	Arg	Phe	Leu	His	Leu	Gln	Cys
				335					340					345
Pro	Phe	His	Phe	Val	Leu	Cys	Pro							
				350										

<210> 47

<211> 1155

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7510660CD1

<400> 47

```

Met Ala Ala Ala Ala Val Gly Asn Ala Val Pro Cys Gly Ala
  1          5          10          15
Arg Pro Cys Gly Val Arg Pro Asp Gly Gln Pro Lys Pro Gly Pro
          20          25          30
Gln Pro Arg Ala Leu Leu Ala Ala Gly Pro Ala Leu Ile Ala Asn
          35          40          45
Gly Asp Glu Leu Val Ala Ala Val Trp Pro Tyr Arg Arg Leu Ala
          50          55          60
Leu Leu Arg Arg Leu Thr Val Leu Pro Phe Ala Gly Leu Leu Tyr
          65          70          75
Pro Ala Trp Leu Gly Ala Ala Ala Ala Gly Cys Trp Gly Trp Gly
          80          85          90
Ser Ser Trp Val Gln Ile Pro Glu Ala Ala Leu Leu Val Leu Ala
          95          100          105
Thr Ile Cys Leu Ala His Ala Leu Thr Val Leu Ser Gly His Trp
          110          115          120
Ser Val His Ala His Cys Ala Leu Thr Cys Thr Pro Glu Tyr Asp
          125          130          135
Pro Ser Lys Ala Thr Phe Val Lys Val Val Pro Thr Pro Asn Asn
          140          145          150
Gly Ser Thr Glu Leu Val Ala Leu His Arg Asn Glu Gly Glu Asp
          155          160          165
Gly Leu Glu Val Leu Ser Phe Glu Phe Gln Lys Ile Lys Tyr Ser
          170          175          180
Tyr Asp Ala Leu Glu Lys Lys Gln Phe Leu Pro Val Ala Phe Pro
          185          190          195
Val Gly Asn Ala Phe Ser Tyr Tyr Gln Ser Asn Arg Gly Phe Gln
          200          205          210
Glu Asp Ser Glu Ile Arg Ala Ala Glu Lys Lys Phe Gly Ser Asn
          215          220          225
Lys Ala Glu Met Val Val Pro Asp Phe Ser Glu Leu Phe Lys Glu
          230          235          240
Arg Ala Thr Ala Pro Phe Phe Val Phe Gln Val Phe Cys Val Gly
          245          250          255
Leu Trp Cys Leu Asp Glu Tyr Trp Tyr Tyr Ser Val Phe Thr Leu
          260          265          270
Ser Met Leu Val Ala Phe Glu Ala Ser Leu Val Gln Gln Gln Met
          275          280          285
Arg Asn Met Ser Glu Ile Arg Lys Met Gly Asn Lys Pro His Met
          290          295          300
Ile Gln Val Tyr Arg Ser Arg Lys Trp Arg Pro Ile Ala Ser Asp
          305          310          315
Glu Ile Val Pro Gly Asp Ile Val Ser Ile Gly Arg Ser Pro Gln
          320          325          330
Glu Asn Leu Val Pro Cys Asp Val Leu Leu Leu Arg Gly Arg Cys
          335          340          345
Ile Val Asp Glu Ala Met Leu Thr Gly Glu Ser Val Pro Gln Met
          350          355          360

```

Lys Glu Pro Ile	Glu Asp Leu Ser Pro Asp Arg Val Leu Asp Leu	365	370	375
Gln Ala Asp Ser	Arg Leu His Val Ile Phe Gly Gly Thr Lys Val	380	385	390
Val Gln His Ile	Pro Pro Gln Lys Ala Thr Thr Gly Leu Lys Pro	395	400	405
Val Asp Ser Gly	Cys Val Ala Tyr Val Leu Arg Thr Gly Phe Asn	410	415	420
Thr Ser Gln Gly	Lys Leu Leu Arg Thr Ile Leu Phe Gly Val Lys	425	430	435
Arg Val Thr Ala	Asn Asn Leu Glu Thr Phe Ile Phe Ile Leu Phe	440	445	450
Leu Leu Val Phe	Ala Ile Ala Ala Ala Tyr Val Trp Ile Glu	455	460	465
Gly Thr Lys Asp	Pro Ser Arg Asn Arg Tyr Lys Leu Phe Leu Glu	470	475	480
Cys Thr Leu Ile	Leu Thr Ser Val Val Pro Pro Glu Leu Pro Ile	485	490	495
Glu Leu Ser Leu	Ala Val Asn Thr Ser Leu Ile Ala Leu Ala Lys	500	505	510
Leu Tyr Met Tyr	Cys Thr Glu Pro Phe Arg Ile Pro Phe Ala Gly	515	520	525
Lys Val Glu Val	Cys Cys Phe Asp Lys Thr Gly Thr Leu Thr Ser	530	535	540
Asp Ser Leu Val	Val Arg Gly Val Ala Gly Leu Arg Asp Gly Lys	545	550	555
Glu Val Thr Pro	Val Ser Ser Ile Pro Val Glu Thr His Arg Ala	560	565	570
Leu Ala Ser Cys	His Ser Leu Met Gln Leu Asp Asp Gly Thr Leu	575	580	585
Val Gly Asp Pro	Leu Glu Lys Ala Met Leu Thr Ala Val Asp Trp	590	595	600
Thr Leu Thr Lys	Asp Glu Lys Val Phe Pro Arg Ser Ile Lys Thr	605	610	615
Gln Gly Leu Lys	Ile His Gln Arg Phe His Phe Ala Ser Ala Leu	620	625	630 ⁹
Lys Arg Met Ser	Val Leu Ala Ser Tyr Glu Lys Leu Gly Ser Thr	635	640	645
Asp Leu Cys Tyr	Ile Ala Ala Val Lys Gly Ala Pro Glu Thr Leu	650	655	660
His Ser Met Phe	Ser Gln Cys Pro Pro Asp Tyr His His Ile His	665	670	675
Thr Glu Ile Ser	Arg Glu Gly Ala Arg Val Leu Ala Leu Gly Tyr	680	685	690
Lys Glu Leu Gly	His Leu Thr His Gln Gln Val Val Met Ile Thr	695	700	705
Gly Asp Asn Pro	Leu Thr Ala Cys His Val Ala Gln Glu Leu His	710	715	720
Phe Ile Glu Lys	Ala His Thr Leu Ile Leu Gln Pro Pro Ser Glu	725	730	735
Lys Gly Arg Gln	Cys Glu Trp Arg Ser Ile Asp Gly Ser Ile Val	740	745	750
Leu Pro Leu Ala	Arg Gly Ser Pro Lys Ala Leu Ala Leu Glu Tyr	755	760	765
Ala Leu Cys Leu	Thr Gly Asp Gly Leu Ala His Leu Gln Ala Thr	770	775	780

```

Asp Pro Gln Gln Leu Leu Arg Leu Ile Pro His Val Gln Val Phe
      785                      790                      795
Ala Arg Val Ala Pro Lys Gln Lys Glu Phe Val Ile Thr Ser Leu
      800                      805                      810
Lys Glu Leu Gly Tyr Val Thr Leu Met Cys Gly Asp Gly Thr Asn
      815                      820                      825
Asp Val Gly Ala Leu Lys His Ala Asp Val Gly Val Ala Leu Leu
      830                      835                      840
Ala Asn Ala Pro Glu Arg Val Val Glu Arg Arg Arg Arg Pro Arg
      845                      850                      855
Asp Ser Pro Thr Leu Ser Asn Ser Gly Ile Arg Ala Thr Ser Arg
      860                      865                      870
Thr Ala Lys Gln Arg Ser Gly Leu Pro Pro Ser Glu Glu Gln Pro
      875                      880                      885
Thr Ser Gln Arg Asp Arg Leu Ser Gln Val Leu Arg Asp Leu Glu
      890                      895                      900
Asp Glu Ser Thr Pro Ile Val Lys Leu Gly Asp Ala Ser Ile Ala
      905                      910                      915
Ala Pro Phe Thr Ser Lys Leu Ser Ser Ile Gln Cys Ile Cys His
      920                      925                      930
Val Ile Lys Gln Gly Arg Cys Thr Leu Val Thr Thr Leu Gln Met
      935                      940                      945
Phe Lys Ile Leu Ala Leu Asn Ala Leu Ile Leu Ala Tyr Ser Gln
      950                      955                      960
Ser Val Leu Tyr Leu Glu Gly Val Lys Phe Ser Asp Phe Gln Ala
      965                      970                      975
Thr Leu Gln Gly Leu Leu Leu Ala Gly Cys Phe Leu Phe Ile Ser
      980                      985                      990
Arg Ser Lys Pro Leu Lys Thr Leu Ser Arg Glu Arg Pro Leu Pro
      995                      1000                     1005
Asn Ile Phe Asn Leu Tyr Thr Ile Leu Thr Val Met Leu Gln Phe
      1010                     1015                     1020
Phe Val His Phe Leu Ser Leu Val Tyr Leu Tyr Arg Glu Ala Gln
      1025                     1030                     1035
Ala Arg Ser Pro Glu Lys Gln Glu Gln Phe Val Asp Leu Tyr Lys
      1040                     1045                     1050
Glu Phe Glu Pro Ser Leu Val Asn Ser Thr Val Tyr Ile Met Ala
      1055                     1060                     1065
Met Ala Met Gln Met Ala Thr Phe Ala Ile Asn Tyr Lys Gly Pro
      1070                     1075                     1080
Pro Phe Met Glu Ser Leu Pro Glu Asn Lys Pro Leu Val Trp Ser
      1085                     1090                     1095
Leu Ala Val Ser Leu Leu Ala Ile Ile Gly Leu Leu Leu Gly Ser
      1100                     1105                     1110
Ser Pro Asp Phe Asn Ser Gln Phe Gly Leu Val Asp Ile Pro Val
      1115                     1120                     1125
Glu Val Leu Leu Leu Asp Phe Cys Leu Ala Leu Leu Ala Asp Arg
      1130                     1135                     1140
Val Leu Gln Phe Phe Leu Gly Thr Pro Lys Leu Lys Val Pro Ser
      1145                     1150                     1155

```

<210> 48

<211> 606

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7510661CD1

<400> 48

```

Met Ala Ala Ala Ala Ala Val Gly Asn Ala Val Pro Cys Gly Ala
  1              5              10              15
Arg Pro Cys Gly Val Arg Pro Asp Gly Gln Pro Lys Pro Gly Pro
      20              25              30
Gln Pro Arg Ala Leu Leu Ala Ala Gly Pro Ala Leu Ile Ala Asn
      35              40              45
Gly Asp Glu Leu Val Ala Ala Val Trp Pro Tyr Arg Arg Leu Ala
      50              55              60
Leu Leu Arg Arg Leu Thr Val Leu Pro Phe Ala Gly Leu Leu Tyr
      65              70              75
Pro Ala Trp Leu Gly Ala Ala Ala Ala Gly Cys Trp Gly Trp Gly
      80              85              90
Ser Ser Trp Val Gln Ile Pro Glu Ala Ala Leu Leu Val Leu Ala
      95              100             105
Thr Ile Cys Leu Ala His Ala Leu Thr Val Leu Ser Gly His Trp
      110             115             120
Ser Val His Ala His Cys Ala Leu Thr Cys Thr Pro Glu Tyr Asp
      125             130             135
Pro Ser Lys Ala Thr Phe Val Lys Val Val Pro Thr Pro Asn Asn
      140             145             150
Gly Ser Thr Glu Leu Val Ala Leu His Arg Asn Glu Gly Glu Asp
      155             160             165
Gly Leu Glu Val Leu Ser Phe Glu Phe Gln Lys Ile Lys Tyr Ser
      170             175             180
Tyr Asp Ala Leu Glu Lys Lys Gln Phe Leu Pro Val Ala Phe Pro
      185             190             195
Val Gly Asn Ala Phe Ser Tyr Tyr Gln Ser Asn Arg Gly Phe Gln
      200             205             210
Glu Asp Ser Glu Ile Arg Ala Ala Glu Lys Lys Phe Gly Ser Asn
      215             220             225
Lys Ala Glu Met Val Val Pro Asp Phe Ser Glu Leu Phe Lys Glu
      230             235             240
Arg Ala Thr Ala Pro Phe Phe Val Phe Gln Val Phe Cys Val Gly
      245             250             255
Leu Trp Cys Leu Asp Glu Tyr Trp Tyr Tyr Ser Val Phe Thr Leu
      260             265             270
Ser Met Leu Val Ala Phe Glu Ala Ser Leu Val Gln Gln Gln Met
      275             280             285
Arg Asn Met Ser Glu Ile Arg Lys Met Gly Asn Lys Pro His Met
      290             295             300
Ile Gln Val Tyr Arg Ser Arg Lys Trp Arg Pro Ile Ala Ser Asp
      305             310             315
Glu Ile Val Pro Gly Asp Ile Val Ser Ile Gly Arg Ser Pro Gln
      320             325             330
Glu Asn Leu Val Pro Cys Asp Val Leu Leu Leu Arg Gly Arg Cys
      335             340             345
Ile Val Asp Glu Ala Met Leu Thr Gly Glu Ser Val Pro Gln Met
      350             355             360
Lys Glu Pro Ile Glu Asp Leu Ser Pro Asp Arg Val Leu Asp Leu
      365             370             375
Gln Ala Asp Ser Arg Leu His Val Ile Phe Gly Gly Thr Lys Val

```


	380		385		390
Val Gln His Ile Pro Pro Gln Lys Ala Thr Thr Gly Leu Lys Pro					
	395		400		405
Val Asp Ser Gly Cys Val Ala Tyr Val Leu Arg Thr Gly Phe Asn					
	410		415		420
Thr Ser Gln Gly Lys Leu Leu Arg Thr Ile Leu Phe Gly Val Lys					
	425		430		435
Arg Val Thr Ala Asn Asn Leu Glu Thr Phe Ile Phe Ile Leu Phe					
	440		445		450
Leu Leu Val Phe Ala Ile Ala Ala Ala Ala Tyr Val Trp Ile Glu					
	455		460		465
Gly Thr Lys Asp Pro Ser Arg Asn Arg Tyr Lys Leu Phe Leu Glu					
	470		475		480
Cys Thr Leu Ile Leu Thr Ser Val Val Pro Pro Glu Leu Pro Ile					
	485		490		495
Glu Leu Ser Leu Ala Val Asn Thr Ser Leu Ile Ala Leu Ala Lys					
	500		505		510
Leu Tyr Met Tyr Cys Thr Glu Pro Phe Arg Ile Pro Phe Ala Gly					
	515		520		525
Lys Val Glu Val Cys Cys Phe Asp Lys Thr Gly Thr Leu Thr Ser					
	530		535		540
Asp Ser Leu Val Val Arg Gly Val Ala Gly Leu Arg Asp Gly Lys					
	545		550		555
Glu Val Thr Pro Val Ser Ser Ile Pro Val Glu Thr His Arg Ala					
	560		565		570
Leu Ala Ser Cys His Ser Leu Met Gln Leu Asp Asp Gly Thr Leu					
	575		580		585
Val Gly Asp Pro Leu Glu Lys Ala Met Leu Thr Ala Val Asp Trp					
	590		595		600
Thr Leu Thr Lys Val Pro					
	605				

<210> 49

<211> 462

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7510680CD1

<400> 49

Met Ala Thr Lys Pro Thr Glu Pro Val Thr Ile Leu Ser Leu Arg			
1	5	10	15
Lys Leu Ser Leu Gly Thr Ala Glu Pro Gln Val Lys Glu Pro Lys			
	20	25	30
Thr Phe Thr Val Glu Asp Ala Val Glu Thr Ile Gly Phe Gly Arg			
	35	40	45
Phe His Ile Ala Leu Phe Leu Ile Met Gly Ser Thr Gly Val Val			
	50	55	60
Glu Ala Met Glu Ile Met Leu Ile Ala Val Val Ser Pro Val Ile			
	65	70	75
Arg Cys Glu Trp Gln Leu Glu Asn Trp Gln Val Ala Leu Val Thr			
	80	85	90
Thr Met Val Phe Phe Gly Tyr Met Val Phe Ser Ile Leu Phe Gly			
	95	100	105

```

Leu Leu Ala Asp Arg Tyr Gly Arg Trp Lys Ile Leu Leu Ile Ser
110 115 120
Phe Leu Trp Gly Ala Tyr Phe Ser Leu Leu Thr Ser Phe Ala Pro
125 130 135
Ser Tyr Ile Trp Phe Val Phe Leu Arg Thr Met Val Gly Cys Gly
140 145 150
Val Ser Gly His Ser Gln Gly Leu Ile Ile Lys Thr Glu Phe Leu
155 160 165
Pro Thr Lys Tyr Arg Gly Tyr Met Leu Pro Leu Ser Gln Val Phe
170 175 180
Trp Leu Ala Gly Ser Leu Leu Ile Ile Gly Leu Ala Ser Val Ile
185 190 195
Ile Pro Thr Ile Gly Trp Arg Trp Leu Ile Arg Val Ala Ser Ile
200 205 210
Pro Gly Ile Ile Leu Ile Val Ala Phe Lys Phe Ile Pro Glu Ser
215 220 225
Ala Arg Phe Asn Val Ser Thr Gly Asn Thr Arg Ala Ala Leu Ala
230 235 240
Thr Leu Glu Arg Val Ala Lys Met Asn Arg Ser Val Met Pro Glu
245 250 255
Gly Lys Leu Val Glu Pro Val Leu Glu Lys Arg Gly Arg Phe Ala
260 265 270
Asp Leu Leu Asp Ala Lys Tyr Leu Arg Thr Thr Leu Gln Ile Trp
275 280 285
Val Ile Trp Leu Gly Ile Ser Phe Ala Tyr Tyr Gly Val Ile Leu
290 295 300
Ala Ser Ala Glu Leu Leu Glu Arg Asp Leu Val Cys Gly Ser Lys
305 310 315
Ser Asp Ser Ala Val Val Val Thr Gly Gly Asp Ser Gly Glu Ser
320 325 330
Gln Ser Pro Cys Tyr Cys His Met Phe Ala Pro Ser Asp Tyr Arg
335 340 345
Thr Met Ile Ile Ser Thr Ile Gly Glu Ile Ala Leu Asn Pro Leu
350 355 360
Asn Ile Leu Gly Ile Asn Phe Leu Gly Arg Arg Leu Ser Leu Ser
365 370 375
Ile Thr Met Gly Cys Thr Ala Leu Phe Phe Leu Leu Leu Asn Ile
380 385 390
Cys Thr Ser Ser Ala Gly Leu Ile Gly Phe Leu Phe Met Leu Arg
395 400 405
Ala Leu Val Ala Ala Asn Phe Asn Thr Val Tyr Ile Tyr Thr Ala
410 415 420
Glu Val Leu Met Ser Ala Ser Ile Leu Gly Ala Leu Cys Leu Phe
425 430 435
Ser Ser Val Cys Val Val Cys Ala Ile Ser Ala Phe Thr Leu Pro
440 445 450
Ile Glu Thr Lys Gly Arg Ala Leu Gln Gln Ile Lys
455 460

```

<210> 50

<211> 366

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7505145CD1

<400> 50

```

Met Gly Trp Gly Gly Gly Gly Gly Cys Thr Pro Arg Pro Pro Ile
 1          5          10          15
His Gln Gln Pro Pro Glu Arg Arg Val Val Thr Val Val Phe Leu
 20          25          30
Gly Leu Leu Leu Asp Leu Leu Ala Phe Thr Leu Leu Leu Pro Leu
 35          40          45
Leu Pro Gly Leu Leu Glu Ser His Gly Arg Ala His Asp Pro Leu
 50          55          60
Tyr Gly Ser Trp Gln Gly Gly Val Asp Trp Phe Ala Thr Ala Ile
 65          70          75
Gly Met Pro Val Glu Lys Arg Tyr Asn Ser Val Leu Phe Gly Gly
 80          85          90
Leu Ile Gly Ser Ala Phe Ser Val Leu Gln Phe Leu Cys Ala Pro
 95          100          105
Leu Thr Gly Ala Thr Ser Asp Cys Leu Gly Arg Arg Pro Val Met
 110          115          120
Leu Leu Cys Leu Met Gly Val Ala Thr Ser Tyr Ala Val Trp Ala
 125          130          135
Thr Ser Arg Ser Phe Ala Ala Phe Leu Ala Ser Arg Leu Ile Gly
 140          145          150
Gly Ile Ser Lys Gly Asn Val Ser Leu Ser Thr Ala Ile Val Ala
 155          160          165
Asp Leu Gly Ser Pro Leu Ala Arg Ser Gln Gly Met Ala Val Ile
 170          175          180
Gly Val Ala Phe Ser Leu Gly Phe Thr Leu Gly Pro Met Leu Gly
 185          190          195
Ala Ser Leu Pro Leu Glu Met Ala Pro Trp Phe Ala Leu Leu Phe
 200          205          210
Ala Ala Ser Asp Leu Leu Phe Ile Phe Cys Phe Leu Pro Glu Thr
 215          220          225
Leu Pro Leu Glu Lys Arg Ala Pro Ser Ile Ala Leu Gly Phe Arg
 230          235          240
Asp Ala Ala Asp Leu Leu Ser Pro Leu Ala Leu Leu Arg Phe Ser
 245          250          255
Ala Val Ala Arg Gly Gln Asp Pro Pro Ser Gly Asp Arg Leu Ser
 260          265          270
Ser Leu Arg Arg Leu Gly Leu Val Tyr Phe Leu Tyr Leu Phe Leu
 275          280          285
Phe Ser Gly Leu Glu Tyr Thr Leu Ser Phe Leu Thr His Gln Arg
 290          295          300
Phe Gln Phe Ser Arg Pro Ser Cys Cys Trp Cys Pro Pro Ser Ser
 305          310          315
Ser Ser Ala Gly Asp Val Leu Cys Pro Cys Trp Ala Trp Gly Cys
 320          325          330
Cys Ser Thr Pro Leu Pro Pro Pro Leu Trp Cys Pro Ala Cys Pro
 335          340          345
Pro Trp Ser Leu Ala Met Ala His Gln Gly Arg Arg Ala Arg Ser
 350          355          360
Trp Val His Cys Ala Ala
 365

```

<210> 51

<211> 295

<212> PRT

<213> Homo sapiens

<220>

```
<221> misc_feature
```

<223> Incyte ID No: 7505162CD1

<400> 51

Met	Ala	Ala	Gln	Gly	Tyr	Gly	Tyr	Tyr	Arg	Thr	Val	Ile	Phe	Ser
1				5					10					15
Ala	Met	Phe	Gly	Gly	Tyr	Ser	Leu	Tyr	Tyr	Phe	Asn	Arg	Lys	Thr
				20					25					30
Phe	Ser	Phe	Val	Met	Pro	Ser	Leu	Val	Glu	Glu	Ile	Pro	Leu	Asp
				35					40					45
Lys	Asp	Asp	Leu	Gly	Phe	Ile	Thr	Ser	Ser	Gln	Ser	Ala	Ala	Tyr
				50					55					60
Ala	Ile	Ser	Lys	Phe	Val	Ser	Gly	Val	Leu	Ser	Asp	Gln	Met	Ser
				65					70					75
Ala	Arg	Trp	Leu	Phe	Ser	Ser	Gly	Leu	Leu	Leu	Val	Gly	Leu	Val
				80					85					90
Asn	Ile	Phe	Phe	Ala	Trp	Ser	Ser	Thr	Val	Pro	Val	Phe	Ala	Ala
				95					100					105
Leu	Trp	Phe	Leu	Asn	Gly	Leu	Ala	Gln	Gly	Leu	Gly	Trp	Pro	Pro
				110					115					120
Cys	Gly	Lys	Val	Leu	Arg	Lys	Trp	Phe	Glu	Pro	Ser	Gln	Phe	Gly
				125					130					135
Thr	Trp	Trp	Ala	Ile	Leu	Ser	Thr	Ser	Met	Asn	Leu	Ala	Gly	Gly
				140					145					150
Leu	Gly	Pro	Ile	Leu	Ala	Thr	Ile	Leu	Ala	Gln	Ser	Tyr	Ser	Trp
				155					160					165
Arg	Ser	Thr	Leu	Ala	Leu	Ser	Gly	Ala	Leu	Cys	Val	Val	Val	Ser
				170					175					180
Phe	Leu	Cys	Leu	Leu	Leu	Ile	His	Asn	Glu	Pro	Ala	Asp	Val	Gly
				185					190					195
Leu	Arg	Asn	Leu	Asp	Pro	Met	Pro	Ser	Glu	Gly	Lys	Lys	Gly	Ser
				200					205					210
Leu	Lys	Glu	Glu	Ser	Thr	Leu	Gln	Glu	Leu	Leu	Leu	Ser	Pro	Tyr
				215					220					225
Leu	Trp	Val	Leu	Ser	Thr	Gly	Tyr	Leu	Val	Val	Phe	Gly	Val	Lys
				230					235					240
Thr	Cys	Cys	Thr	Asp	Trp	Gly	Gln	Phe	Phe	Leu	Ile	Gln	Glu	Lys
				245					250					255
Gly	Gln	Ser	Ala	Leu	Val	Gly	Gly	Thr	Val	Gln	Leu	Arg	Glu	Pro
				260					265					270
Ser	Pro	Trp	Pro	Val	Ala	Val	His	Asp	Gly	Trp	His	Asp	Ser	Val
				275					280					285
His	Val	Pro	Leu	Pro	Gly	Asn	Ser	Asp	Gln					
				290					295					

<210> 52

<211> 229

<212> PRT

<213> Homo sapiens

<220>

```
<221> misc_feature
```

<223> Incyte ID No: 7505469CD1

<400> 52

Met	Glu	Ala	Arg	Glu	Pro	Gly	Arg	Pro	Thr	Pro	Thr	Tyr	His	Leu
1				5					10					15
Val	Pro	Asn	Thr	Ser	Gln	Ser	Gln	Val	Glu	Glu	Asp	Val	Ser	Ser
				20					25					30
Pro	Pro	Gln	Arg	Ser	Ser	Glu	Thr	Met	Gln	Leu	Lys	Lys	Glu	Ile
				35					40					45
Ser	Leu	Leu	Asn	Gly	Val	Ser	Leu	Val	Val	Gly	Asn	Met	Ile	Gly
				50					55					60
Ser	Gly	Ile	Phe	Val	Ser	Pro	Lys	Gly	Val	Leu	Val	His	Thr	Ala
				65					70					75
Ser	Tyr	Gly	Met	Ser	Leu	Ile	Val	Trp	Ala	Ile	Gly	Gly	Leu	Phe
				80					85					90
Ser	Val	Val	Gly	Ala	Leu	Cys	Tyr	Ala	Glu	Leu	Gly	Thr	Thr	Ile
				95					100					105
Thr	Lys	Ser	Gly	Ala	Ser	Tyr	Ala	Tyr	Ile	Leu	Glu	Ala	Phe	Gly
				110					115					120
Gly	Phe	Ile	Ala	Phe	Ile	Arg	Leu	Trp	Val	Ser	Leu	Leu	Val	Val
				125					130					135
Glu	Pro	Thr	Gly	Gln	Ala	Ile	Ile	Ala	Ile	Thr	Phe	Ala	Asn	Tyr
				140					145					150
Ile	Ile	Gln	Pro	Ser	Phe	Pro	Ser	Cys	Asp	Pro	Pro	Tyr	Leu	Ala
				155					160					165
Cys	Arg	Leu	Leu	Ala	Ala	Cys	Ile	Cys	Leu	Leu	Thr	Phe	Val	
				170					175					180
Asn	Cys	Ala	Tyr	Val	Lys	Trp	Gly	Thr	Arg	Val	Gln	Asp	Thr	Phe
				185					190					195
Thr	Tyr	Ala	Lys	Val	Val	Ala	Leu	Ile	Ala	Ile	Ile	Val	Met	Gly
				200					205					210
Leu	Val	Lys	Leu	Cys	Gln	Glu	Ile	Cys	Pro	Trp	Pro	Leu	Gly	Phe
				215					220					225
Leu	Cys	Gln	Leu											

<210> 53

<211> 637

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7505475CD1

<400> 53

Met	Asn	Met	Lys	Gln	Lys	Ser	Val	Tyr	Gln	Gln	Thr	Lys	Ala	Leu
1				5					10					15
Leu	Cys	Lys	Asn	Phe	Leu	Lys	Lys	Trp	Arg	Met	Lys	Arg	Glu	Ser
				20					25					30
Leu	Leu	Glu	Trp	Gly	Leu	Ser	Ile	Leu	Leu	Gly	Leu	Cys	Ile	Ala
				35					40					45
Leu	Phe	Ser	Ser	Ser	Met	Arg	Asn	Val	Gln	Phe	Pro	Gly	Met	Ala
				50					55					60
Pro	Gln	Asn	Leu	Gly	Arg	Val	Asp	Lys	Phe	Asn	Ser	Ser	Ser	Leu
				65					70					75

Met	Val	Val	Tyr	Thr	Pro	Ile	Ser	Asn	Leu	Thr	Gln	Gln	Ile	Met	80	85	90
Asn	Lys	Thr	Ala	Leu	Ala	Pro	Leu	Leu	Lys	Gly	Thr	Ser	Val	Ile	95	100	105
Gly	Ala	Pro	Asn	Lys	Thr	His	Met	Asp	Glu	Ile	Leu	Leu	Glu	Asn	110	115	120
Leu	Pro	Tyr	Ala	Met	Gly	Ile	Ile	Phe	Asn	Glu	Thr	Phe	Ser	Tyr	125	130	135
Lys	Leu	Ile	Phe	Phe	Gln	Gly	Tyr	Asn	Ser	Pro	Leu	Trp	Lys	Glu	140	145	150
Asp	Phe	Ser	Ala	His	Cys	Trp	Asp	Gly	Tyr	Gly	Glu	Phe	Ser	Cys	155	160	165
Thr	Leu	Thr	Lys	Tyr	Trp	Asn	Arg	Gly	Phe	Val	Ala	Leu	Gln	Thr	170	175	180
Ala	Ile	Asn	Thr	Ala	Ile	Ile	Glu	Ile	Thr	Thr	Asn	His	Pro	Val	185	190	195
Met	Glu	Glu	Leu	Met	Ser	Val	Thr	Ala	Ile	Thr	Met	Lys	Thr	Leu	200	205	210
Pro	Phe	Ile	Thr	Lys	Asn	Leu	Leu	His	Asn	Glu	Met	Phe	Ile	Leu	215	220	225
Phe	Phe	Leu	Leu	His	Phe	Ser	Pro	Leu	Val	Tyr	Phe	Ile	Ser	Leu	230	235	240
Asn	Val	Thr	Lys	Glu	Arg	Lys	Lys	Ser	Lys	Asn	Leu	Met	Lys	Met	245	250	255
Met	Gly	Leu	Gln	Asp	Ser	Ala	Phe	Trp	Leu	Ser	Trp	Gly	Leu	Ile	260	265	270
Tyr	Ala	Gly	Phe	Ile	Phe	Ile	Ile	Ser	Ile	Phe	Ile	Thr	Ile	Ile	275	280	285
Ile	Thr	Phe	Thr	Gln	Ile	Ile	Val	Met	Thr	Gly	Phe	Met	Val	Ile	290	295	300
Phe	Ile	Pro	Phe	Phe	Leu	Tyr	Gly	Leu	Ser	Leu	Val	Ala	Leu	Val	305	310	315
Phe	Leu	Leu	Ser	Val	Leu	Leu	Lys	Lys	Ala	Val	Leu	Thr	Asn	Leu	320	325	330
Val	Val	Phe	Leu	Leu	Thr	Leu	Phe	Trp	Gly	Cys	Leu	Gly	Phe	Thr	335	340	345
Val	Phe	Tyr	Glu	Gln	Leu	Pro	Ser	Ser	Leu	Glu	Trp	Ile	Leu	Asn	350	355	360
Ile	Cys	Ser	Pro	Phe	Ala	Phe	Thr	Thr	Gly	Met	Ile	Gln	Ile	Ile	365	370	375
Lys	Leu	Asp	Tyr	Asn	Leu	Asn	Gly	Val	Ile	Phe	Pro	Asp	Pro	Ser	380	385	390
Gly	Asp	Ser	Tyr	Thr	Met	Ile	Ala	Thr	Phe	Ser	Met	Leu	Leu	Leu	395	400	405
Asp	Gly	Leu	Ile	Tyr	Leu	Leu	Leu	Ala	Leu	Tyr	Phe	Asp	Lys	Ile	410	415	420
Leu	Pro	Tyr	Gly	Asp	Glu	Arg	His	Tyr	Ser	Pro	Leu	Phe	Phe	Leu	425	430	435
Asn	Ser	Ser	Ser	Cys	Phe	Gln	His	Gln	Arg	Thr	Asn	Ala	Lys	Val	440	445	450
Ile	Glu	Lys	Glu	Ile	Asp	Ala	Glu	His	Pro	Ser	Asp	Asp	Tyr	Phe	455	460	465
Glu	Pro	Val	Ala	Pro	Glu	Phe	Gln	Gly	Lys	Glu	Ala	Ile	Arg	Ile	470	475	480
Arg	Asn	Val	Lys	Lys	Glu	Tyr	Lys	Gly	Lys	Ser	Gly	Lys	Val	Glu	485	490	495

Ala	Leu	Lys	Gly	Leu	Leu	Phe	Asp	Ile	Tyr	Glu	Gly	Gln	Ile	Thr
				500					505					510
Ala	Ile	Leu	Gly	His	Ser	Gly	Ala	Gly	Lys	Ser	Ser	Leu	Leu	Asn
				515					520					525
Ile	Leu	Asn	Gly	Leu	Ser	Val	Pro	Thr	Glu	Gly	Ser	Val	Thr	Ile
				530					535					540
Tyr	Asn	Lys	Asn	Leu	Ser	Glu	Met	Gln	Asp	Leu	Glu	Glu	Ile	Arg
				545					550					555
Lys	Ile	Thr	Gly	Val	Cys	Pro	Gln	Phe	Asn	Val	Gln	Phe	Asp	Ile
				560					565					570
Leu	Thr	Val	Lys	Glu	Asn	Leu	Ser	Leu	Phe	Ala	Lys	Ile	Lys	Gly
				575					580					585
Ile	His	Leu	Lys	Glu	Val	Glu	Gln	Glu	Val	Gln	Arg	Ile	Leu	Leu
				590					595					600
Glu	Leu	Asp	Met	Gln	Asn	Ile	Gln	Asp	Asn	Leu	Ala	Lys	His	Leu
				605					610					615
Ser	Glu	Gly	Gln	Lys	Arg	Lys	Leu	Thr	Phe	Gly	Ile	Thr	Ile	Leu
				620					625					630
Gly	Asp	Pro	Gln	Ile	Glu	Lys								
				635										

<210> 54

<211> 90

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7505568CD1

<400> 54

Met	Ala	Arg	Lys	Gln	Asn	Arg	Asn	Ser	Lys	Glu	Leu	Gly	Leu	Val
1				5					10					15
Pro	Leu	Thr	Asp	Asp	Thr	Ser	His	Ala	Gly	Pro	Pro	Gly	Pro	Gly
				20					25					30
Arg	Ala	Leu	Leu	Glu	Cys	Asp	His	Leu	Arg	Ser	Gly	Val	Pro	Gly
				35					40					45
Gly	Arg	Arg	Arg	Lys	Asp	Trp	Ser	Cys	Ser	Leu	Leu	Val	Ala	Ser
				50					55					60
Leu	Ala	Gly	Ala	Phe	Gly	Ser	Ser	Phe	Leu	Tyr	Gly	Tyr	Asn	Leu
				65					70					75
Ser	Val	Val	Asn	Ala	Pro	Thr	Pro	Glu	Ala	His	Phe	Ala	Gly	Gln
				80					85					90

<210> 55

<211> 327

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7506953CD1

<400> 55

Met Lys Thr Lys Leu Asn Ile Tyr Asn Met Gln Phe Leu Leu Phe

1	5	10	15
Val Phe Leu Val Trp Asp Pro Ala Arg Leu Val Leu Ala Asn Ile			
	20	25	30
Gln Glu Asp Glu Ala Lys Asn Asn Ile Thr Ile Phe Thr Arg Ile			
	35	40	45
Leu Asp Arg Leu Leu Asp Gly Tyr Asp Asn Arg Leu Arg Pro Gly			
	50	55	60
Leu Gly Asp Ala Tyr Thr Thr Ser Glu Val Thr Tyr Ile Trp Thr			
	65	70	75
Tyr Asn Ala Ser Asp Ser Val Gln Val Ala Pro Asp Gly Ser Arg			
	80	85	90
Leu Asn Gln Tyr Asp Leu Leu Gly Gln Ser Ile Gly Lys Glu Thr			
	95	100	105
Ile Lys Ser Ser Thr Gly Glu Tyr Thr Val Met Thr Ala His Phe			
	110	115	120
His Leu Lys Arg Lys Ile Gly Tyr Phe Val Ile Gln Thr Tyr Leu			
	125	130	135
Pro Cys Ile Met Thr Val Ile Leu Ser Gln Val Ser Phe Trp Leu			
	140	145	150
Asn Arg Glu Ser Val Pro Ala Arg Thr Val Phe Gly Val Thr Thr			
	155	160	165
Val Leu Thr Met Thr Thr Leu Ser Ile Ser Ala Arg Asn Ser Leu			
	170	175	180
Pro Lys Val Ala Tyr Ala Thr Ala Met Asp Trp Phe Ile Ala Val			
	185	190	195
Cys Tyr Ala Phe Val Phe Ser Ala Leu Ile Glu Phe Ala Thr Val			
	200	205	210
Asn Tyr Phe Thr Lys Arg Gly Trp Ala Trp Asp Gly Lys Ser Val			
	215	220	225
Val Asn Asp Lys Lys Lys Glu Lys Ala Ser Val Met Ile Gln Asn			
	230	235	240
Asn Ala Tyr Ala Val Ala Val Ala Asn Tyr Ala Pro Asn Leu Ser			
	245	250	255
Lys Asp Pro Val Leu Ser Thr Ile Ser Lys Ser Ala Thr Thr Pro			
	260	265	270
Glu Pro Asn Lys Lys Pro Glu Asn Lys Pro Ala Glu Ala Lys Lys			
	275	280	285
Thr Phe Asn Ser Val Ser Lys Ile Asp Arg Met Ser Arg Ile Val			
	290	295	300
Phe Pro Val Leu Phe Gly Thr Phe Asn Leu Val Tyr Trp Ala Thr			
	305	310	315
Tyr Leu Asn Arg Glu Pro Val Leu Gly Val Ser Pro			
	320	325	

<210> 56

<211> 40

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7510176CD1

<400> 56

Met Lys Phe Phe Ser Tyr Ile Leu Val Tyr Arg Arg Phe Leu Phe			
1	5	10	15

Val Val Phe Thr Val Leu Val Leu Leu Pro Leu Pro Ile Val Leu
 20 25 30
 His Thr Lys Leu Ile Leu Thr Phe Pro Arg
 35 40

<210> 57
 <211> 104
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 7510541CD1

<400> 57
 Met Glu Ala Pro Leu Gln Thr Glu Met Val Glu Leu Val Pro Asn
 1 5 10 15
 Gly Lys His Ser Glu Gly Leu Leu Pro Val Ile Thr Pro Met Ala
 20 25 30
 Gly Asn Gln Arg Val Glu Asp Pro Ala Arg Ser Cys Met Glu Gly
 35 40 45
 Lys Ser Phe Leu Gln Lys Ser Pro Ser Lys Glu Pro His Phe Thr
 50 55 60
 Asp Phe Glu Gly Lys Thr Ser Phe Gly Met Ser Val Phe Asn Leu
 65 70 75
 Ser Asn Ala Ile Met Gly Ser Gly Ile Leu Gly Leu Ala Tyr Ala
 80 85 90
 Met Ala Asn Thr Gly Ile Ile Leu Phe Leu His Pro Cys Leu
 95 100

<210> 58
 <211> 296
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 7510923CD1

<400> 58
 Met Glu Ala Pro Leu Gln Thr Glu Met Val Glu Leu Val Pro Asn
 1 5 10 15
 Gly Lys His Ser Glu Gly Leu Leu Pro Val Ile Thr Pro Met Ala
 20 25 30
 Gly Asn Gln Arg Val Glu Asp Pro Ala Arg Ser Cys Met Glu Gly
 35 40 45
 Lys Ser Phe Leu Gln Lys Ser Pro Ser Lys Glu Pro His Phe Thr
 50 55 60
 Asp Phe Glu Gly Lys Thr Ser Phe Gly Met Ser Val Phe Asn Leu
 65 70 75
 Ser Asn Ala Ile Met Gly Ser Gly Ile Leu Gly Leu Ala Tyr Ala
 80 85 90
 Met Ala Asn Thr Gly Ile Ile Leu Phe Leu Phe Leu Leu Thr Ala
 95 100 105
 Val Ala Leu Leu Ser Ser Tyr Ser Ile His Leu Leu Leu Lys Ser
 110 115 120

```

Ser Gly Val Val Gly Ile Arg Ala Tyr Glu Gln Leu Gly Tyr Arg
      125                      130                      135
Ala Phe Gly Thr Pro Gly Lys Leu Ala Ala Ala Leu Ala Ile Thr
      140                      145                      150
Leu Gln Asn Ile Gly Ala Met Ser Ser Tyr Leu Tyr Ile Ile Lys
      155                      160                      165
Ser Glu Leu Pro Leu Val Ile Gln Thr Phe Leu Asn Leu Glu Glu
      170                      175                      180
Lys Thr Ser Asp Trp Tyr Met Asn Gly Asn Tyr Leu Val Ile Leu
      185                      190                      195
Val Ser Val Thr Ile Ile Leu Pro Leu Ala Leu Met Arg Gln Leu
      200                      205                      210
Gly Tyr Leu Gly Tyr Ser Ser Gly Phe Ser Leu Ser Cys Met Val
      215                      220                      225
Phe Phe Leu Ile Ala Val Ile Tyr Lys Lys Phe His Val Pro Cys
      230                      235                      240
Pro Leu Pro Pro Asn Phe Asn Asn Thr Thr Gly Asn Phe Ser His
      245                      250                      255
Val Glu Ile Val Lys Glu Lys Val Gln Leu Gln Val Glu Pro Glu
      260                      265                      270
Ala Ser Ala Phe Cys Thr Pro Ser Tyr Phe Thr Leu Asn Ser Gln
      275                      280                      285
Val Leu Thr Gly Gln Gly Lys Ala Gly Ala Gln
      290                      295

```

<210> 59

<211> 1364

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7510984CD1

<400> 59

```

Met Pro Leu Ala Phe Cys Gly Ser Glu Asn His Ser Ala Ala Tyr
  1                      5                      10                      15
Arg Val Asp Gln Gly Val Leu Asn Asn Gly Cys Phe Val Asp Ala
      20                      25                      30
Leu Asn Val Val Pro His Val Phe Leu Leu Phe Ile Thr Phe Pro
      35                      40                      45
Ile Leu Phe Ile Gly Trp Gly Ser Gln Ser Ser Lys Val His Ile
      50                      55                      60
His His Ser Thr Trp Leu His Phe Pro Gly His Asn Leu Arg Trp
      65                      70                      75
Ile Leu Thr Phe Met Leu Leu Phe Val Leu Val Cys Glu Ile Ala
      80                      85                      90
Glu Gly Ile Leu Ser Asp Gly Val Thr Glu Ser His His Leu His
      95                      100                      105
Leu Tyr Met Pro Ala Gly Met Ala Phe Met Ala Ala Val Ala Ser
      110                      115                      120
Val Val Tyr Tyr His Asn Ile Glu Thr Ser Asn Phe Pro Lys Leu
      125                      130                      135
Leu Ile Ala Leu Leu Val Tyr Trp Thr Leu Ala Phe Ile Thr Lys
      140                      145                      150
Thr Ile Lys Phe Val Lys Phe Leu Asp His Ala Ile Gly Phe Ser

```

	155	160	165
Gln Leu Arg Phe Cys Leu Thr Gly Leu Leu Val Ile Leu Tyr Gly			
	170	175	180
Met Leu Leu Leu Val Glu Val Asn Val Ile Arg Val Arg Arg Tyr			
	185	190	195
Ile Phe Phe Lys Thr Pro Arg Glu Val Lys Pro Pro Glu Asp Leu			
	200	205	210
Gln Asp Leu Gly Val Arg Phe Leu Gln Pro Phe Val Asn Leu Leu			
	215	220	225
Ser Lys Gly Thr Tyr Trp Trp Met Asn Ala Phe Ile Lys Thr Ala			
	230	235	240
His Lys Lys Pro Ile Asp Leu Arg Ala Ile Gly Lys Leu Pro Ile			
	245	250	255
Ala Met Arg Ala Leu Thr Asn Tyr Gln Arg Leu Cys Glu Ala Phe			
	260	265	270
Asp Ala Gln Val Arg Lys Asp Ile Gln Gly Thr Gln Gly Ala Arg			
	275	280	285
Ala Ile Trp Gln Ala Leu Ser His Ala Phe Gly Arg Arg Leu Val			
	290	295	300
Leu Ser Ser Thr Phe Arg Ile Leu Ala Asp Leu Leu Gly Phe Ala			
	305	310	315
Gly Pro Leu Cys Ile Phe Gly Ile Val Asp His Leu Gly Lys Glu			
	320	325	330
Asn Asp Val Phe Gln Pro Lys Thr Gln Phe Leu Gly Val Tyr Phe			
	335	340	345
Val Ser Ser Gln Glu Phe Leu Ala Asn Ala Tyr Val Leu Ala Val			
	350	355	360
Leu Leu Phe Leu Ala Leu Leu Leu Gln Arg Thr Phe Leu Gln Ala			
	365	370	375
Ser Tyr Tyr Val Ala Ile Glu Thr Gly Ile Asn Leu Arg Gly Ala			
	380	385	390
Ile Gln Thr Lys Ile Tyr Asn Lys Ile Met His Leu Ser Thr Ser			
	395	400	405
Asn Leu Ser Met Gly Glu Met Thr Ala Gly Gln Ile Cys Asn Leu			
	410	415	420
Val Ala Ile Asp Thr Asn Gln Leu Met Trp Phe Phe Phe Leu Cys			
	425	430	435
Pro Asn Leu Trp Ala Met Pro Val Gln Ile Ile Val Gly Val Ile			
	440	445	450
Leu Leu Tyr Tyr Ile Leu Gly Val Ser Ala Leu Ile Gly Ala Ala			
	455	460	465
Val Ile Ile Leu Leu Ala Pro Val Gln Tyr Phe Val Ala Thr Lys			
	470	475	480
Leu Ser Gln Ala Gln Arg Ser Thr Leu Glu Tyr Ser Asn Glu Arg			
	485	490	495
Leu Lys Gln Thr Asn Glu Met Leu Arg Gly Ile Lys Leu Leu Lys			
	500	505	510
Leu Tyr Ala Trp Glu Asn Ile Phe Arg Thr Arg Val Glu Thr Thr			
	515	520	525
Arg Arg Lys Glu Met Thr Ser Leu Arg Ala Phe Ala Ile Tyr Thr			
	530	535	540
Ser Ile Ser Ile Phe Met Asn Thr Ala Ile Pro Ile Ala Ala Val			
	545	550	555
Leu Ile Thr Phe Val Gly His Val Ser Phe Phe Lys Glu Ala Asp			
	560	565	570
Phe Ser Pro Ser Val Ala Phe Ala Ser Leu Ser Leu Phe His Ile			

575	580	585
Leu Val Thr Pro Leu Phe Leu Leu Ser	Ser Val Val Arg Ser Thr	
590	595	600
Val Lys Ala Leu Val Ser Val Gln Lys	Leu Ser Glu Phe Leu Ser	
605	610	615
Ser Ala Glu Ile Arg Glu Glu Gln Cys	Ala Pro His Glu Pro Thr	
620	625	630
Pro Gln Gly Pro Ala Ser Lys Tyr Gln	Ala Val Pro Leu Arg Val	
635	640	645
Val Asn Arg Lys Arg Pro Ala Arg Glu	Asp Cys Arg Gly Leu Thr	
650	655	660
Gly Pro Leu Gln Ser Leu Val Pro Ser	Ala Asp Gly Asp Ala Asp	
665	670	675
Asn Cys Cys Val Gln Ile Met Gly Gly	Tyr Phe Thr Trp Thr Pro	
680	685	690
Asp Gly Ile Pro Thr Leu Ser Asn Ile	Thr Ile Arg Ile Pro Arg	
695	700	705
Gly Gln Leu Thr Met Ile Val Gly Gln	Val Gly Cys Gly Lys Ser	
710	715	720
Ser Leu Leu Leu Ala Ala Leu Gly Glu	Met Gln Lys Val Ser Gly	
725	730	735
Ala Val Phe Trp Ser Ser Ser Leu Pro	Asp Ser Glu Ile Gly Glu	
740	745	750
Asp Pro Ser Pro Glu Arg Glu Thr Ala	Thr Asp Leu Asp Ile Arg	
755	760	765
Lys Arg Gly Pro Val Ala Tyr Ala Ser	Gln Lys Pro Trp Leu Leu	
770	775	780
Asn Ala Thr Val Glu Glu Asn Ile Ile	Phe Glu Ser Pro Phe Asn	
785	790	795
Lys Gln Arg Tyr Lys Met Val Ile Glu	Ala Cys Ser Leu Gln Pro	
800	805	810
Asp Ile Asp Ile Leu Pro His Gly Asp	Gln Thr Gln Ile Gly Glu	
815	820	825
Arg Gly Ile Asn Leu Ser Gly Gly Gln	Arg Gln Arg Ile Ser Val	
830	835	840
Ala Arg Ala Leu Tyr Gln His Ala Asn	Val Val Phe Leu Asp Asp	
845	850	855
Pro Phe Ser Ala Leu Asp Ile His Leu	Ser Asp His Leu Met Gln	
860	865	870
Ala Gly Ile Leu Glu Leu Leu Arg Asp	Asp Lys Arg Thr Val Val	
875	880	885
Leu Val Thr His Lys Leu Gln Tyr Leu	Pro His Ala Asp Trp Ile	
890	895	900
Ile Ala Met Lys Asp Gly Thr Ile Gln	Arg Glu Gly Thr Leu Lys	
905	910	915
Asp Phe Gln Arg Ser Glu Cys Gln Leu	Phe Glu His Trp Lys Thr	
920	925	930
Leu Met Asn Arg Gln Asp Gln Glu Leu	Glu Lys Glu Thr Val Thr	
935	940	945
Glu Arg Lys Ala Thr Glu Pro Pro Gln	Gly Leu Ser Arg Ala Met	
950	955	960
Ser Ser Arg Asp Gly Leu Leu Gln Asp	Glu Glu Glu Glu Glu Glu	
965	970	975
Glu Ala Ala Glu Ser Glu Glu Asp Asp	Asn Leu Ser Ser Met Leu	
980	985	990
His Gln Arg Ala Glu Ile Pro Trp Arg	Ala Cys Ala Lys Tyr Leu	

995	1000	1005
Ser Ser Ala Gly Ile Leu Leu Leu Ser Leu Leu Val Phe Ser Gln		
1010	1015	1020
Leu Leu Lys His Met Val Leu Val Ala Ile Asp Tyr Trp Leu Ala		
1025	1030	1035
Lys Trp Thr Asp Ser Ala Leu Thr Leu Thr Pro Ala Ala Arg Asn		
1040	1045	1050
Cys Ser Leu Ser Gln Glu Cys Thr Leu Asp Gln Thr Val Tyr Ala		
1055	1060	1065
Met Val Phe Thr Val Leu Cys Ser Leu Gly Ile Val Leu Cys Leu		
1070	1075	1080
Val Thr Ser Val Thr Val Glu Trp Thr Gly Leu Lys Val Ala Lys		
1085	1090	1095
Arg Leu His Arg Ser Leu Leu Asn Arg Ile Ile Leu Ala Pro Met		
1100	1105	1110
Arg Phe Phe Glu Thr Thr Pro Leu Gly Ser Ile Leu Asn Arg Phe		
1115	1120	1125
Ser Ser Asp Cys Asn Thr Ile Asp Gln His Ile Pro Ser Thr Leu		
1130	1135	1140
Glu Cys Leu Ser Arg Ser Thr Leu Leu Cys Val Ser Ala Leu Ala		
1145	1150	1155
Val Ile Ser Tyr Val Thr Pro Val Phe Leu Val Ala Leu Leu Pro		
1160	1165	1170
Leu Ala Ile Val Cys Tyr Phe Ile Gln Lys Tyr Phe Arg Val Ala		
1175	1180	1185
Ser Arg Asp Leu Gln Gln Leu Asp Asp Thr Thr Gln Leu Pro Leu		
1190	1195	1200
Leu Ser His Phe Ala Glu Thr Val Glu Gly Leu Thr Thr Ile Arg		
1205	1210	1215
Ala Phe Arg Tyr Glu Ala Arg Phe Gln Gln Lys Leu Leu Glu Tyr		
1220	1225	1230
Thr Asp Ser Asn Asn Ile Ala Ser Leu Phe Leu Thr Ala Ala Asn		
1235	1240	1245
Arg Trp Leu Glu Val Arg Met Glu Tyr Ile Gly Ala Cys Val Val		
1250	1255	1260
Leu Ile Ala Ala Val Thr Ser Ile Ser Asn Ser Leu His Arg Glu		
1265	1270	1275
Leu Ser Ala Gly Leu Val Gly Leu Gly Leu Thr Tyr Ala Leu Met		
1280	1285	1290
Val Ser Asn Tyr Leu Asn Trp Met Val Arg Asn Leu Ala Asp Met		
1295	1300	1305
Glu Leu Gln Leu Gly Ala Val Lys Arg Ile His Gly Leu Leu Lys		
1310	1315	1320
Thr Glu Ala Glu Ser Tyr Glu Gly Leu Leu Gly Glu Arg Leu Arg		
1325	1330	1335
Glu Arg Gly Gly Glu Glu Ser Lys Glu Glu Cys Val Trp Val Gly		
1340	1345	1350
Gly His Lys Gly Ala Trp Gly Trp Gly Gly Thr Phe Gly Tyr		
1355	1360	

<210> 60

<211> 895

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7509332CB1

<400> 60

```

gagcacggag attcggcacg aggaggaaaa gcagcaaacc agatggagaa ggaaggccaa 60
aaagataagt agaaagctgg accatgagct ccttgagggc agggactgaa tggttactat 120
gtccccaggg cccagcatga ccttctcctg gattcctcat ctcccttctg tgacctgtgt 180
ctccatcagtt ttctcctccg gcattctttt cttacaggat tcttacctca ggaatagatg 240
gacatggcct ggcatgatgat gcagctgctg cttctggcct tggtagctgc tgcggggagt 300
gccagcccca ggagtgcgcg gcccaggacg gacctgctca atgtctgcat gaacgccaa 360
caccacaaga cacagcccg ccccgaggac gagctgtatg gccagtgcag tccctggaag 420
aagaatgcct gctgcacggc cagcaccagc caggagctgc acaaggacac ctcccgctg 480
tacaacttta actgggatca ctgtgagcgc tggtagggag actgtcgcac ctccctacacc 540
tgcaaaagca actggcacaaggctggaat tggacctcag ggattaatga gtgtccggcc 600
ggggccctct gcagcacctt tgaagtctac ttccctactc cagccgccct ttgtgaaggc 660
ctctggagcc actccttcaa ggtcagcaac tatagtgcag ggagcggccg ctgcatccag 720
atgtggtttg actcagccca gggcaacccc aatgaggagg tggccaagtt ctatgctgcg 780
gccatgaatg ctggggcccc gtctcgtggg attattgatt cctgatccaa gaagggtcct 840
ctgggggttct tccaacaacc tattctaata gacaaatcca catgaaaaaa aaaaa 895

```

<210> 61

<211> 1623

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7509102CB1

<400> 61

```

cagcaaaagg ctgacctgac ctctgatgc tcaggagaag ccatggggccc ctccctgtcct 60
gtgttctctgt ccttcacaaa gctcggcctg tggtaggctcc ttctgacccc agcagggtgga 120
gaggaagcta agcggcccacc tcccagggtc cctggagacc cactctctct tcccagctccc 180
acggcattgc cgcaggggagg ctgcataacc gagactgagg accggctctt caaacacctc 240
ttccgggggt acaaccgctg ggcgcgcccgt gtgcccaaca cttcagacgt ggatgagaag 300
aaccaaaatga tgaccaccaa cgtctggcta aaacaggagt ggagcgacta caaactgcgc 360
tggaacccca ctgatttttg caacatcaca tctctcaggg tcccttctga gatgatctgg 420
atccccgaca ttgttctcta caacaaaact gcaagatgaa gtttggctcc tggacttatg 480
acaaggccaa gatcgacctg gagcagatgg agcagactgt ggacctgaag gactactggg 540
agagcggcga gtgggccatc gtcaatgcc cgggcaccta caacagcaag aagtacgact 600
gctgcgcgga gatctacccc gacgtcacct acgccttcgt catccggcgg ctgccgctct 660
tctacacccat caacctcacc atcccctgcc tgctcatctc ctgcctcact gtgctggtct 720
tctacctgcc ctccgactgc ggcgagaaga tcacgctgtg catttcgggtg ctgctgtcac 780
tcaccgtctt cctgctgctc atcactgaga tcatcccgct cacctcgctg gtcaccccgc 840
tcatcggcga gtacctgctg ttcacatga tcttcgtcac cctgtccatc gtcacaccg 900
tcttcgtgct caatgtgcac caccgctccc ccagcaccca caccatgcc cactgggtgc 960
ggggggccct tctgggctgt gtgcccgggt ggcttctgat gaaccggccc ccaccaccg 1020
tggagctctg ccacccctta cgctgaagc tcagcccctc ttatcactgg ctggagagca 1080
acgtggatgc cgaggagagg gaggtggtgg tggaggagga ggacagatgg gcatgtgcag 1140
gtcatgtggc cccctctgtg ggcacccctc gcagccacgg ccacctgcac tctggggcct 1200
caggtcccaa ggctgaggct ctgctgcagg aggtgagct gctgctatca ccccatatgc 1260
agaaggcact ggaagggtgt cactacattg ccgaccacct gcggtctgag gatgctgact 1320
cttcggtgaa ggaggactgg aagtatgttg ccatggctat cgacaggatc ttccctctggc 1380
tgtttatcat cgtctgcttc ctggggacca tcggcctctt tctgcctccg ttcctagctg 1440
gaatgatctg actgcacctc cctcagctg gctcccaggg caaaggggag ggttcttggg 1500
tgtggaaggg ctttgaacaa tgttttagatt tggagatgag cccaaagtgc caggggagaac 1560

```

agccaggtga ggtgggaggt tggagagcca ggtgaggtct ctctaagtca ggctgggggtt 1620
gaa 1623

<210> 62
<211> 1802
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 7509132CB1

<400> 62
gaatcagctg tgacgagccg catcagctta tactggcgca gtgtgctgga atgcgtcctt 60
caggatcggt tctttcatct tcgccgcccc tgcgcgtcca gctcttctaa gacgagatgc 120
cgtcgggctt ccaacagata ggctccgaag atggggaacc ccctcagcag cgagtgcactg 180
ggacctgggt ccttgctgtg ttctctgcgg tgcttggtct cctgcagttt gggtagaaca 240
ttgggggtcat caatgccctt cagaaggtga ttgaacagag ctacaatgag acgtggctgg 300
ggaggcaggg gcctgaggga ccagctcca tccctccagg caccctcacc accctctggg 360
ccctctccgt ggccatcttt tccgtggcg gcatgatttc ctctctctc attggtatca 420
tctctcagtg gcttggaagg aaaaggcca tgctggtcaa caatgtcctg gcggtgctgg 480
ggggcagcct catgggcctg gccaatgctg ctgcctccta tgaaatgtct atccttgga 540
gattctcat tggcgctac tcaggtgctg ggcttgaggt ccctcctggg cactgccagc 600
ctgtggccac tgctcctggg cctcacagtg ctacctgcc tctgcagct ggtcctgctg 660
ccctctgtc ccgagagccc ccgtacctc tacatcatcc agaactctga ggggcctg 720
agaaagagtc tgaagcgct gacaggtgg gccgatgttt ctggagtgt ggtgagctg 780
aaggatgaga agcggaagct ggagcgtgag cggccactgt ccctgctcca gctcctggg 840
agccgtaccc accggcagcc cctgatcatt gcggtcgtgc tgcagctgag ccagcagctc 900
tctggcatca atgctgtttt ctattattcg accagcatct tcgagacagc aggggtaggc 960
cagcctgcct atgccaccat aggagctgggt gtggtcaaca cagtcttcac cttggtctcg 1020
gtgttggtgg tggagcgggc ggggcgccgg acgctccatc tctgggcct ggcgggcatg 1080
tgtggctgtg ccctcctgat gactgtggct ctgctcctgc tggagcgagt tccagccatg 1140
agctacgtct ccattgtggc catctttggc ttctgtggcat tttttgagat tggccctggc 1200
cccattcctt ggttcatcgt ggccgagctc ttcagccagg gaccccgccc ggcagccatg 1260
gctgtggctg gtttctccaa ctggacgagc aacttcatca ttggcatggg tttccagtat 1320
gttgccgagg ctatggggcc ctacgtcttc cttctatttg cggctcctct gctgggcttc 1380
ttcatcttca ctttcttaag agtacctgaa actcgaggcc ggacgtttga ccagatctca 1440
gctgccttcc accggacacc ctctcttcta gagcaggagg tgaaaccag cacagaactt 1500
gagtatttag ggccagatga gaacgactga ggggccaggc aggggtggga gagccagctc 1560
tctctaccgg gccagagac cccttctttt cctctgcagc actttaaccc tctcttccct 1620
attatttccg ggtggaaaag aatccctgca gcctggtaga attgggaagc tgggggaagg 1680
gtggtctgag cacccttca ttccctcgt gtgactctct tggattattt atgtgtgtg 1740
gtttggcctg ggccatcagg gtgggacct ctccctccc tcttcttcc ccatccct 1800
tt 1802

<210> 63
<211> 2139
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 7509136CB1

<400> 63
agcctttggt gaagattgga tcgaaatcag accaatggac aagctctggc cgtgggtgg 60

```

ggacgggcct ggagtagaac tggaacgaga aggatgaaga gatgagcaca aaggtgtact 120
tagacctgga gtggactgac tacaggctga gctgggaccc tgcggagcac gacggcatcg 180
attcgctccg catcacggcg gaatccgtgt ggctccctga cgtggtgcta ctgaacaaca 240
atgatgggaa ttttgacgtg gctctggaca ttagcgtcgt ggtgtcctcc gacggctccg 300
tgcgttgga acccccgggc atctatcgca gcagctgcag catccaggtc acctacttcc 360
ccttcgactg gcagaattgc actatggtgt tcagctccta cagctacgac agctcggagg 420
tcagcctgca gacaggcctg ggtcctgacg ggcaaggcca tcaggaaatc cacattcatg 480
aagggacttt cattgagaat ggccagtggg agattatcca caagccctct cggctaatacc 540
agcctccagg cgatcctagg ggaggagggg aaggacagcg ccaggaagtc atcttctacc 600
tcacatcccg ccgcaagcct ctcttctacc tggccaacgt cattgcccc tgcacacctca 660
tcactcttct ggccatcttc gtcttctacc tggcaccaga tgcagtcac cttagtgtcg 720
tggtttctca cctgcaccac cgctcaccac acaccacca aatgccccct tgggtccgtg 780
agatcttcat tcacaaactt ccgctgtacc tgcgtctaaa aaggcccaaa cccgagagag 840
acctgatgcc ggagccccct cactgttctt ctccaggaag tggctggggg cggggaacag 900
atgaatatth catccggaag ccgccaagtg attttctctt ccccaaacc aataggttcc 960
agcctgaact gtctgcccct gatctgccc gatttatcga tggccaacac cgggctgtgg 1020
ccctgcttcc ggagctacgg gaggtcgtct cctctatcag ctacatcgct cgacagctgc 1080
aggaacagga ggaccacgat gcgctgaagg aggactggca gtttgtggcc atggtagtgg 1140
accgctctt cctgtggact ttcacatctt tcaccagcgt tgggacccta gtcacttctc 1200
tggacgccac gtaccacttg cccctccag accccttctc ttgaagactg gagggttgag 1260
accagggccc cctgccagtt gaagtgaag tttggtgata ctgtcaagcc ccatccttct 1320
ctgcctctta actccttcac gaggaatctg ggctcttctt ttcgtttctg gggactgcat 1380
tggactgagg gctgggtagg caggtgtctt ggaccacct gaaatgcagt atcatctgat 1440
ttactctttg ggatcttgaa gaagctcttt tgggtatcaa cacctaggtc gccagtgaat 1500
tagaacacag aacaggaact agattataag ccttatgagg tcaagaaatg tgacttggcc 1560
gggcgcggtg gctcacgcct gtaatcccag cactttggga ggccaaggcg ggcggatcac 1620
ctgaggtcgg gagtttgaga ccagcccag caacatggag aaacctgtc tctactaaaa 1680
atacaaaatt agccaggtgt ggtggtacat gcctgtaatc ccagctacta gggaggctga 1740
ggcaggagaa tcactcgaa ccgggaggca gaggttgca tgagtcaaga tcacgccatt 1800
gcactccagc ctgggcaaca agagcgaaac tccatctcaa aaaaaaaaaa gtgtcttgtt 1860
cactgcagca tgcccagtgc cacgcacagg tgctgacct tagtaagtgc ttaacatttg 1920
ttgaataggg gaaagaaatt tccggaagta aatacagcaa ttaataatgt ttataagctg 1980
ggcatggtcg ctcaggccag taatcccagt gacttaggag gctgaggtgg gaggattact 2040
tgaacccac agtttgagac cagcctgggc aacatagtga gaccctgtct ctaaaaaaat 2100
aaaaatagaa ataaagtagt gcttattggt tgcaaaaaa 2139

```

<210> 64

<211> 1461

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7509178CB1

<400> 64

```

cacaagctcc ggtagcccat ggagccctgg cctctcctcc tgctctttag cctttgctca 60
gctggcctcg tcctgggctc cgaacatgag acccgtctgg tggcaaagct atttaaagac 120
tacagcagcg tggcgggcc agtgaagac caccgccagg tcgtggaggc caccgtgggc 180
ctgcagctga tacagctcat caatgtggat gaagtaaata agatcgtgac aaccaatgtg 240
cgtctgaaac agaactgcag catgaagctg ggcacctgga cctacgacgg ctctgtctgt 300
gccatcaacc cggaaagcga ccagccagac ctgagcaact tcatggagag cggggagtgg 360
gtgatcaagg agtcccgggg ctggaagcac tccgtgacct attcctgctg ccccgacacc 420
ccctacctgg acatcaccta ccacttcgtc atgcagcgcc tgcccctcta ctctcatctc 480
aacgtcatca tcccctgctt gctcttctcc ttcttaactg gcttggtatt ctacctgccc 540
acagactcag gggagaagat gactctgagc atctctgtct tactgtcttt gactgtgttc 600

```



```

cttctggtca tcgtggagct gatccccctc acgtccagtg ctgtgccctt gattggaaaa 660
tacatgctgt tcaccatggt gttcgtcatt gcctccatca tcatcactgt catcgatc 720
aacacacacc accgctcacc cagcacccat gtcatgccca actgggtgcg gaagggtttt 780
atcgacacta tcccaaatat catgtttttc tccacaatga aaagaccatc cagagaaaag 840
caagacaaaa agattttttac agaagacatt gatattctctg acattttctgg aaagccaggg 900
cctccaccca tgggcttcca ctctccccctg atcaaacacc ccgaggtgaa aagtgccatc 960
gagggcatca agtacatcgc agagaccatg aagtcagacc aggagtctaa caatgcggcg 1020
gcagagtgga agtacgttgc aatggtgatg gaccacatac tctcggagt cttcatgctt 1080
gtttgcatca tcggaaccct agccgtgttt gcaggtcgac tcattgaatt aaatcagcaa 1140
ggatgagcag aaaatgagct gagcttagct ctgccctgga acctaccaga gcagagaagg 1200
gcaggagagg aagatttgtc tacttgctcc actgcactt atcaaactg ttatattcca 1260
tacttattat tgatgataag atttaccttt atgtaagttt atggccttga agtggtttca 1320
tattgcttct ccttttagtt ctgctgtctc cctgaagagt gaacctctt tagtaaatga 1380
aactaatcac taaaaaaagt gttcatttcc agtgtctgga agagtttttg ccaggataac 1440
cgaggtttct gttgcattgc a 1461

```

<210> 65

<211> 738

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7509214CB1

<400> 65

```

gacagcggcc tggctaactc ctgccaggca gtgcccttcc cggagcgtgc cctcgccgct 60
gagctcccct gaacagcagc tgcagcagcc atggccccgc cctgggtgcc cgccatgggc 120
ttcacgctgg cgcccagcca tggggtacgg ctccctacctg gtctggaaag agctgggagg 180
cttcacagag aaggctgtgg ttcccctggg cctctacact gggcagctgg ccttgaactg 240
ggcatggccc cccatcttct ttggtgcccc acaaatgggc tgggccttgg tggatctcct 300
gctggtcagt gggggcggcg cagccactac cgtggcctgg taccaggtga gcccgctggc 360
cgcccgccct ctctaccctt acctggcctg gctggccttc gcgaccacac tcaactactg 420
cgtatggcgg gacaaccatg gctggcgtgg gggacggcgg ctgccagagt gagtggccgg 480
cccaccaggg actgcagctg caccagcagg tgccatcacg cttgtgatgt ggtggccgtc 540
acgctttcat gaccactggg cctgctagtc tgtcagggcc ttggcccagg ggtcagcaga 600
gcttcagagg tggccccacc tgagccccc cccgggagca gtgtcctgtg ctttctgcat 660
gcttagagca tgttcttggg acatggaatt ttataagctg aataaagttt ttgacttctt 720
ttaaaaaaaa aaaaaaaaa 738

```

<210> 66

<211> 2106

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7509244CB1

<400> 66

```

agcctttggt gaagattgga tcgaaatcag accaatggac aagctctggc cgtgggtggt 60
ggacgggcct ggagtagaac tggaaacgaga aggatgaaga gatgagcaca aagggtgtact 120
tagacctgga gtggactgac tacaggctga gctgggacct tgcggagcac gacggcatcg 180
attcgctccg catcacggcg gaatccgtgt ggctccctga cgtggtgcta ctgaacaaca 240
atgatgggaa ttttgacgtg gctctggaca ttagcgtcgt ggtgtcctcc gacggctccg 300
tgcggttgga acccccgggc atctatcgca gcagctgcag catccaggtc acctacttcc 360

```

```

ccttcgactg gcagaattgc actatggtgt tcagctccta cagctacgac agctcggagg 420
tcagcctgca gacaggcctg ggtcctgacg ggcaagggca tcaggaaatc cacattcatg 480
aagggacttt cattgagaat ggccagtggg agattatcca caagccctct cggctaattc 540
agcctccagg cgatcctagg ggaggaggag aaggacagcg ccaggaagtc atcttctacc 600
tcatcatccg ccgcaagcct ctcttctacc tggccaacgt cattgccccca tgcatacctca 660
tcactcttct ggccatcttc gtcttctacc tgccaccaga tgaggagag aagatggggc 720
tctcaatctt tgccctgctg acccttactg tgttcctgct gctgctggct gacaaagtac 780
ctgagacctc actatcagta cccattatta tcaagtacct catgtttacc atggtcctcg 840
tcaccttctc agtcacacct agtgcctggt ttctcaacct gcaccaccgc tcaccaccaca 900
cccaccaaat gccccttttg gtccgtcaga tcttcattca caaacttccg ctgtacctgc 960
gtctaaaaag gcccacccc gagagagacc tgatgccgga gctacgggag gtcgtctcct 1020
ctatcagcta catgctcga cagctgcagg aacaggagga ccacgatgcg ctgaaggagg 1080
actggcagtt tgtggccatg gtagtgacc ccctcttctg gtggactttc atcatcttca 1140
ccagcgttgg gaccctagtc atcttctctg acgccacgta ccacttgccc cctccagacc 1200
cctttccttg aagactggag ggttgagacc caggcccccct gccagttgaa gtgagagttt 1260
ggtgatactg tcaagcccca tccttctctg cctcttaact ccttcacgag gaatctgggc 1320
ctcttatttc gtttctgggg actgcattgg actgagggct gggtaggcag gtgtcttgga 1380
cccacctgaa atgcagtatc atctgattta ctctttggga tcttgaagaa gctcttttgg 1440
gtatcaacac ctaggtcgcc agtgaaatag aacacagaac aggaactaga ttataagcct 1500
tatgaggtca agaaatgtga cttggccggg cgcggtggct cagcctgta atcccagcac 1560
tttgggaggc caaggcgggc ggatcacctg aggtcgggag tttgagacca gcccagacca 1620
catggagaaa ccctgtctct actaaaaata caaaattagc caggtgtggt ggtacatgcc 1680
tgtaatccca gctactaggg aggtcaggc aggagaatca ctggaacccg ggaggcagag 1740
gttgacagta gtcaagatca cgccattgca ctccagcctg ggcaacaaga gcgaaactcc 1800
atctcaaaaa aaaaaaagtg tcttgttcac tgcagcatgc ccagtgccac gcacaggtgc 1860
tgacctatag taagtgccta acatttgttg aataggggaa agaaatttcc ggaagtaaat 1920
acagcaatta ataattgtta taagctgggc atggctgctc aggccagtaa tcccagtgac 1980
ttaggaggct gaggtgggag gattacttga aaccacagt ttgagaccag cctgggcaac 2040
atagttagac cctgtctcta aaaaaataaa aatagaaata aagtagtgct tattgtttgc 2100
aaaaaa 2106

```

<210> 67

<211> 2334

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7509256CB1

<400> 67

```

ctcagagccgc tcgagccgcg ggcggctggg acgcagctgc ccccgctcgg cgcccgctgc 60
acccttagca gccactgcc cctgggcccg gagcctccac gatctcgccc ggcgattgtg 120
ggcaggggag cctccggatc gatcttctga aattcaagtt ttcaagatga agtttttatt 180
gacaactgcc tttttaattt taatttcctt gtgggtggaa gaagcctatt ctaaggaaaa 240
gtcttcaaaag aaagggaagg ggaaaaagaa gcagtatcta tgcccactc agcagtcagc 300
agaggacctt gcccgagtac ctgccaaact cactagcaat atcttgaaca ggttatttgt 360
cagttatgat ccaggataa gaccaaactt caaaggcatt cctgttgatg tagtagtcaa 420
catttttatt aacagttttg gatccattca agaaacaaca atggactata gagttaacat 480
cttctgaga caaaaatgga atgacccag gctgaagctc ccagtgatt ttaggggttc 540
agatgcactg acagtggatc caacaatgta caagtgttta tggaaacctg attttatttt 600
tgcaaatgaa aaaagtgcc attttcatga tgtgaccag gaaaacatcc tcctctttat 660
tttctgtgat ggagatgtcc ttgtcagcat gaggttatct attactcttt catgcccttt 720
ggacttgaca ttgtttccca tggatacaca acgttgcaag atgcaactgg agagcttttg 780
ttacacaact gatgatttac gatttatctg gcagtcagga gatcctgtgc aattagaaaa 840
aattgccttg cctcaatttg atatcaaaaa ggaagatatt gaatatggta actgtacaaa 900

```

```

atactataaa ggcacgggct actacacatg cgtggaagtc atcttcaccc tgaggaggca 960
ggtcggccttt tacatgatgg ggtctacgc cccaaccctg ctcatgtgtg ttctctcctg 1020
gctttccttc tggatcaacc cggacgcgag tgctgccaga gtgcccctgg gttggtgaga 1080
ccagatgcaa aaaagtgtgt acttctaagt ctgatctgag atctaatagac ttcagcattg 1140
ttggaagctt accaagagat tttgaactat ccaattatga ctgctatgga aaacccattg 1200
aagttaacaa cggacttggg aaatctcagg ctaagaacaa caagaagcct cccctgcga 1260
aacctgttat tccaacagca gcaaagcgaa ttgatcttta tgcaagagca ttgtttcctt 1320
tctgtctctt gttcttcaat gttatatatt ggtctatata tttatgataa atcttttcca 1380
tttgtacaaa ataaatttcc atttcattgt gacctactcc tttcataaat gccaatctgt 1440
gagaactttt gaattttcat agcaacattg cattttggat gccatttgat tgtaataaaa 1500
ctgtggcacc ttaattttga atggcagcat gatcatgtaa tatctgtgct ctaataacga 1560
tgtatatatg tatagtgaac atattgctta gtaacaaatg aaggacaagc atactacata 1620
atataatcca tacaattctc ttcagttagt gtaaactgca aatactacag ataattctga 1680
taataaaatg atatgcacgc tgaatcctgc tatggtcacc attctaagt atgtagtatt 1740
tcaaatttcc ttccttgtaa ctttcaaaga aagccatctt attcttgtaa aattttagat 1800
ggtattatca cagattttaa aaggttgat tacatattgt ttaaactttg taagtagaaa 1860
tatatctgtt ataattatac aggtctgtg gagaaataaa gttcaaaaaa tattaatttg 1920
taaaatcagc tcgtttttaa gtgtgcttgt gttgtcaaaa atactagata gtaatacaca 1980
gtgagcattt ttaaacaag ggaacctat atttatgtaa ctgtatactg aattctgaca 2040
aaataaaaaa agatacctta ttgacgaaat atttaggata aacaaaattc tatttaatcc 2100
accttaaaac ctaaatgtat tttcatggat ttcatttgtt ggtacatatt acacaaaaca 2160
ttgtgcctta aaatgagtca tacatctttt aaattggaat gcagtaatag atatgtgatt 2220
ttacatcatt tttaagaac caaggggaag taataagttg aaaaagaaat ccataactat 2280
taaaagattt taactttttt attttattaa aatgcttgca tattttaagt aaaa 2334

```

<210> 68

<211> 1475

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7509395CB1

<400> 68

```

ccacggccag tgtgtcgaac tcggtacttc acaagctccg gtagcccatg gagccctggc 60
ctctcctcct gctcttttagc ctttgctcag ctggcctcgt cctggggctcc gaacatgaga 120
cccgctcgtg ggcaaagcta tttaaagact acagcagcgt ggtgcggcca gtggaagacc 180
accgccaggt cgtggaggtc accgtgggcc tgcagctgat acagctcatc aatgtggatg 240
aagtaaatca gatcgtgaca accaataact gcagcatgaa gctgggcacc tggacctacg 300
acggctctgt cgtggccatc aacccggaaa gcgaccagcc agacctgagc aacttcatgg 360
agagcgggga gtgggtgatc aaggagtccc ggggctggaa gcaactcctg acctattcct 420
gctgccccga caccctctac ctggacatca cctaccactt cgtcatgcag cgcctgcccc 480
tctacttcat cgtcaacgct atcatccct gcctgctctt ctccttctta actggcctgg 540
tattctacct gccacagac tcaggggaga agatgactct gagcatctct gtcttactgt 600
ctttgactgt gttccttctg gtcacgtgg agctgatccc ctccacgtcc agtgctgtgc 660
ccttgattgg aaaatacatg ctgttcacca tgggtgtcgt cattgcctcc atcatcatca 720
ctgtcatcgt catcaacaca caccaccgct caccagcac ccatgtcatg cccaactggg 780
tgcggaaggt ttttatcgac actatcccaa atatcatgtt tttctccaca atgaaaagac 840
catccagaga aaagcaagac aaaaagattt ttacagaaga cattgataac tctgacattt 900
ctggaaagcc agggcctcca cccatgggct tccactctcc cctgatcaaa caccctgagg 960
tgaaaagtgc catcgagggc atcaagtaca tcgcagagac catgaagtca gaccaggagt 1020
ctaacaatgc ggccgcagag tgggaagtac ttgcaatggt gatggaccac atactcctcg 1080
gagtcttcat gcttggttgc atcatcgaa ccctagccgt gtttgaggt cgactcattg 1140
aattaaatca gcaaggatga gcagaaaatg agctgagctt agctctgccc tggaacctac 1200
cagagcagag aagggcagga gaggaagatt tgtctacttg ctccactcgc acttatcaaa 1260

```

```

cgtgttatat tccataactta ttattgatga taagatttac ctttatgtaa gtttatggcc 1320
ttgaagtgtt ttcatattgc ttctcccttt agttctgctg tctccctgaa gagtgaaccc 1380
tcttttagtaa atgaaactaa tctaataaaa aagtgttcat ttccagtgtc tggaagagtt 1440
tttgccagga taaccgaggt ttctgttgca ttgca 1475

```

<210> 69

<211> 1295

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7503287CB1

<400> 69

```

ccaggacccg ccgccgggctg ccggcttgcc gaagccccct caggatcccc tcaacaagga 60
tggaactgaa ggcgaggag gaggaggtgg gtggcggtcca gccggtgagc atccaggcct 120
tcgccagcag ctccacactg caccggcctgg ccacacatctt ctccctacgag cggctgtctc 180
tgaagcgggc actgtgggccc ctgtgcttcc tgggctcgct ggctgtgctg ctgtgtgtgt 240
gcacggagcg tgtgcagtac tacttccact accaccatgt caccaagctc gacgaggtgg 300
ctgcctctca gcttaccttc cctgctgtca cgctgtgcaa cctcaacgag ttccgcttta 360
gccaaagtct caagaatgac ctgtatcatg ctggggagct gctggccctg ctcaacaaca 420
ggtatgagat accagacaca cagatggcag atgaaaagca gctggagata ctgcaggaca 480
aagccaactt ccgcagcttc aaacccaaac ccttcaacat gcgtgagttc tacgaccgag 540
ctgggacaga cattcgagac atgctgctct cctgccactt ccgggggggag gtctgcagcg 600
ctgaagactt caaggtgggc ttcacacgct atggaaagtg ctacacgttc aactcggggc 660
gagatgggcg gcccgggctg aagaccatga aggggtgggac gggcaatggg ctggaaatca 720
tgctggacat ccagcaggac gactacctgc ctgtgtgggg ggagactgac gagacgtcct 780
tcgaagcagg catcaaagtg cagatctttc ctcttgtctg tggttaaggaa ggagtcttga 840
ccatagagtc ctctctctgc ctctatccca ttctttttac atttaacaaa actaatctaa 900
aaaagaacta aaaagggaga acggggcaag ggacctcagg ctgccccctc ctccctccatg 960
ctgcctcccc tagctcccag cctgaattct gtctatctag ctgtctgcca tctgagtgct 1020
catctacatt ctgctgccac cagtcaccaa agggcccttc cagtgggggg tggaagggat 1080
ctctggggtc tggaatttgg ccccaaacca gagaatgtac ctttaagggg agggctagtgt 1140
tgggggaggg aggttcccc agccttaaga gaccctctca gccagtgac tgtcccaaaa 1200
cccaagtctc ctggcaggaa ctaaaacctc agccccactc tctcacacca tgtggaatct 1260
cgtggggggtc ggggatcccc ttaagaagtg gtaat 1295

```

<210> 70

<211> 1386

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7503320CB1

<400> 70

```

tgcagctccg ggactcaaca tgcgctgtct gccgggaggg gtctgggtgg cgctggccgc 60
gtcgctcctg cacgtgtccc tgcaaggcga gttccagagg aagctttaca aggagctggt 120
caagaactac aatcccttgg agaggccgt ggccaatgac tcgcaaccac tcaccgtcta 180
cttctccctg agcctcctgc agatcatgga cgtggatgag aagaaccaag ttttaaccac 240
cacgaccccg acgggggcaa gatgccaaag tggaccagag tcaccttctt gaactggtgc 300
gcgtgggttc tgcaaatgaa gagggccggg gaggacaagg tgcggccggc ctgccagcac 360
aagcagcggc gctgcagcct ggccagtgtg gagatgagcg ccgtggcgcc gccggccgcc 420
agcaacggga acctgctgta catcggtctc cgcggcctgg acggcggtgca ctgtgtcccc 480

```

```

acccccgact ctggggtagt gtgtggccgc atggcctgct cccccacgca cgatgagcac 540
ctcctgcacg gcgggcaacc ccccgagggg gaccggact tggccaagat cctggaggag 600
gtccgctaca ttgccaaccg cttccgctgc caggacgaaa gcgaggcggg ctgcagcgag 660
tggaagtctg ccgcctgtgt ggtggaccgc ctgtgcctca tggccttctc ggtcttcacc 720
atcatctgca ccatcggcac cctgatgtcg gctcccaact tcgtggaggc cgtgtccaaa 780
gactttgcgt aaccacgcct ggttctgtac atgtggaaaa ctacagatg ggcaaggcct 840
ttggcttggc gagatttggg ggtgctaata caggacagca ttacacgcca caactccagt 900
gttcccttct ggctgtcagt cgtgttgctt acggtttctt tgttacttta ggtagtagaa 960
tctcagcact ttgtttcata ttctcagatg ggctgataga tctccttggc acatccgtac 1020
catcggtcag cagggccact gagtagtcat tttgcccatt agcccactgc ctggaaagcc 1080
cttcggagag ctcccatggt ctccctacca ccgagacagt tggttttgca tgtctgcagt 1140
aaggtctacc tgaaaattca acatttgcct tttgcttgtg taaaaacca gattgaagct 1200
aaaataaacc agactcata aatcctttcc aataattgac tgggtgaagg aaaacaaaaa 1260
acaaaaacta aaaacctctt agcttttctg caattcaact ttttattttt atttttattt 1320
ctatcaaaga cggtagagag aaacagcttg atgctgtttc tacattaaaa aaaaaatttg 1380
tcggtc

```

<210> 71

<211> 2213

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7503335CB1

<400> 71

```

gttactggga gggggcttgc tgtggccctg tcaggaagag tagagctctg gtccagctcc 60
gcgcagggag ggaggctgtc accatgccgg cctgctgcag ctgcagtgat gttttccagt 120
atgagacgaa caaagtcact cggatccaga gcatgaatta tggcaccatt aagtggttct 180
tccacgtgat catcttttcc tacgtttgct ttgctctggt gagtgacaag ctgtaccagc 240
ggaaagagcc tgtcatcagt tctgtgcaca ccaagggtga ggggatagca gaggtgaaag 300
aggagatcgt ggagaatgga gtgaagaagt tgggtgcacag tgtctttgac accgcagact 360
acaccttccc tttgcagggg aactctttct tcgtgatgac aaactttctc aaaacagaag 420
gccaaagaca gcggttgtgt cccgagtatc ccaccgcag gacgctctgt tcctctgacc 480
gaggttgtaa aaagggtatg atggaccgcg agagcaaagg aattcagacc ggaagggtgtg 540
tagtgcataa aggggaaccag aagacctgtg aagtctctgc ctggtgcccc atcgaggcag 600
tggaagaggg ccccggcctt gctctcttga acagtgcgca aaacttctct gtgctcatca 660
agaacaatat cgacttcccc ggccacaact acaccacgag aaacatcctg ccagggtttaa 720
acatcacttg taccttccac aagactcaga atccacagtg tcccattttc cgactaggag 780
acatcttccg agaacaggcg ataatttttc agatgtggca attcagatac gccaaagtact 840
acaaggaaaa caatgttgag aaacggactc tgataaaagt cttcgggatac cgttttgaca 900
tcttggtttt tggcaccgga ggaaaatttg acattatcca gctggttgtg tacatcggtc 960
caaccctctc ctacttcggt ctggccgctg tgttcacgca cttcctcatc gacacttact 1020
ccagtaactg ctgtcgctcc catatttatc cctggtgcaa gtgctgtcag ccctgtgttg 1080
tcaacgaata ctactacagg aagaagtgcg agtccattgt ggagccaaag ccgacattaa 1140
agtatgtgtc ctttgtggat gaatcccaca ttaggatggt gaaccagcag ctactaggga 1200
gaagtctgca agatgtcaag ggccaagaag tcccaagacc tgcgatggac ttcacagatt 1260
tgtccaggct gcccttggcc ctccatgaca caccctcgat tcttggacaa ccagaggaga 1320
tacagtgtct tagaaaaggag gcgactccta gatccaggga tagccccgtc tgggtgccagt 1380
gtggaagctg cttcccatct caactocctg agagccacag gtgcctggag gagctgtgct 1440
gccggaaaaa gccgggggcc tgcataacca cctcagagct gttcaggaag ctggtcctgt 1500
ccagacacgt cctgcagttc ctctgtctct accaggagcc cttgctggcg ctggatgttg 1560
attccaccaa cagccggctg cggcactgtg cctacaggtg ctacgccacc tggcgcttcg 1620
gctcccagga catggctgac tttgccatcc tgcccagctg ctgccgctgg aggatccgga 1680
aagagtttcc aaagagtga gggcagtaca gtggcttcaa gagtccctac tgaagccagg 1740

```

```

caccgtggct cactgtctgta atcccagcgc tttggggaggc cgaggcaggc agatcacctg 1800
aggctcgggag ttggagaccc gcctggctaa caaggcgaaa tcctgtctgt actaaaaata 1860
caaaaatcag ccagacatgg tggcatgcac ctgcaatccc agctactcgg gaggtgagg 1920
cacaagaatc acttgaaccc gggaggcaga ggttgtagtg agcccagatt gtgccactgc 1980
tctccagcct gggaggcaca gcaaactgtc ccaaaaaaaa caaaagagtc cttaccaata 2040
gccgggggct tgcagtaccc atgttaactt gaccattttac caagcaattg aacttcacct 2100
gcaaagctct gtggccactt ttccagccaa agggaaatat gcttcacctc ggtggccctc 2160
ggggtctgaa gcaaaggggc ctggttaaac aacaaaaaat ccttaaattg agc 2213

```

<210> 72

<211> 1289

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7503952CB1

<400> 72

```

gagaaattga ggggcattcc atctggtagg caagtttgca tttctccttt ttgggatctg 60
cccaggaatg ttgtcaagtg taatggctcc cctgtgggcc tgcacccctg ttgctgcagg 120
aattctagcc acagatacac atcatcccca ggattctgct ctgtatcatc tcagcaagca 180
gctattacag aaatatcata aagaagttag acctgtttac aactggacca aggccaccac 240
agtctacctg gacctgttcg tccatgctat attggatgtg gatgcagaga atcaaatatt 300
aaagacaagt gtatggtacc aagaggtctg gaatgatgaa tttttatcct ggaactccag 360
catgtttgat gagattagag agatctccct acctctaagt gccatctggg ccccgatat 420
catcatcaat gagtttgtgg acattgaaag ataccctgac cttccctatg tttatgtgaa 480
ctcatctggg accattgaga actataagcc catccagggt gtctctgcgt gcagtttaga 540
gacatatgct tttccatttg atgtccagaa ttgcagcctg accttcaaga gcattctgca 600
tacagtggaa gacgtagacc tggcctttct gaggagccca gaagacattc agcatgaca 660
aaaggcgttt ttgaatgaca gtgagtggga acttctatct gtgtcctcca catacagcat 720
cctgcagagc agcgctggag gatttgcaca gattcagttt aatggcactt cttcaccatc 780
tgcattggct tcttggttct cagcttagct aagtcctatg tgttgggtcaa attcctccat 840
gatgagcagc gtggtggaca ggagcagccc ttcttgtgcc ttcgagggga caccgatgct 900
gacaggccta gagtggaaac cagggcccaa cgtgctgtgg taacagagtc ctgctgtat 960
ggagagcacc tggccagcc aggaaccctg aaggaagtct ggtcgcagct tcaatctatc 1020
agcaactacc tccaaactca ggaccagaca gaccaacagg aggcagagtg gctggctctc 1080
ctgtcccgtt ttgaccgaat gctcttccaa agctaccttt tcatgctggg gatctacacc 1140
atcactctgt gctccctctg ggcactgtgg ggcggcgtgt gaagactgaa gtgttcttca 1200
gtaattgtgc tggcacttag gagagagagg agggggaata atagtgggtt aaaaagcttt 1260
ctgggtcggg tgtggtggtt cttgcctat 1289

```

<210> 73

<211> 1358

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7504530CB1

<400> 73

```

cgctcgaggc cgccctggga gagctgagag gcaggctctg gactggggac acagggatag 60
ctgagcccca gctgggggtg gaagctgagc caggacaggt cacggaggaa caagatcaag 120
atgcgctgta actgagaagc cccaaggcg gaggtgaga atcagagaca ttccagcaga 180
catctacaaa tctgaaagac aaaacatggt tcaagcatcc gggcacaggc ggtccaccg 240

```

```

tggctccaaa atggtctcct ggtccgtgat agcaaagatc caggaaatac tgcagaggaa 300
gatggtgcga gagttcctgg ccgagttcat gagcacatat gtcatgatgg tattcggcct 360
tggttccgtg gcccatatgg ttctaaataa aaaatatggg agctaccttg gtgtcaactt 420
gggttttggc ttcggagtca ccatgggagt gcacgtggca ggccgcatct ctggagccca 480
catgaacgca gctgtgacct ttgctaactg tgcgctgggc cgcgtgccct ggaggaagtt 540
tccggtctat gtgctggggc agttcctggg ctcccttctg gcggctgcca ccatctacag 600
tctcttctac acggccattc tccacttttc ggggtggacag ctgatgggtga ccggtcccgt 660
cgctacagct ggcatttttg ccacctacct tcctgatcac atgacattgt ggcggggcct 720
cctgaatgag gcgtggctga ccgggatgct ccagctgtgt ctcttcgcca tcacggacca 780
ggagaacaac ccagcactgc caggaacaga ggcgctggtg ataggcatcc tcgtggtcat 840
catcgggggtg tcccttggca tgaacacagg atatgccatc aaccctgcc ggacctgcc 900
cccccgcatc ttcaccttca ttgctggttg gggcaaacag gtcttcagggt ggcatcatct 960
acctggtctt cattggtctc accatcccac gggagcccct gaaattggag gattctgttg 1020
cgtatgaaga ccacgggata accgtattgc ccaagatggg atctcatgaa cccacgatct 1080
ctccccctac ccccgctctc gtgagccctg ccaacagatc ttcagtccac cctgccccac 1140
ccttacatga atccatggcc ctgagcact tctaagcaga gattatttgt gatcccatcc 1200
attcccaat aaagcaaggc ttgtccgaca gcagtacccc cacttcctgg gggcctcctg 1260
tggttgggct tccctcctgg gttcttacag gagctccagg gctatgtctt agcccaaggg 1320
gtagagggtga ggcacctaag gccttccatc cccgggag 1358

```

<210> 74

<211> 2232

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7509303CB1

<400> 74

```

ggaccctaga cctctgcagc ccataccagg tctcatggag gggaacaagc tggaggagca 60
ggactctagc cctccacagt ccactccagg gctcatgaag gggaacaagc gtgaggagca 120
ggggctgggc cccgaacctg cggcgcccca gcagcccacg gcggaggagg aggcctgat 180
cgagttccac cgctcctacc gagagctctt cgagttcttc tgcaacaaca ccaccatcca 240
cggcgccatc cgcctggtgt gctcccagca caaccgcatg aagacggcct tctgggcagt 300
gctgtggctc tgcacctttg gcatgatgta ctggcaattc ggctgcttt tcggagagta 360
cttcagctac cccgtcagcc tcaacatcaa cctcaactcg gacaagctcg tcttccccgc 420
agtgaccatc tgcaccctca atccctacag gtaccgggaa attaaagagg agctggagga 480
gctggaccgc atcacagagc agacgctctt tgacctgtac aaatacagct ccttcaccac 540
tctcgtggcc ggctcccgcg gccgtcgcga cctgcggggg actctgcgcg accccttgca 600
gcgcctgagg gtcccgcctc cgcctcacgg ggcccgctga gcccgtagcg tggcctccag 660
cttgcgggac aacaaccccc aggtggactg gaaggactgg aagatcggct tccagctgga 720
attactctca cttccaccac ccgatgtatg gaaactgcta tactttcaat gacaagaaca 780
actccaacct ctggatgtct tccatgcctg gaatcaacaa cggctctgtc ctgatgctgc 840
gcgcagagca gaatgacttc attcccctgc tgtccacagt gactggggcc cgggtaatgg 900
tgcacgggca ggatgaacct gcctttatgg atgatggtgg ctttaacttg cggcctggcg 960
tggagacctc catcagcatg aggaaggaaa ccctggacag acttgggggc gattatggcg 1020
actgcaccaa gaatggcagt gatgttcctg ttgagaacct ttacccttca aagtacacac 1080
agcaggtgtg tattcactcc tgcttccagg agagcatgat caaggagtgt ggctgtgcct 1140
acatcttcta tccgcgggcc cagaacgttg agtactgtga ctacagaaag cacagttcct 1200
gggggtactg ctactataag ctccaggttg acttctctc agaccacctg ggctgtttca 1260
ccaagtgccg gaagccatgc agcgtgacca gctaccagct ctctgctggt tactcacgat 1320
ggccctcggt gacatcccag gaatgggtct tccagatgct atcgcgacag aacaattaca 1380
ccgtcaacaa caagagaaat ggagtggcca aagtcaacat cttcttcaag gagctgaact 1440
acaaaaccaa ttctgagtct ccctctgtca cgatgggtcac cctcctgtcc aacctgggca 1500
gccagtggag cctgtggttc ggctcctcgg tggtgtctgt ggtggagatg gctgagctcg 1560

```

```

tctttgacct gctggtcac c atgttctc t tgctgctccg aagggtccga agccgatact 1620
gggtctccagg ccgagggggc aggggtgctc aggaggtagc ctccaccctg gcatcctccc 1680
ctccttccca cttctgcccc cccccatgt ctctgtcctt gtcccagcca ggccctgctc 1740
cctctccagc cttgacagcc cctccccctg cctatgccac cctgggcccc cgcccatctc 1800
cagggggctc tgcagggggc agttcctcca cctgtcctct gggggggccc tgagagggaa 1860
ggagagggttt ctcacaccaa ggcagatgct cctctggtgg gaggggtgctg gccctggcaa 1920
gattgaagga tgtgcagggc ttcctctcag agccgcccc aactgccgttg atgtgtggag 1980
gggaagcaag atgggtaagg gctcaggaag ttgctccaag aacagtagct gatgaagctg 2040
cccagaagtg ccttggtctc agccctgtac cccttggtac tgcctctgaa cactctggtt 2100
tccccaccca actgcggtta agtctctttt tcccttggat cagccaagcg aaacttggag 2160
ctttgacaag gaactttcct aagaaaccgc tgataaccag gacaaaacac aaccaaggta 2220
cacgcaggca tg                                     2232

```

<210> 75

<211> 2230

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7509910CB1

<400> 75

```

gttactggga gggggcttgc tgtggccctg tcaggaagag tagagctctg gtccagctcc 60
gcgcaggggag ggaggctgtc accatgccgg cctgctgcag ctgcagtgat gttttccagt 120
atgagacgaa caaagtcact cggatccaga gcatgaatta tggcaccatt aagtggttct 180
tccacgtgat catcttttcc tacgtttgct ttgctctggt gagtgacaag ctgtaccagc 240
ggaaagagcc tgtcatcagt tctgtgcaca ccaaggtgaa ggggtagca gaggtgaaag 300
aggagatcgt ggagaatgga gtgaagaagt tgggtgcacag tgtctttgac accgcagact 360
acaccttccc tttgcagggg aactctttct tctgtatgac aaactttctc aaaacagaag 420
gccaaagaca gcggttgtgt cccgagtatc ccaccgcgag gacgctctgt tcctctgacc 480
gaggttgtaa aaagggatgg atggaccgcg agagcaaagg aattcagacc ggaagggtgtg 540
tagtgcataa aggaaccag aagacctgtg aagtctctgc ctggtgcccc atcgaggcag 600
tggaagaggg cccccggcct gctctcttga acagtgccga aaacttact gtgtcatca 660
agaacaatat cgaactcccc ggccacaact acaccacgag aaacatcctg ccaggtttaa 720
acatcacttg taccttccac aagactcaga atccacagtg tccattttc cgactaggag 780
acatcttccg agaaacaggc gataattttt cagatgtggc aattcagggc ggaataatgg 840
gcattgagat ctactgggac tgcaacctag accgttgggt ccatcactgc cgtcccaaat 900
acagtttccg tcgccttgac gacaagacca ccaacgtgtc cttgtaccct ggctacaact 960
tcagatacgc caagtactac aaggaaaaca atgttgagaa acggactctg ataaaagtct 1020
tcgggatccg ttttgacatc ctggtttttg gcaccggagg aaaatttgac attatccagc 1080
tggttgtgta catcggtcca accctctcct acttcggtct ggtaagagat tctcttttcc 1140
atgcttttagg aaaatggttt ggagaaggaa gtgactaacg cagcgcttgt ctgcattctc 1200
cccaggccgc tgtgttcac cacttctc tgcacactta ctccagtaac tgctgtcgtc 1260
cccatattta tccctggtgc aagtgtgtc agccctgtgt ggtcaacgaa tactactaca 1320
ggaagaagtg cgagtccatt gtggagccaa agccgacatt aaagtatgtg tcctttgtgg 1380
atgaatccca cattaggatg gtgaaccagc agctactagg gagaagtctg caagatgtca 1440
aggccaaga agtcccaaga cctgcgatgg acttcacaga tttgtccagg ctgcccctgg 1500
cctccatga cacaccccc attcctggac aaccagagga gatacagctg cttagaaagg 1560
aggcgactcc tagatccagg gatagcccc tctggtgcca gtgtggaagc tgcctcccat 1620
ctcaactccc tgagagccac aggtgcctgg aggagctgtg ctgccgaaa aagccggggg 1680
cctgcatcac cactcagag ctgttcagga agctggtcct gtccagacac gtccctgcagt 1740
tcctcctgct ctaccaggag cccttgctgg cgctggatgt ggattccacc aacagccggc 1800
tgcggcactg tgcctacagg tgctacgcca cctggcgctt cggctcccag gacatggtctg 1860
actttgccat cctgcccagc tgctgccgct ggaggatccg gaaagagttt ccgaagagt 1920
aagggcagta cagtggcttc aagagtctt actgaagcca ggcaccgtgg ctcacgtctg 1980

```



```

taatcccagc gctttgggag gccgaggcag gcagatcacc tgaggctcggg agttgggagac 2040
ccgcctggct aacaaggcga aatcctgtct gtactaaaaa tacaaaaatc agccagacat 2100
gggtggcatgc acctgcaatc ccagctactc gggaggctga ggcacaagaa tcacttgaac 2160
ccgggaggca gaggttgtag tgagcccaga ttgtgccact gctctccagc ctgggaggca 2220
cagcaaaactg                                     2230

```

<210> 76

<211> 5966

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7509982CB1

<400> 76

```

gcttggtctg gctacacccc ttttcagaaa ccaggctgtg taagagctgc tggagtaggc 60
accattttaa agaaaaaatg aagaagcagc aataaagaag ttgtaatcgt tacctagaca 120
aacagagAAC tggttttgac agtgtttcta gagtgttttt tattattttc ctgacagttg 180
tgttccacca tgattacttt ctcttccagc gaataggcta aatgaatatg aaacagaaaa 240
gcgtgtatca gcaaaccaaa gcacttctgt gcaagaatth tcttaagaaa tggaggatga 300
aaagagagag cttatttgaa tggggcctct caatacttct aggactgtgt attgctctgt 360
tttccagttc catgagaaat gtccagtttc ctggaatggc tcctcagaaat ctgggaaggg 420
tagataaatt taatagctct tctttaatgg ttgtgtatac accaatatct aatttaacc 480
agcagataat gaataaaaca gcacttgctc ctcttttgaa aggaacaagt gtcattgggg 540
caccaataaa aacacacatg gacgaaatac ttctggaaaa ttaccatat gctatgggaa 600
tcattcttaa tgaaactttc tcttataagt taatattttt ccagggatat aacagtccac 660
tttggaaga agatttctca gctcattgct gggatggata tggtgagttt tcatgtacat 720
tgaccaaata ctggaataga ggatttgtgg ctttacaac agctattaat actgccatta 780
tagaaatcac aaccaatcac cctgtgatgg aggagtgtat gtcagttact gctataacta 840
tgaagacatt acctttcata actaaaaatc ttcttcacaa tgagatgttt attttattct 900
tcttgcttca tttctcccca cttgtatatt ttatatcact caatgtaaca aaagagagaa 960
aaaagtctaa gaatttgatg aaaatgatgg gtctccaaga ttcagcattc tggctctcct 1020
ggggtctaat ctatgctggc ttcattctta ttatttccat attcattaca attatcataa 1080
cattcaccca aattatagtc atgactggct tcatggctat atttataccc ttttttttat 1140
atggcttata tttggtagct ttggtgttcc tgctgagtgt gctgttaaag aaagctgtcc 1200
tcaccaattt ggttgtgttt ctctttacc 1260
tttatgaaca acttcttca tctctggagt ggattttgaa tattttagc ccttttgcc 1320
ttactactgg aatgattcag attatcaaac tggattataa cttgaatggg gtaattttt 1380
ctgacccttc aggagactca tatacaatga tagcaacttt ttctatgttg cttttggatg 1440
gtctcatcta cttgctattg gcattatact ttgacaaaat tttaccctat ggagatgagc 1500
gccattatc tcttttattt ttcttgaatt catcatcttg tttccaacac caaaggacta 1560
atgctaaggt tattgagaaa gaaatcgatg ctgagcatcc ctctgatgat tattttgaac 1620
cagtagctcc tgaattccaa ggaaaagaag ccatcagaat cagaaatgtt aagaagggaat 1680
ataaaggaaa atctggaaaa gtggaagcat tgaaaggctt gctctttgac atatatgaag 1740
gtcaaatcac ggcaatcctg ggtcacagtg gagctggcaa atcttccactg ctaaattatc 1800
ttaatggatt gtctgttcca acagaaggat cagttaccat ctataataaa aatctctctg 1860
aaatgcaaga cttggaggaa atcagaaaaga taactggcgt ctgtcctcaa ttcaatgttc 1920
aatttgacat actcaccgtg aaggaaaacc tcagcctgtt tgctaaaaata aaagggattc 1980
atctaaagga agtggaaaca gaggtacaac gaattattt ggaattggac atgcaaaaca 2040
ttcaagataa ccttgctaaa catttaagt aaggacagaa aagaaagctg acttttggga 2100
ttaccatttt aggagatcct caaattttgc ttttagatga accaactact ggattggatc 2160
ccttttccag agatcaagtg tggagcctcc tgagagagcg tagagcagat catgtgatcc 2220
ttttcagtac ccagtcctat gatgaggctg acatcctggc tgatagaaaa gtgatcatgt 2280
ccaatgggag actgaagtgt gcaggttctt ctatgttttt gaaaagaagg tggggtcttg 2340
gatatcacct aagttttacat aggaatgaaa tatgtaaccc agaacaaata acatccttca 2400

```

ttactcatca	catccccgat	gctaaattaa	aaacagaaaa	caaagaaaag	cttgtatata	2460
ctttgccact	ggaaaggaca	aatacatttc	cagatctttt	cagtgatctg	gataagtgtt	2520
ctgaccaggg	agtgacaggt	tatgacattt	ccatgtcaac	tctaaatgaa	gtctttatga	2580
aactggaagg	acagtcaact	atcgaacaag	gtaaagccat	ttgtataaat	ttcgaacaag	2640
tggagatgat	aagagactca	gaaagcctca	atgaaatgga	gctggctcac	tcttccttct	2700
ctgaaatgca	gacagctgtg	agtgacatgg	gcctctggag	aatgcaagtc	tttgccatgg	2760
cacggctccg	tttcttaaaag	ttaaaacgtc	aaactaaagt	gttattgacc	ctattattgg	2820
tatttggaat	cgcaatatte	cctttgattg	ttgaaaatat	aatatatgct	atgttaaagt	2880
aaaagatcga	ttgggaattt	aaaaacgaat	tgtattttct	ctctcctgga	caacttcccc	2940
aggaaccccg	taccagcctg	ttgatcatca	ataacacaga	atcaaatatt	gaagatttta	3000
taaaatcact	gaagcatcaa	aataactttt	tggaaagtaga	tgactttgaa	aacagaaatg	3060
gtactgatgg	cctctcatac	aatggagcta	tcabagtttc	tggtaaacaa	aaggattata	3120
gattttcagt	tgtgtgtaat	accaagagat	tgcactgttt	tccaattctt	atgaatatta	3180
tcagtaatgg	gctacttcaa	atgtttaatc	acacacaaca	tattcgaatt	gagtcaagcc	3240
catttcctct	tagccacata	ggactctgga	ctgggttgcc	ggatggttcc	tttttcttat	3300
ttttggttct	atgtagcatt	tctccttata	tcaccatggg	cagcatcagt	gattacaaga	3360
aaaatgctaa	gtcccagcta	tggatttcag	gcctctacac	ttctgcttac	tggtgtgggc	3420
aggcactagt	ggacgtcagc	ttcttcattt	taattctcct	tttaatgtat	ttaattttct	3480
acatagaaaa	catgcagtac	cttcttatta	caagccaaat	tgtgtttgct	ttggttatag	3540
ttactcctgg	ttatgcagct	tctcttgtct	tcttcatata	tatgatata	tttatttttc	3600
gcaaaaggag	aaaaaacagt	ggcctttggg	cattttactt	cttttttgcc	tccaccatca	3660
tgttttccat	cactttaatc	aatcattttg	acctaagtat	attgattacc	accatgggtat	3720
tggttccttc	atataccttg	cttggattta	aaactttttt	ggaagtgaga	gaccaggagc	3780
actacagaga	atttccagag	gcaaattttg	aattgagtgc	cactgatttt	ctagtctgct	3840
tcatacccta	ctttcagact	ttgtatttcg	tttttgttct	aagatacatg	gaactaaaat	3900
gtggaaagaa	aagaatgcga	aaagatcctg	ttttcagaat	ttcccccaa	agtagagatg	3960
ctaagccaaa	tccagaagaa	cccatagatg	aagatgaaga	tattcaaaca	gaaagaataa	4020
gaacagtcac	tgctctgacc	acttcaatct	tagatgagaa	acctgttata	attgccagct	4080
gtctacacaa	agaatatgca	ggccagaaga	aaagttgctt	ttcaaagagg	aagaagaaaa	4140
tagcagcaag	aaatatctct	ttctgtgttc	aagaagggtga	gattttggga	ttgctaggac	4200
ccagtgggtg	tggaaaaagt	tcacttatta	gaatgatata	tgggatcaca	aagccaactg	4260
ctggagaggt	ggaactgaaa	ggctgcagtt	cagttttggg	ccacctgggg	tactgccctc	4320
aagagaacgt	gctgtggccc	atgctgacgt	tgagggaaca	cctggagggtg	tatgctgccg	4380
tcaaggggct	caggggaagcg	gacgcgaggc	tcgccatcgc	aagattagtg	agtgccttca	4440
aaactgcata	gctagtgaa	gttcctgtgc	agaaattaac	agcaggaatc	acgagaaagt	4500
tgtgttttgt	gctgagcctc	ctgggaaact	ccactgtctt	gctcctggat	gaaccatcta	4560
cgggcataga	ccccacaggg	cagcagcaaa	tgtggcaggc	aatccaggca	gtcgttaaaa	4620
acacagagag	agggtgtcctc	ctgaccaccc	ataacctggc	tgaggcggaa	gccttgtgtg	4680
accgtgtggc	catcatgggtg	tctggaaggc	ttagatgcat	tggctccatc	caacacctga	4740
aaaacaaact	tggcaaggat	tacattctag	agctaaaagt	gaaggaaacg	tctcaagtga	4800
ctttggtcca	cactgagatt	ctgaagcttt	tcccacaggc	tgcaaggcag	gaaagggtatt	4860
cctctttgtt	aacctataag	ctgcccggtg	cagacgttta	ccctctatca	cagacctttc	4920
acaaattaga	agcagtgaag	cataacttta	acctggaaga	atacagcctt	tctcagtga	4980
cactggagaa	ggtattctta	gagctttcta	aagaacagga	agtaggaaat	tttgatgaag	5040
aaattgatac	aacaatgaga	tggaaactcc	tccctcattc	agatgaacct	taaaacctca	5100
aacctagtaa	ttttttgttg	atctcctata	aacttatgtt	ttatgtaata	attaatagta	5160
tgtttaattt	taaagatcat	ttaaaattaa	catcagggtat	attttgtaaa	tttagttaac	5220
aaatacataa	attttaaaaa	tattcttctc	ctcaaacata	ggggtgatag	caaacctgtg	5280
ataaaggcaa	tacaaaatat	tagtaaagtc	acccaaagag	tcaggcactg	ggtattgtgg	5340
aaataaaact	atataaaact	agaatttttt	aaaaatatga	cttttttacc	ttttacaaaa	5400
cattctcttg	ctgaaatatg	tgaagggtat	attcagtagc	caagagttgc	atgactactt	5460
cacaccagtt	catgatataa	caggtataca	ggttttcttt	tataaccaac	tacaactcaa	5520
gagtcttctg	aaagtgttcc	agaaattgct	ttaaaactca	aaagtaaggg	gccagggtga	5580
gtggctcacg	cctgtaatcc	cagcactttg	ggaggccgag	gcagggtggat	cacaagggtca	5640
ggagttcgag	actagcctgg	ccaatatggt	gaaactccat	ctctaataaa	aatacaaaaa	5700
ttagccgggc	gttggcattt	gcctgtagtc	ctagctattc	gggagggtga	gggaggagaa	5760

ttgcttgaac ccgggaggca gaggttgcag tgagccatgt gctagtgcac tccagcctgg 5820
gtgacagagt gagactctgt caaaaaaaaaa aaaaacaaaa aaaaaaacia aaaaccttca 5880
agggttttga ggtctttggc cacaatttga gagccccctt tggaagggtt tcccttttac 5940
ttttgaataa agggtcgga tttggc 5966

<210> 77

<211> 2071

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7510082CB1

<400> 77

ccgggtagtg agcggaggga caggaagggt agggcaagaa agggagaggg gacaggaggg 60
aagggtgggc caaagcgggt agaaaggagg gccagccagt tgcgtggggg agagtggccg 120
aggcccgggg gcaggagtgc agggctctga ggcggggaga ggagaggaga gaagagccgc 180
ggggggccca gcccgagcc aggatgcccg cgccgcgcgc ccgggagcag cccgcgctgc 240
ccggggagcg ccagccgctg ctgcctcgcg gtgcgcgggg ccctcgacgg tggcgcgggg 300
cggcgggcgc ggccgtgctg ctggtggaga tgctggagcg cgccgccttc ttcggcgta 360
ccgccaacct cgtgctgtac ctcaacagca ccaacttcaa ctggaccggc gagcaggcga 420
cgcgcgccgc gctggtattc ctgggcgcct cctacctgct ggcgcccggt ggcggtggc 480
tggccgacgt gtacctgggc cgctaccgcg cggctcgctg cagcctgctg ctctacctgg 540
ccgcctcggg cctgctgccc gccaccgcct tccccgacgg ccgcagctcc ttctgcggag 600
agatgccccg gtcgcccgtg ggacctgcct gccctcgcc cggctgcccg cgctcctcgc 660
ccagccccca ctgcgcgccc gtccctctacg cgggcctgct gctactcggc ctggccgcca 720
gctccgtccg gagcaacctc acctccttcg gtgcccacca ggtgatggat ctcgcccgcg 780
acgccaccgc cgcttcttc aactggtttt actggagcat caacctgggt gctgtgctgt 840
cgctgctggt ggtggcggtt attcagcaga acatcagctt cctgctgggc tacagcatcc 900
ctgtgggctg tgtgggcctg gcatttttca tcttcctctt tgccaccccc gtcttcatca 960
ccaagcccc gatgggcagc caagtgtcct ctatgcttaa gctcgctctc caaaactgct 1020
gccccagct gtggcaacga cactcgcca gagaccgtoa atgtgcccgc gtgctggccg 1080
acgagaggto tccccagcca ggggcttccc cgcaagagga catcgccaac ttccagggtg 1140
tggtgaagat cttgcccgtc atggtgaccc tggtgcccta ctggatggtc tacttccaga 1200
tgagtgccac ctatgtcctg cagggtcttc acctccacat cccaaacatt ttccagcca 1260
acccggccaa catctctgtg gccctgagag ccaggggcag cagctacacg atcccggaag 1320
cctggctcct cctggccaat gttgtggtgg tgctgattct ggtccctctg aaggaccgct 1380
tgatcgaccc tttactgctg cggtgcaagc tgcttccctc tgctctgcag aagatggcgc 1440
tggggatggt ctttggtttt acctccgtca ttgtggcagg agtcctggag atggagcgct 1500
tacactacat ccaccacaac gagaccgtgt cccagcagat tggggaggto ctgtacaacg 1560
cgccaccact gtccatctgg tggcagatcc ctacgtacct gctcattggg atcagtga 1620
tctttgccag catcccaggc ctggagtgtg cctactcaga ggccccgcgc tccatgcagg 1680
gcgccatcat gggcatcttc ttctgcctgt cgggggtggg ctactgttg ggctccagcc 1740
tagtggcact gctgtccttg cccgggggct ggctgcactg ccccaaggac tttgggaaca 1800
tcaacaattg ccgatggac ctctacttct tctgctggc tggcattcag gccgtcacgg 1860
ctctcctatt tgtctggatc gctggacgct atgagagggc gtcccagggc ccagcctccc 1920
acaggccggt tcagcacgga caggggctcg acaggcccta tccaggcccc ttggtttact 1980
ctaccggaaa gaacggcagc agtcccagct ctggtttcct tctcggttta ttctgttaga 2040
atgaaatggt ccataaata agggcatggt c 2071

<210> 78

<211> 3703

<212> DNA

<213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 7510367CB1

<220>
 <221> unsure
 <222> (1) ... (3703)
 <223> a, t, c, g, or other

<400> 78
 cggacggtgg gggcggtgac gtagtggttg tgccccgttc ttgccccctc agtactagag 60
 tctccggctt cgctcacgcg ccttgggcat aagagtcctc tcgttggtcc cggaggtggg 120
 gttgcgctca caagggcgga cgcgcgcac ggtggcggcc actgcatcgc gtccccacctc 180
 cgcggccctg ggcgcgcgtg tgtcgacggg ccccgagcct atgacgggac agggccagtc 240
 ggcgtccggg tcgtcggcgt ggagcacggg attccgccac gtccggtatg agaacctgat 300
 agcgggctg agcggcggtg tcttatccaa ccttgcgctg catccgctcg acctcgtgaa 360
 gatccgcttc gccggaacaa tcctgtgagt ttatgatata tgctatacag atgaggataa 420
 cagaagtga ctaacttgcc caagtcacaa gtttgtaaag atggatctgg gatttaaacc 480
 cagtgaatga tggattggaa ctgagaccga aatataatgg aattttacat tgcttgacta 540
 ccatttgtaa acttgatgga ctacggggac tttatcaagg agtaaccca aatatatggg 600
 gtgcaggttt atcctgggga ctctactttt tcttttaca tgccatcaag tcatataaaa 660
 cagaaggag agctgaacgt ttagaggcaa cagaatacct tgcctcagct gctgaagctg 720
 gagccatgac cctctgcatt acaaacccat tatgggtaac aaaaactcgc cttatgttac 780
 agtatgatgc tgttggttaac tccccacacc gacaatataa aggaatgttt gatacacttg 840
 tgaaaatata taagtatgaa ggtgtgcgtg gattatataa gggatttggt cctgggctgt 900
 ttggaacatc gcatgggtgc cttcagttta tggcatatga attgctgaag ttgaagtaca 960
 accagcatat caatagatta ccagaagccc agttgagcac agtagaatat atatctgttg 1020
 cagcactatc caaaatattt gctgtcgcag caacataccc atatcaagtc gtaagagctc 1080
 gtcttcagga tcaacacatg ttttacagtg gtgtaataga tgtaatcaca aagacatgga 1140
 ggaaagaagg cgtcgggtga ttttacaagg gaattgctcc taatttgatt agagtgaactc 1200
 cagcctgctg tattaccttt gtggtatatg aaaacgtctc acatttttta cttgacctta 1260
 gagaaaagag aaagtaagct caaagaggac aattccagta tatctgcccc aggcagcaac 1320
 aagctctttt gtgtttaagg cataaaagaa gaattctgca tagaaacatg gctcatattc 1380
 gaaattgctc tatagtcatt agaagccaga gaactgctaa gtctcctgca atgtttttct 1440
 gctttttgcc tccccatat atatggaact tggctacctc tgcctgaaat ggctgccatc 1500
 aacacaaatg taaaactgac acgaaggata gagtttcaca gatttctacg ttttattggt 1560
 ggaagctgat ttgcaacatt tgctaaatgg attagatgaa tgtaactctt tttgtgagct 1620
 tacttgctg gattgcttta aaattaacct ttgtgcaata ccaagaaaat agctctttta 1680
 aagaatgtct ttgtatgtct caaggtaaat taaggattta ctgaataagg tgttgaccaa 1740
 atccagacca ttttatttta tttttttatt ttttttttt ttgagatgga gtcttgcttt 1800
 gtcgcccagg ctggagtga gtggcgtgat ctcagctcac tgcaacctcc acctccggg 1860
 ttcacgccat tctcctgcct cagcctcctg agtagctggg actacaggca cctgccacca 1920
 cgcctggcta actttttttt atatttttag tagaaatggg gtttcacat gttagccagg 1980
 atggtctcaa tctcctgacc ttgtgatccg cctgccttgg cctcccaaag tgctgggatt 2040
 acaggcgtga gccactgcgc ctggccagac catttttaga ttgggaaatt ttagtgagaa 2100
 aaaatgcact gtaaatatgc tttagtttta attcagttgg gatgcactac ctacgaaaa 2160
 ttgagaaact atatacttct cagagaaata tctgacatct attgtcattc cattgctatt 2220
 ttttttcccc agagacttcc ataattttaa ataaaatcct agatccagtt cttgtttttt 2280
 ggcataaata cttaatctat tttaaattta taaaatctga gcttctagga tccagctgtg 2340
 tcaaccttta tttagcatat ataactataa atcacttatt acagatgcta aatagatcac 2400
 cttttacaga tgctgaaatg tttgggatat gtttggtgac aaggtaaatg gaaatgagaa 2460
 actttatact tcagttttca gatatatgga tctagatccc aaataaatga ttaactttca 2520
 ttggtttctc aaattcagggt tgaatacaaa attaatagcc ttatttgatt ttacttttat 2580
 gagtcatgtg agacatctat aaatataaaa gggcctgtac ccaaaggatg ccggaatact 2640
 agtattttta tttatcgtaa acatccacga gtgctgttgc actaccatct atttgttgta 2700
 aataaaagtg ttgttttcaa agccatcttt aaatagttct ttaaaaatag gtcttttttt 2760

tataatatttgg aaaaggcatt gttttttaag taaagataaa atggtaagta cctaattgta 2820
tttactgtaa tataacatgc agatgaatgc tttataagtt aaatatgatg tattttttca 2880
tactttctgga ttatactata attcatatga aatcttgata ttagtcccca cacggaaaaa 2940
gtgaactgca gttgatattt ggtgtttaag atagcaccat tgtttaaata ccgcctatgt 3000
actcccaaat gaataaaaca taattcttgt cctctgagag catacaagct tgtgtgatag 3060
ataaatatgc attaaataat tacagctata gattaagaac tcgtaaggaa tatctcacia 3120
agcctggtaa gagttctgac agaagagaac tcaatttcag tcattcaaca acaaatagtc 3180
actcaactcc tgctcttttg cagggtacgtc accaagcact gaggatatag caataaataa 3240
gccagacaat attcctgccc tcagggaatt ttcattcttg tgtaagtgc agaaaaggaa 3300
atatatgcat aatgtaattt cagggtattta atgctataaa taaaactaca gcagaacggg 3360
ggaatagtgt tgctatctta ggtagtatgg ttggggctcag gaaaggtctc tgagatagta 3420
tttggaacat ttgaaagaa gtgaggaagc gagccacagt gagaggaaac acattctagg 3480
cagagaggac aggaagtaaa aagggcctga tggaaggact aaagttggat agaggggatg 3540
ggtgagcaca aaacggagtt ggcaaattgg ccttgccgta tgtgtggaaa gaccaggtg 3600
ggacgccang ccctctgttc aaaataccgt tccattctc gtttgccctg gcggatatta 3660
caccctatgt tatgggtccg ccttcaaagg cgtaaacacc cct 3703

<210> 79

<211> 1171

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7510413CB1

<400> 79

gagcacggag attcggcagc aggaggaaaa gcagcaaacc agatggagaa ggaaggccaa 60
aaagataagt agaaagctgg accatgagct ccttgagggc agggactgaa tggttactat 120
gtccccaggc cccagcatga ccttctcctg gattcctcat cttccttctg tgacctgtgt 180
ctccatcagt ttctcctccg gcatcttttt cttacaggat tcttacctca ggaatagatg 240
gacatggcct ggcagatgat gcagctgctg cttctggcct tgggtgactgc tgcggggagt 300
gcccagccca ggagtgcgcg ggccaggagc gacctgctca atgtctgcat gaacgccaaag 360
caccacaaga cacagcccag ccccgaggac gagctgtatg gccagggtgg agctcctcaa 420
gggcccctcc caggaagtgt tcctctggat gacctacctg gggcagagga gccagaatat 480
ggaggagatg gctgtggtgg ggagagactt agtctctgtg cttccccacc cagtgcagtc 540
cctggaagaa gaatgcctgc tgcacggcca gcaccagcca ggagctgcac aaggacacct 600
ccgcctgta caactttaac tgggatcact gtggtaagat ggaaccacc tgcaagcgcc 660
actttatcca ggacagctgt ctctgagtgc tcaccaacc tggggccctg gatccggcag 720
gtcaaccaga gctggcgcaa agagcgcatt ctgaacgtgc ccctgtgcaa agaggactgt 780
gagcgtcgtt gggaggactg tcgcacctcc tacacctgca aaagcaactg gcacaaaggc 840
tggaattgga cctcagggat taatgagtgt ccggccgggg ccctctgcag cacccttgag 900
tcctacttcc cactccagc cgccctttgt gaaggcctct ggagccactc cttcaaggtc 960
agcaactata gtcgagggag cggccgctgc atccagatgt ggtttgactc agcccagggc 1020
aaccccaatg aggaggtggc caagttctat gctgcccga tgaatgctgg ggccccgtct 1080
cgtgggatta ttgattctg atccaagaag ggtcctctgg ggttcttcca acaacctatt 1140
ctaatagaca aatccacatg aaaaaaaaaa a 1171

<210> 80

<211> 323

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1721303CB1

<400> 80

```

ccaagactcc aaaatggcgt cagttggtga gtgtccggcc ccagtaccag tgaaggacaa 60
gaaacttctg gaggtcaaac tgggggagct gccaaagctgg atcttgatgc gggacttcag 120
tcctagtggc attttcggag cgtttcaaag agagcacgag cggctccgca aataccactg 180
aagaggacac actctgcacc cccccacccc acgaccttgg cccgagcccc tccgtgagga 240
acacaatctc aatcgttgct gaatcctttc atatcctaata aggaattaac ctccaaataa 300
aacatgactg gtacgtgtaa..aaa 323

```

<210> 81

<211> 1221

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7502007CB1

<400> 81

```

attaactcag ctgggagttg aagagccgat gggcagcagg cagacttgag tctcctttct 60
gtccatgggc tggggccact gtctcaggtc caccctgggc tccaaaatgg tctcctgggc 120
cgtgatagca aagatccagg aaatactgca gaggaagatg gtgcgagagt tcctggccga 180
gttcctgagc acatatgtca tgatggtatt cggccttggc tccgtggccc atatggttct 240
aaataaaaaa tatgggagct accttgggtg caacttgggt tttggcttcg gagtccacct 300
gggagtgac gtggcaggcc gcatctctgg agcccacatg aacgcagctg tgacctttgc 360
taactgtgcg ctgggcccgc tggcctggag gaagtttccg gtctatgtgc tggggcagtt 420
cctgggctcc ttcctggcgg ctgccacct ctacagtctc ttctacacgg ccattctcca 480
cttttcgggt ggacagctga tggtgaccgg tcccgtcgct acagctggca tttttgccac 540
ctaccttctc gatcacatga cattgtggcg gggcttctc aatgaggcgt ggctgaccgg 600
gatgtccag ctgtgtctct tcgccatcac ggaccaggag aacaaccag cactgccagg 660
aacagaggcg ctggtgatag gcatcctcgt ggtcatcatc ggggtgtccc ttggcatgaa 720
cacaggatat gccatcaacc cgtcccggga cctgcccccc cgcattctca ccttcattgc 780
tggttggggc aaacaggtct tcaggtgga tcactctacc ggtcttcatt ggctccacca 840
tcccacggga gccctgaaa ttggaggatt ctgtggcgta tgaagaccac gggataaccg 900
tattgccaa gatgggatct catgaaccca cgatctctcc cctcaccccc gtctctgtga 960
gccctgcca cagatcttca gtccaccctg ccccaccctt acatgaatcc atggccctag 1020
agcacttcta agcagagatt atttgtgat ccatccattc cccaataaag caaggcctgt 1080
ccgacaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1140
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaagg gggggggggcg 1200
cgggggcccc gacaaggggg g 1221

```

<210> 82

<211> 2008

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7506439CB1

<400> 82

```

gcagcctcag aaggtgtgag cagtgccac gagaggcagg ctggctggga catgagggtg 60
gcagagggca ggcaagctgg cccttgggtg gcctcgctcc gagcactcgg aggcactcct 120
atgcttggaa agctcgctat gctgtgtgg gtccagcagg cgctgctcgc cttgctcctc 180
cccacactcc tggcacagg agaaagccagg aggagccgaa acaccaccag gcccgctctg 240
ctgaggctgt cggattacct tttgaccaac tacaggaagg gtgtgcgccc cgtgaggggac 300
tggaggaagc caaccaccgt atccattgac gtcattgtct atgccatcct caacgtggat 360

```

```

gagaagaatc aggtgctgac cacctacatc tggtagccgc agtactggac t gatgagttt 420
ctccagtgga accctgagga ctttgacaac atcaccaagt tgtccatccc caccgacagc 480
atctgggtcc cggacattct catcaatgag ttcgtggatg tggggaagtc tccaaatc 540
ccgtacgtgt atattcggca tcaacatctc tttgtggcgc ttgccagaaa aggtgaaatc 600
cgacaggagt gtcttcatga accagggaga gtgggagttg ctgggggtgc tgcctactt 660
tcgggagttc agcatggaaa gcagtaacta ctatgcagaa atgaagttct atgtgggtcat 720
ccgccggcgg cccctcttct atgtgggtcag cctgctactg cccagcatct tctcatggt 780
catggacatc gtgggcttct acctgcccc caacagtggc gagagggtct ctttcaagat 840
tacactcctc ctgggctact cgggtcttct gatcatcgtt tctgacacgc tgccggccac 900
tgccatcggc actcctctca ttggtgtcta ctttgtgggt tgcattggctc tgctgggtgat 960
aagtttgcc gagaccatct tcattgtgcg gctgggtgcac aagcaagacc tgcagcagcc 1020
cgtgctgctc tggctgcgct acctggttct ggagagaatc gcctggctac tttgctgag 1080
ggagcagtc acttcccaga ggccccagc caccctccaa gccaccaaga ctgatgactg 1140
ctcagccatg ggaaaccact gcagccacat gggaggaccc caggacttct agaagagccc 1200
gagggacaga tgtagccctc cccaccacc tggggaggcc tcgctggcgg tgtgtgggct 1260
gctgcaggag ctgtcctcca tccggcaatt cctggaaaag cgggatgaga tccgagaggt 1320
ggccccagac tggctgcgct tgggtctcgt gctggacaag ctgctattcc acatttacct 1380
gctggcgggt ctggcctaca gcataccct ggttatgctc tgggtccatct ggcagtacgc 1440
ttgagtgggt acagcccagt ggaggagggg gtacagtcct ggttaggtgg ggacagagga 1500
tttctgctta ggccctcag gaccagggga atgccagggga cattttcaag acacagacaa 1560
agtcccgtgc cctgtttcca atgccaatc atctcagcaa tcacaagcca aggtctgaac 1620
ccttccacca aaaactgggt gttcaaggcc cttacacct tgtccaccc ccagcagctc 1680
accatggctt taaaacatgc tctcttagat caggagaaac tcgggcactc cctaagtcca 1740
ctctagttgt ggacttttcc ccattgacct tcacctgaat aagggaactt ggaattctgc 1800
ttctctttca caactttgct tttaggttga aggcaaaacc aactctctac tacacagggc 1860
tgataactct gtacgaggct tctctaacc ctagtgtctt tttttcttc acctcacttg 1920
tggcagcttc cctgaacact catccccat cagatgatgg gagtgggaag aataaaatgc 1980
agtgaaccc taaaaaaaaa aaaaaggg 2008

```

<210> 83

<211> 1080

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7509243CB1

<400> 83

```

ggaggagggc agggcaggcg gcagcctggg cacaggcccc taggtgctta ctctcacct 60
gtttcccacc tctcccccat agccagcccc acggccctgg cagggtcctg gccacagcat 120
gccagtgct gggtctctga gctgctgggg tggccgggtg ctgcccctgc tgctggccta 180
tgtctgctac ctgctgctcg gtgccactat cttccagctg ctgagagaggc aggcggaggc 240
tcagtccagg gaccagtttc agttggagaa gctgcgcttc ctggagaact acacctgct 300
ggaccagtgg gccatggagc agtttgtgca ggtcatcatg gaagcctggg tgaaagggtg 360
gaaccccaaa ggcaactcta ccaacccag caactgggac tttggcagca gtttcttct 420
tgcaggcaca gtgctcacta ccatagggca ctgacagcag ctgctacacc ccctcggcca 480
gaaaactcac tccatcccac cccaaggaaa ccatcagatc caggatatgg gaacctggca 540
cccagcacag aggcaggtta ggtcttctgt gtcttctatg ccctgttggg catcccgct 600
aacgtgatct tctcaacca cctgggcaca gggctgcgtg cccatctggc cgccattgaa 660
agatgggagg accgtccag gcgctccag gtactgcaag tcctgggcct ggctctgttc 720
ctgaccctgg ggacgctggt cattctcctc tttccaccca tgggtcttcag ccatgtggag 780
ggctggagct tcagcgaggg cttctacttt gctttcatca ctctcagcac cattggcttt 840
ggggactatg ttgttggcac agaccccagc aagcattata tctcagtgtg tcggagcctg 900
gcagccatct ggatcctcct gggcctggcg tggctggcgc tgatcctccc actgggcccc 960
ctgcttctgc acagatgctg ccagctctgg ctgctcagta ggggcctcgg cgtcaaggat 1020

```

ggggcagcct ctgacccag tgggctcccc aggcctcaga agatcccat ctctgcatga 1080

<210> 84

<211> 2412

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7509404CB1

<400> 84

```

ctcgagccgc tcgagccgcg ggcggctggg acgcagctgc ccccgctcgg cgccccgtgc 60
acccttagca gccactgcca cctgggcccc gagcctccac gatctcgccc ggcgattgtg 120
ggcaggggcg cctccggatc gatcttctga aattcaagtt ttcaagatga agtttttatt 180
gacaactgcc tttttaattt taatttcctt gtgggtggaa gaagcctatt ctaaggaaaa 240
gtcttcaaag aaagggaagg ggaaaaagaa gcagtatcta tgcccatcag agagattgta 300
ccattgaatg acagcatttt catacttcag tctgtatgta ctaagaaggt cagcagtcag 360
cagaggacct tgcccagagta cctgccaact ccactagcaa tatcttgaac aggttatttg 420
tcagttatga tcccaggata agaccaaact tcaaaggcat tcctgttgat gtagtagtca 480
acatttttat taacagtttt ggatccattc aagaaacaac aatggactat agagttaaca 540
tcttcctgag acaaaaatgg aatgacccca ggctgaagct ccccgatgat tttaggggtt 600
cagatgcact gacagtggat ccaacaatgt acaagtgttt atggaaacct gatttatttt 660
ttgcaaatga aaaaagtgcc aattttcatg atgtgaccca ggaaaacatc ctcctcttta 720
tttttcgtga tggagatgtc cttgtcagca tgaggttatc tattactctt tcatgccctt 780
tggacttgac attgtttccc atggatacac aacggttgcaa gatgcaactg gagagctttg 840
gttacacaac tgatgattta cgatttatct ggcagtcagg agatcctgtg caattagaaa 900
aaattgcctt gcctcaattt gatatacaaa aggaagatat tgaatatggt aactgtacaa 960
aatactataa aggcacgggc tactacacat gcgtggaagt catcttcacc ctgaggaggc 1020
aggtcggctt ttacatgatg ggggtctacg ccccaaccct gctcattgtt gttctctcct 1080
ggctttcctt ctggatcaac ccggacgcga gtgctgccag agtgcccctg gggttggtgag 1140
accagatgca aaaaagtgtg tacttctaag tctgatctga gatctaataa cttcagcatt 1200
gttggaagct taccaagaga ttttgaacta tccaattatg actgctatgg aaaaccatt 1260
gaagttaaca acggacttgg gaaatctcag gctaagaaca acaagaagcc tccccctgcg 1320
aaacctgtta ttccaacagc agcaaagcga attgatcttt atgcaagagc attgtttctc 1380
ttctgcttct tgttcttcaa tggtatata tgggtctata atttatgata aatcttttcc 1440
atttgtacaa aataaaattc catttcattg tgacctactc ctttcataaa tgccaatctg 1500
tgagaacttt tgaattttca tagcaacatt gcatttttga tgccatttga ttgtaataaa 1560
actgtggcac cttaattttg aatggcagca tgatcatgta atatctgtgc tctaataacg 1620
atgtatata gtatagtga catattgctt agtaacaaat gaaggacaag catactacat 1680
aatataatcc atacaattct cttcagttag tgtaaaactgc aaatactaca gataattctg 1740
ataataaaat gatatgcacg ctgaatcctg ctatggtcac cattctaata tatgtagtat 1800
ttcaaatctt cttccttgta actttcaaag aaagccatct tattcttgta aaattttaga 1860
tggtattatc acagatttaa aaaggttgta ttacatattg tttaaacttt gtaagtagaa 1920
atatatctgt tataattata caggctctgt ggagaaataa agttcaaaaa atattaattt 1980
gtaaaatcag ctcgttttta agtgtgcttg tgttgtaaaa aatatcagat agtaatacac 2040
agtgagcatt tttaaacaaa gggaaacctt tatttatgta actgtatact gaattctgac 2100
aaaataaaaa aagatacctt attgacgaaa tatttaggat aaacaaaatt ctattttaatc 2160
caccttaaaa cctaaatgta ttttcattga tttcatttgt tgggtacatat tacacaaaac 2220
attgtgcctt aaatgagtc atacatcttt taaattggaa tgtagtaata gatatgtgat 2280
tttcatcat ttttaagaaa ccaaggggaa gtaataagtt gaaaaagaaa tccataacta 2340
ttaaaagatt ttaacttttt tattttatta aaatgcttgc atattttaag taaaaaaaaa 2400
aaaaaaaaa cc 2412

```

<210> 85

<211> 1004

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7509439CB1

<400> 85

```
ggctcgggac gcgcgccatt gtgttggtac ccgggaattc ggccattatg gccgggggac 60
cttcagcagg gctgtggcta ccatgttctc tcgcgcgggt gtcgctgggc tgcgcgcctg 120
gaccttgacg ccgcaatgga ttcaagttcg aaatatggca actttgaaag atataccag 180
gagactaaag tccatcaaaa acatccagaa aattaccaag tctatgaaa tggtagcggc 240
agcaaaatat gcccgagctg agagagagct gaaaccagct cgaatatatg gattgggac 300
tttagctctg tatgaaaaag ctgatatcaa ggggcctgaa gacaagaaga aacacctcct 360
tattggtgtg tcctcagatc gaggactgtg tgggtgtatt cattcctcca ttgctaaaca 420
gatgaaaagc gaggttgcta cactaacagc agctgggaaa gaagttatgc ttgttggaat 480
tggtgacaaa atcagaggca tactttatag ttctttgcag gtgctgaagg aaaggaatga 540
tgatagtgtg tggacaact caggaaatca ccaccacca taccctaaag acctgatcca 600
tggactcatt ctgaccagt ttctggtggca ttcaaagaag tgggaagaaa gccccccact 660
tttgagatg cgtcagtcatt tgcccttgaa ttactaaatt ctggatatga atttgatgaa 720
ggctccatca tctttaataa attcaggtct gtcattcctc ataagacaga agaaaagccc 780
atcttttccc ttttaataccg ttgcaagtgc tgacagcatg agtatctatg acgatattga 840
tgctgacgtg ctgcaaatta ccaagaatac aatctggcca acatcatcta ctactctctg 900
aaggagtcca ccactagtga gcagagtgcc aggatgacag ccatggacaa tgccagcagg 960
ctttccacac ctgcgccgta ctatagtccg gtcgtcactt ggtc 1004
```

<210> 86

<211> 5231

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7510202CB1

<400> 86

```
atgagcaaga gacgcatgag cgtgggctcag caaacatggg ctcttctctg caagaactgt 60
ctcaaaaaat ggagaatgaa aagacagacc ttgttggaat ggctcttttc atttcttctg 120
gtactgtttc tgtacctatt tttctccaat ttacatcaag ttcatgacac tcctcaaatg 180
tcttcaatgg atctgggacg tgtagatagt tttaatgata ctaattatgt tattgcattt 240
gcacctgaat ccaaaactac ccaagagata atgaacaaag tggcttcagc cccattccta 300
aaaggaagaa caatcatggg gtggcctgat gaaaaaagca tggatgaatt ggatttgaac 360
tattcaatag acgcagttag agtcatcttt actgatacct tctcctacca tttgaagt 420
tcttggggac atagaatccc catgatgaaa gagcacagag accattcagc tcaactgtca 480
gcagtgaatg aaaaaatgaa gtgtgaaggt tcagagttct gggagaaaagg ctttgtagct 540
tttcaagctg cattaatgc tgctatcata gaaatcgcaa caaatcattc agtgatggaa 600
cagctgatgt cagttactgg tgtacatatg aagatattac cttttgttgc ccaaggagga 660
gttgcaactg attttttcat tttcttttgc attatttctt tttctacatt tatatactat 720
gtatcagtag atgttacaca agaaagacaa tacattacgt cattgatgac aatgatggga 780
ctccgagagt cagcattctg gctttcctgg gggttgatgt atgctggcct catccttatt 840
atggccactt taatggctct tattgtaaaa tctgcacaaa ttgtcgtcct gactggtttt 900
gtgatggctt tcacctctt tctcctctat ggctgtctt tgataacttt agctttcctg 960
atgagtgtgt tgataaagaa acctttcctt acgggcttgg ttgtgtttct ccttattgtc 1020
ttttggggga tcttgggatt cccagcattg tatacacatc ttcttgcat tttggaatgg 1080
actttgtgtc ttcttagccc ctttgccttc actgttggga tggccagct tatacatttg 1140
gactatgatg tgaattctaa tgcccacttg gattcttcac aaaatccata cctcataata 1200
```

```

gctactcttt tcatgttggt ttttgacacc cttctgtatt tggatttgac attatatttt 1260
gacaaaattt tgcccgctga atatggacat cgatgttctc ccttgttttt cctgaaatcc 1320
tgtttttggt ttcaacacgg aagggctaata catgtgggtcc ttgagaatga aacagattct 1380
gacctaactc ctaatgactg ttttgaacca gtgtctccag aattctgtgg gaaggaagcc 1440
atcagaatca aaaatcttaa aaaagaatat gcaggggaagt gtgagagagt agaagccttg 1500
aaaggtgtgg tgtttgacat atatgaaggc cagatcactg ccctccttg tccagtgga 1560
gctggaaaaa ctaccctgtt aaacatactt agtgggttgt cagttccaac atcaggttca 1620
gtcactgtct ataactcacac actttcaaga atggctgata tagaaaatat cagcaagttc 1680
actggatttt gtccacaatc caatgtgcaa tttggatttc tcaactgtga agaaaacctc 1740
aggctgtttg ctaaaaataaa agggattttg ccacatgaag tggagaaaaga ggttttgcta 1800
ttggatgaag cgactgctgg attggatcct ctttcaaggc accgaatatg gaatctcctg 1860
aaagagggga aatcagacag agtaattctc ttcagcacc agtttataga tgaggctgac 1920
attctggcgg acaggaaggt gttcatatcc aatgggaagc tgaagtgtgc aggtctctct 1980
ctgttcctta agaagaaatg gggcataggc taccatttaa gtttgcactc gaatgaaagg 2040
tgtgatccag agagtataac atcactgggt aagcagcaca tctctgatgc caaattgaca 2100
gcacaaagtg aagaaaaact tgtatatatt ttgccttttg aaaggacaaa caaatttcca 2160
gaactttaca gggatcttga tagatgttct aaccaaggca ttgaggatta tgggtgttcc 2220
ataacaactt tgaatgaggt gtttctgaaa ttagaaggaa aatcaactat tgatgaatca 2280
gatattggaa tttggggaca attacaaact gatggggcaa aagatatagg aagccttgtt 2340
gagctggaac aagttttgtc ttccttccac gaaacaagga aaacaatcag tggcgtggcg 2400
ctctggaggc agcaggtctg tgcaatagca aaagttcgct tcctaaagtt aaagaaagaa 2460
agaaaaagcc tgtggactat attattgctt tttggattta gctttatccc tcaacttttg 2520
gaacatctat tctacgagtc atatcagaaa agttaccctg gggaactgtc tccaaataca 2580
tacttctctc caccaggaca acaaccacag gatcctctga cccatttact ggtcatcaat 2640
aagacagggt caaccattga taacttttta cattcactga ggcgacagaa catagctata 2700
gaagtggatg cctttggaac tagaaatggc acagatgacc catcttaca tggtgctatc 2760
attgtgtcag gtgatgaaaa ggatcacaga ttttcaatag catgtaatac aaaacggctg 2820
aattgctttc ctgtcctcct ggatgtcatt agcaatggac tacttggaat ttttaattcg 2880
tcagaacaca ttcagactga cagaagcaca ttttttgaag agcatatgga ttatgagtat 2940
gggtaccgaa gtaacacctt cttctggata ccgatggcag cctctttcac tccatacatt 3000
gcaatgagca gcattggtga ctacaaaaaa aaagctcatt ccagctacg gatttcaggc 3060
ctctaccctt ctgcatactg gtttggccaa gcaactgggt atgtttccct gtactttttg 3120
atcctcctgc taatgcaaat aatggattat atttttagcc cagaggagat tatattttata 3180
attcaaaacc tgtaatttca aatcctgtgt agtattggct atgtctcatc tctgtttttc 3240
ttgacatatg tgatttcatt catttttcgc aatgggagaa aaaatagtgg catttggta 3300
tttttcttct taattgtggt catcttctcg atagttgcta ctgatctaaa tgaatatgga 3360
tttctagggc tatttttttg caccatgtta atacctccct tcacattgat tggctctcta 3420
ttcatttttt ctgagatttc tctgtattcc atggattact taggagcttc agaactctgaa 3480
attgtatacc tggcactgct aataccttac cttcattttc tcatttttct tttcattctg 3540
cgatgcctag aaatgaactg caggaagaaa ctaatgagaa aggatcctgt gttcagaatt 3600
tctccaagaa gcaacgctat ttttccaaac ccagaagagc ctgaaggaga ggaggaagat 3660
atccagatgg aaagaatgag aacagtgaat gctatggctg tgcgagactt tgatgagaca 3720
cccgtcatca ttgccagctg tctacggaag gaatatgcag gcaaaaagaa aaattgcttt 3780
tctaaaagga agaaaacaa tgccacaaga aatgtctctt tttgtgttaa aaaaggtgaa 3840
gttataggac tgtaggaca caatggagct ggtaaaagta caactattaa gatgataact 3900
ggagacacaa aaccaactgc aggacagggt attttgaaag ggagcgggtg aggggaacct 3960
ctgggcttcc tggggactgc cctcaggag aatgcgctgt ggcccaacct gacagtgagg 4020
cagcacctgg aggtgtacgc tgccgtgaaa ggtctcagga aaggggacgc aatgatcgcc 4080
atcacacggg tagtgatgc gctcaagctg caggaccagc tgaaggctcc cgtgaagacc 4140
ttgtcagagg gaataaagcg aaaggtagcg gcagggttg ttgttgcctc gcaagtgcg 4200
tagatgggaa ccagaggggc tgttcctccc gttgcagctg tgctttgtgc tgagcatcct 4260
ggggaacccg tcagtgggtg tcttgatga gccgtcgacc gggatggacc ccgaggggca 4320
gcagcaaatg tggcaggtga ttcggggcac ctttagaaac acggagaggg gcgcctcct 4380
gaccaccac tacatggcag aggtgagggc ggtgtgtgac cgagtggcca tcatgggtgc 4440
aggaaggctg agatgtattg gttccatcca acacctgaaa agcaaatttg gcaaagacta 4500
cctgctggag atgaagctga agaacctggc acaaatggag cccctccatg cagagatcct 4560

```

```

gaggcttttc cccagggctg ctcagcagga aaggttctcc tccctgatgg tctataagtt 4620
gcctgttgag gatgtgcgac ctttatcaca ggctttcttc aaattagaga tagttaaaca 4680
gagtttcgac ctggaggagt acagcctctc acagtctacc ctggagcagg ttttcctgga 4740
gctctccaag gaggaggagc tgggtgatct tgaagaggac tttgatccct cgggtgaagtg 4800
gaaactcctc ctgcaggaag agccttaaag ctccaaatac cctatatctt tctttaatcc 4860
tgtgactctt ttaaagataa tattttatag ccttaatatg ccttatatca gaggtggtac 4920
aaaatgcatt tgaactcat gcaataatta tctcagtag tatttcttac agtgagacaa 4980
caggcgatgt cagtgagggc gatcataggg cataagccta agccatacca tgcagccttt 5040
gtgccagcaa ccaaatccca tgtttcctac tgtgttaagt ttaaaaatgc atttattata 5100
gaattgtcta catttctgag gatgtcatgg agaatgctta attttcttcc tctgaacttc 5160
aaaatattaa atattttctt atttattttt ttgattaaag tataaattaa gacaccctat 5220
tgacttccgg g 5231

```

<210> 87

<211> 3269

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7510203CB1

<400> 87

```

ggcttttgta ctgggtgctc ttgggaactt aaaggcccag gtctctgaga acattctcat 60
atcttcagag aagagaaaagg agtcaggttt agaatgggtc ttttgtaaaa acaaaaattt 120
ttaaactctg aaagattttt atgcagaggg atgtgaccac ctgcaagttt actgggagag 180
aaataggagg aaatgaagct ccagccagat attaggaatt gagcgaagca tgagaaaaag 240
ctctgcagta atgagaagta accctggaca gagtggcagg catagctctg gcggctctct 300
tggggatgga cattcgctcc tctctgctgg tcggaatcaa gggtttacaag gatggacttg 360
agtcctgctc gaggtctagg ggtatccaga gcagggtggg ttagagaggg aggcctaaga 420
gtcctgctcg aggtctaggg gtatcctgct aggggtgggt agacggggag gcctgagagg 480
atgagaggtg ggatctgcac acgcactgag aaaggcatag tatagactca gaacagtcct 540
ctcccaatct ccccttctac cctccaggac ctccctctga gattctgcca ctggtacaag 600
ctgtcccaa agcctgggct gagaatggac aagagtctga ctcagccaca gccagtcag 660
tacagaaccc agagaaaaca aaggaggggc tggaggagga gcagagcaca tctggctgcc 720
tgctgcagga agaaagcaag aaggagggcg ccgtggcctt gcacgtgtac caagcttac 780
ggaaggccgt gggccagggc ttggccttag ccatcctctt ctctctgctt ctcagccaag 840
ccacgcgga cgtgctgac tgggtggctc cccactggat ctctcagctg aaggctgaga 900
atagctccca ggaggcgcaa ccctccacca gccagcttc tatggggctc ttctctccgc 960
agctgctcct cttttccctt ggaaacctct acatcccagt gttccactg cccaaagctg 1020
cccccaatgg ctctcagac atccgtttct acctaccgt gtatgcgacc attgctggtg 1080
taaattccct ctgcaccctt ctccgggcag tgctctttgc agcaggcacc cttcaagcag 1140
ctgccactct gcatcgccgc ctgctgcatc gagtccttat ggcaccagtg actttcttca 1200
atgccacacc cacgggcccgg atcctaaacc gcttctcctc tgatgtggcc tgtgcggtg 1260
acagcctgcc cttcatectc aacatcctcc tggccaacgc ggcaggcctg ctggggctcc 1320
tggcgtgctc gggctctggc ctgccctggc tgctgctcct gctgccgect ttgagcatca 1380
tgtactatca cgtgcagcgc cactacaggg cctcctcacg ggagctgcgg cgcctgggca 1440
gcctcaccct gtctccactg tatagccatc tggccgatac cttggctggc ctctctgtgc 1500
tccgggccac aggggccacc tacaggtttg aggaggagaa cctgcgactc cttgagctaa 1560
accagaggtg ccagtttgcc accagtgcga caatgcagtg gctggacatt cggctacagc 1620
tcatgggggc ggcagtggtc agcgctatcg caggcatcgc tctgggtgcag caccagcagg 1680
gcctcgctaa cccagggctg gtgggcttgt cgctgtctta tgccctgtcc ctgacgggcc 1740
tgctctcggg cctggtgagc agcttcacac agacagaggc catgctggtg agcgtcgagc 1800
ggctggaaga gtacacctgt gacctgcccc aggaacccca gggccagcca ctgcaggtgg 1860
gcctgtaccc ccaccccagg ccaaagctct ggaaccctga agggcccagt ctccctcaca 1920
attcctttct ttttgccac ccatctttct cagctcccat aacctctctt catgatgacc 1980

```

```

acaattcttc accatgtccc ttcttcccca tctctcatte tctcattcct ctcacactgt 2040
ccatttctca ttatttctccc ctcttcacca tctctcctca tctcccttat ctccctttcc 2100
ccgtctgtct cccacccatg gacccaccca gctgggcacc ggctggctga cccagggggg 2160
cgtggagttc caggacgtgg tgttggcgta ccggccaggg ctgccaatg ccctggatgg 2220
agtacacctc tgcgtgcagc ctggagagaa gttgggcata gtggggccga caggctcccg 2280
caagtcttcc ctgttggtgg tgccttcccg gctgctagag cccagttcag ggcgagtgt 2340
gctggacggc gtggacacca gccagctgga gctggcccag ctcagatccc agttggctat 2400
catccccag gagccctttt tgttcagtgg gactgttcgg gaaaacctg acccccagg 2460
cctacataag gacagggcct tgtggcaggc cctgaagcag tgccacctga gtgagtgat 2520
tacatccatg ggtggtctgg atggtgagct gggtaggggg ggccggagct tatctcttgg 2580
gcagaggcag ctgttggtgt tggccagggc tctctcaca gatgccaa ga tcctgtgtat 2640
cgatgaggcc acagcaagtg tggaccagaa gacagaccag ctgctccagc agaccatctg 2700
caaagccttt gccaaacaaga cagtgtgcac cattgcccat aggtcaaca cgatcctgaa 2760
ctcagaccgg gtgctggtgc tacaagcggg gagagtggta gagctggact ccccgccac 2820
cctgcgcaac cagccccact ccctgttcca gcagctgctg cagagcagcc agcaggagt 2880
ccctgcctca ctcgagggtc cctgagccca atcccacacc ctgcagagtt ctccctctc 2940
tctgatccag gccgggcta tacagaggtg ctggctgctt gtttacattc tcctctggg 3000
ctctacctct ccacacttcc ccagaaggga aaagggcacc ctggattact ctttggaat 3060
cactccttgg tgggcagcat cctgaggctt cccagaacc aggcctctgc tctggccctc 3120
ttgcatctgg aacgccaggt gggtttttct ggcataggag cccacttgca tttcatagt 3180
tttatttgat aaaattccat cttacattct gtgtattaaa aaaataatat ttctggtgtg 3240
agaaaaaaaa aaaaaaaaaa atggttcgg 3269

```

<210> 88

<211> 7706

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7510208CB1

<400> 88

```

gcgccccgcc cccgcgcggg cgatgccag cggcgcggcg ggctgcgggg cccggcgggg 60
cgcgcagagg agcgggcccgc ggcgtgagg cggcggagcg tggccccgcc atgggcttcc 120
tgcaccagct gcagctgctg ctctggaaga acgtgacgct caaacgccgg agcccggtgg 180
tcctggcctt cgatctcttc atccccctgg tgcgttctt tatcctgctg gggctgcgac 240
agaagaagcc accatctcc gtgaaggaa tctccttcta cacagcggcg cccctgacgt 300
ctgccggcat cctgcctgtc atgcaatcgc tgtgcccgga cggccagcga gacgagttcg 360
gcttcttgca gtacgccaac tccacggtca cgcagctgct tgagcgctg gaccgcgtgg 420
tggaggaagg caacctgttt gaccagcgc gcccagcct gggctcagag ctcgaggccc 480
tacgccagca tctggaggcc ctcatgctg gcccgggac ctcggggagc cacctggaca 540
gatccacagt gtcttcttcc tctctggact cggtgccag aaaccgcag gagctctggc 600
gtttcctgac gcaaaacttg tcgtgccc aatagcacgg ccaagcactc ttggccgccc 660
gtgtggaccc gcccgaggtc taccacctgc tctttggtcc ctcatctgcc ctggattcac 720
agtctggcct ccacaagggt caggagccct ggagccgct agggggcaat cccctgttcc 780
ggatggagga gctgctgctg gctcctgccc tctggagca gctcacctgc acgcccggct 840
cgggggagct gggccggatc ctactgtgc ctgagagtc gaaggagacc ctgcagggt 900
accgggatgc tgtctgcagt gggcaggctg ctgcgcgtgc caggcgcttc tctgggctgt 960
ctgctgagct ccggaaccag ctggacgtgg ccaaggtctc ccagcagctg ggcctggatg 1020
cccccaacgg ctcgactcc tcgccacagg cgccaccccc acggaggctg caggcgcttc 1080
tgggggacct gctggatgcc cagaagggtc tgcaggatgt ggatgtcctg tcggccctgg 1140
ccctgctact gcccagggt gctgcaactg gccggacccc cggaccccca gccagtgggt 1200
cgggtggggc ggccaatggc actggggcag gggcagtcac gggccccaac gccaccgtg 1260
aggagggcgc accctctgct gcagcactgg ccaccccgga cacgctgcag ggccagtgt 1320
cagccttctg acagctctgg gccggcctgc agcccatctt gtgtggcaac aaccgcacca 1380

```

ttgaaccgga	ggcgctgcgg	cggggcaaca	tgagctccct	gggcttcacg	agcaaggagc	1440
agcggaacct	gggcctcctc	gtgcacctca	tgaccagcaa	ccccaaaatc	ctgtacgcgc	1500
ctgcgggctc	tgaggctgcac	cgcgctcatcc	tcaaggccaa	cgagactttt	gcttttgtgg	1560
gcaacgtgac	tcaactatgcc	caggtctggc	tcaacatctc	ggcgagagatc	cgagacttcc	1620
tgagagcagg	caggctgcag	caacacctgc	gctggctgca	gcagtatgta	gcagagctgc	1680
ggctgcaccc	cgaggcactg	aacctgtcac	tggatgagct	gccgccggcc	ctgagacagg	1740
acaacttctc	gctgcccagt	ggcatggccc	tctgcagca	gctggatacc	attgacaacg	1800
cggcctgcgg	ctggatccag	ttcatgtcca	aggtgagcgt	ggacatcttc	aagggtctcc	1860
ccgacgagga	gagcattgtc	aactacaccc	tcaaccaggc	ctaccaggac	aacgtcactg	1920
tttttgccag	tgtgatcttc	cagacccgga	aggacggctc	gctcccgctc	cacgtgcaact	1980
acaagatccg	ccagaactcc	agcttcaccg	agaaaaccaa	cgagatccgc	cgcgctact	2040
ggcgccctgg	gccaataact	ggcgccgctc	tctacttcc	ctacggcttc	gtctggatcc	2100
aggacatgat	ggagcgccgc	atcatcgaca	cttttgtggg	gcacgacgtg	gtggagccag	2160
gcagctacgt	gcagatgttc	ccctaccctc	gtacacacg	cgatgacttc	ctgtttgtca	2220
ttgagcacat	gatgccgctg	tgcatggtga	tctcctgggt	ctactccgtg	gccatgacca	2280
tccagcacat	cgtggcgagg	aaggagcacc	ggctcaagga	ggtgcgcggg	ccgggactct	2340
ccctggaggc	gcgggctggc	agggaggggc	ggcgctcctc	ccggggcctg	ccccaagccc	2400
ctggcccacc	cgcagggtgat	gaagaccatg	ggcctgaaca	acgcgggtgca	ctgggtggcc	2460
tggttcatca	ccggctttgt	gcagctgtcc	atctccgtga	cagcactcac	cgccatcctg	2520
aagtacggcc	aggtgcttat	gcacagccac	gtggctcatca	tctggctctt	cctggcagtc	2580
tacgcggtgg	ccaccatcat	gttctgtctc	ctgggtgtctg	tgctgtactc	caaggccaag	2640
ctggcctcgg	cctgcggtgg	catcatctac	ttcctgagct	acgtgcccta	catgtacgtg	2700
gcgatccgag	aggaggtggc	gcataataag	atcacggcct	tcgagaagtg	catcgcgctc	2760
ctcatgtcca	cgacggcctt	tggtctgggc	tctaagta	tcgcgctgta	tgaggtggcc	2820
ggcgtgggca	tccagtggca	caccttcagc	cagtccccgg	tgagggggga	cgacttcaac	2880
ttgctcctgg	ctgtcaccat	gctgatgggt	gacgccgtgg	tctatggcat	cctcactgtg	2940
tacattgagg	ctgtgcaccc	aggcatgtac	ggcgctgccc	ggccctggta	cttcccactg	3000
cagaagtcct	actggctggg	cagtggcgcg	acagaagcct	gggagtggag	ctggccgtgg	3060
gcacgcaccc	ccgcctcag	tgatcatggg	gaggaccagg	cctgtgccat	ggagagccgg	3120
cgctttgagg	agaccctggg	catggaggag	gagcccaccc	acctgcctct	ggttgtctgc	3180
gtggacaaac	tcaccaaggt	ctacaaggac	gacaagaagc	tggccctgaa	caagctgagc	3240
ctgaacctct	acgagaacca	ggtggtctcc	ttcttggggc	acaacggggc	gggcaagacc	3300
accaccatgt	ccatcctgac	cggcctgttc	cctccaacgt	cggttccgc	caccatctac	3360
gggcacgaca	tccgcacgga	gatggatgag	atccgcaaga	acctgggcat	gtgcccgcag	3420
cacaatgtgc	tctttgaccg	gtcacgggtg	gaggaaacac	tctggttcta	ctcacggctc	3480
aagagcatgg	ctcaggagga	gatccgcaga	gagatggaca	agatgatcga	ggacctggag	3540
ctctccaaca	aacggcactc	actggtgcag	acattgtcgg	gtggcatgaa	gcgcaagctg	3600
tccgtgggca	tcgcttctgt	ggcgcgctct	cgcgccatca	tcctggacga	gcccacggcg	3660
ggcggtggacc	cctacgcgcg	ccgcgccatc	tgggacctca	tcctgaagta	caagccaggc	3720
cgcaccatcc	ttctgtccac	ccaccacatg	gatgaggctg	acctgcttgg	ggaccgcatt	3780
gccatcatcg	tcccatggga	agctcaagtg	ctgcggctcc	ccgctcttcc	tcaagggcac	3840
ctatggcgac	gggtaccgcc	tcacgtgggt	caagcgcccc	gccgagccgg	ggggccccc	3900
agagccaggg	ctggcatcca	gccccccagg	tcggggcccc	ctgagcagct	gctccgagct	3960
ccaggtgtcc	cagttcatcc	gcaagcatgt	ggcctcctgc	ctgctggtct	cagacacaag	4020
cacggagctc	tcctacatcc	tgcccagcga	ggccgccaag	aagggggctt	tcgagcgctc	4080
cttccagcac	ctggagcgca	gcctggatgc	actgcacctc	agcagcttcg	ggctgatgga	4140
cacgaccctg	gagggaagtgt	tcctcaaggt	gtcggaggag	gatcagtcgc	tggaagaacag	4200
tgaggccgat	gtgaaggagt	ccaggaagga	tggtctccct	ggggcgagg	gccccgcgtc	4260
tggggagggt	cacgtgggca	atctggcccc	gtgctcggag	ctgaccagct	cgaggcatc	4320
gctgcagtcg	gcgtcatctg	tgggctctgc	ccgtggcgac	gagggaagctg	gctacaccga	4380
cgtctatggc	gactaccgcc	ccctctttga	taaccacacg	gaccagaca	atgtcagcct	4440
gcaagagggtg	gaggcagagg	ccctgtcgag	ggtcggccag	ggcagccgca	agctggacgg	4500
cggttggtg	aagggtgcgc	agttccacgg	gctgctggtc	aaacgcttcc	actgcgcccc	4560
ccgcaactcc	aaggcactct	tctcccagat	cttgcgtgca	gccttcttcg	tctgcgtggc	4620
catgaccgtg	gccctgtccg	tcccggagat	tggtgatctg	cccccgctgg	tcctgtcacc	4680
ttcccagtac	cacaactaca	cccagccccg	tggcaatttc	atcccctacg	ccaacgagga	4740

```

gcgcccgcgag taccggctgc ggctatcgcc cgacgccagc cccagcagc tcgtgagcac 4800
gttccggctg ccgtcggggg tgggtgccac ctgctgctc aagtctcccg ccaacggctc 4860
gctggggccc acgttgaacc tgagcagcgg ggagtcggcg ctgctggcgg ctcggttctt 4920
cgacagcatg tgtctggagt cttcacaca ggggctgcca ctgtccaatt tcgtgccacc 4980
cccaccctcg cccgccccat ctgactcgcc agcgtccccg gatgaggacc tgcaggcctg 5040
gaacgtctcc ctgccgccca ccgctgggcc agaaatgtgg acgtcggcac cctccctgcc 5100
gcgcctggta cgggagcccg tccgctgcac ctgctctgcg cagggcaccg gcttctctctg 5160
cccagcagtg gtgggcgggc acccgcccca gatgcgggtg gtcacaggcg acatcctgac 5220
cgacatcacc ggccacaatg tctctgagta cctgctcttc acctccgacc gcttccgact 5280
gcaccgggtat ggggccatca cctttgaaa cgtcctgaag tccatcccag cctcatttg 5340
caccagggcc ccacccatgg tgcggaagat cgcggtgcgc agggctgccc aggttttcta 5400
caacaacaag ggctatcaca gcatgcccac ctacctcaac agcctcaaca acgccatcct 5460
gcgtgccaac ctgcccaga gcaaggcaca cccggcggct tacggcatca ccgtcaccaa 5520
ccaccccatg aataagacca gcgccagcct ctccctggat tacctgctgc agggcacgga 5580
tgtctgcatc gccatcttca tcatcgtggc catgtccttc gtgccggcca gcttcgttgt 5640
cttcctctgt gccgagaagt ccaccaaggc caagcatctg cagtttgtca gcggctgcaa 5700
ccccatcatc tactggctgg cgaactacgt gtgggacatg ctcaactacc tgggtccccg 5760
tacctgctgt gtcacatcc tgtttgtgtt cgacctgccg gcctacacgt cgcccaccaa 5820
cttcctctgc gtccctctcc tcttctctgt ctatgggtgg tccatcacgc ccatcatgta 5880
cccgccctcc ttctgggttc aggtccccag ctccgcctac gtgttctca ttgtcatcaa 5940
tctcttcatc ggcatcaccg ccaccgtggc cacttctctg ctacagctct tcgagcacga 6000
caaggacctg aaggttgtca acagttacct gaaaagctgc tctctcattt tcccaacta 6060
caacctgggc cacgggctca tggagatggc ctacaacgag tacatcaacg agtactacgc 6120
caagattggc cagtttgaca agatgaagtc cccgttcgag tgggacattg tcaccccgcg 6180
actgggtggc atggcggttg agggcgctcg gggcttctc ctgaccatca tgtgccagta 6240
caacttctcg cggcggccac agcgcatgcc tgtgtctacc aagcctgtgg aggatgatgt 6300
ggacgtggcc agtgagcggc agcgagtgtc ccggggagac gccgacaatg acatggta 6360
gattgagaac ctgaccaagg tctacaagtc ccggaagatt ggccgtatcc tggccgttga 6420
ccgcctgtgc ctgggtgtgc gtccctggcg gtgcttcggg ctccctggcg tcaacggtgc 6480
gggcaagacc agcaccttca agatgctgac cggcgacgag agcacgacgg gggcgagggc 6540
cttcgtcaat ggacacagcg tctgaagga gctgtccag gtgcagcaga gcctcggcta 6600
ctgcccgcag tgtgacgcgc tgttcgacga gctcacggcc cgggagcacc tgcagctgta 6660
cacgcggctg cgtgggatct cctggaagga cgaggcccg gtggtgaagt gggctctgga 6720
gaagctggag ctgaccaagt acgcagacaa gccggtggc acctacagcg gcggcaaca 6780
gcggaagctc tccacggcca tcgccctcat tgggtacca gccttcatct tccctggacga 6840
gccaccaca ggcattggacc ccaaggcccg gcgcttctc tggaaacctc tctcgcacct 6900
catcaagaca gggcgttcag tgggtgctgac atcacacagc atggaggagt gcgaggcgct 6960
gtgcacgcgg ctggccatca tgggtgaacgg tcgcctgcgg tgcctgggca gcatccagca 7020
cctgaagaac cggtttgag atggctacat gatcacggtg cggaccaaga gcagccagag 7080
tgtgaaggac gtggtgcggt tcttcaaccg caacttcccg gaagccatgc tcaaggagcg 7140
gcaccacaca aaggtgcagt accagctcaa gtcggagcac atctcgctgg ccaggtgtt 7200
cagcaagatg gagcaggtgt ctggcgtgct gggcatcgag gactactcgg tcagccagac 7260
cacactggac aatgtgttcg tgaactttgc caagaagcag agtgacaacc tggagcagca 7320
ggagacggag ccgcatccg cactgcagtc cccctctcgg ctgcttctc agcctgctcc 7380
ggccccggtc tgccccacg gagctccggg cacttgtggc agacgagccc gaggacctgg 7440
acacggagga cgaggccctc atcagcttcg aggaggagcg ggcccagctg tccttcaaca 7500
cggacacgct ctgctgacca ccagagctg ggcaggggag gacacgctcc actgaccacc 7560
cagagctggg ccagggactc aacaatgggg acagaagtcc cccagtgcct gccagggcct 7620
ggagtggagg ttcaggacca aggggttctt ggtcctccag cccctgtact cggccatgcc 7680
ctgcggtcac tgcgggtgcc gggcct 7706

```

<210> 89

<211> 3159

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7510446CB1

<400> 89

```

agcaagagca gaggcttaag gagctacact gggggaagga caggggcaag caggccaagg 60
cctggccggg gctcgggggg agggaaatag gagcaatccc ggtcacagca gctggggggt 120
gaacaaagct ggtggggtag tgacccccag taccagtata tgccctttga aactgcacc 180
agctacggac tgccctctga gaatgggggc ctccagcaca ggctccggaa ggatgcaggc 240
ccccgccaca acgtccaccc cacacagatt tatggccatc acaaagaaca attctcagac 300
agggagcagg acatagggat gcccagaag acaggctcca gttctaccgt ggacagcaag 360
gatgaggatc actattctaa atgtcaaggat gatggggact gaggaataaa gaaatctgga 420
gtagaaacag attgtatcca ccgcctggga caggtgggtga gaagaaaatt aggggaagac 480
tggatctttc tgggtcttct gggactgctg atggctcttg tcagctggag catggactac 540
gtcagtgcc aagccttca ggcctacaag tggctctacg cgcagatgca gccagcctt 600
cctctgcagt tcttggctg ggtcaccttc ccactagtcc tcatctctt cagcgcctc 660
ttctgccacc tcatctctcc ccaggctgtt ggctctggaa tccccgaaat gaagacaata 720
cttcgtgggg ttgtcctgaa ggaatacctc acaatgaaag cttttgtggc caaggttgtc 780
gccctgactg cgggcctggg cagtggcatc cccgtgggga aagagggcc cttcgtccac 840
attgccagca tctgtgctgc tgtcctcagc aaattcatgt ctgtgttctg cgggttatat 900
gagcagccat actactactc tgatatcctg acggtgggct gtgctgtggg agtcggctgt 960
tgttttggga caccacttg aggagtcta ttagcatcg aggtcacctc cactacttt 1020
gctgttcgga actactggag aggattctt gcagccacgt tcagcgctt tgtgtttcga 1080
gtgctggcag tgtggaacaa ggatgtgtc accatcactg ctctgttcag aaccaatttc 1140
cgaatggatt tcccccttga cctgaaggaa ctaccagctt ttgctgccat cgggatttgc 1200
tgtgggctcc tgggagctgt atttgtgtat ctgcatcgcc aagtcatgct cgggtgccga 1260
aagcacaagg cctcagcca gtttcttgct aagcacgcc tgctgtatcc tgggaattgtt 1320
acctttgtca ttgcctcatt caccttccca ccaggaaagg gtcaattcat ggctggagag 1380
ttgatgcccc gcgaagccat cagtactttg tttgacaaca atacatgggt gaaacacgag 1440
ggtgatcctg agagcctggg ccagtcagct gtgtggattc acccccggt caacgttgc 1500
atcatcatct ttctcttctt cgtcatgaag ttctggatgt ccatcgtggc caccactatg 1560
cccataccct gcggaggctt catgcctgtg tttgtgctag gagctgcatt tgggaaggctg 1620
gtaggagaaa tcatggccat gctctttcct gatggtatgt tgtttgatga catcatctac 1680
aagatcctac ctgggggcta tgcagtaatt ggagcagcag cgctgactgg tgccgtttcc 1740
cacacagtct ccacagctgt gatttgcttc gaattaacgg gtcagattgc tcacatcctg 1800
cccagatgg tggctgttat cttggccaac atgggtggcc agagcctgca gccctctctc 1860
tatgacagca taccatcagg caagaagcta cctacttg ctagacctgg ctggaaccag 1920
ctcagcaaat ataccatctt tgttgaggac atcatggtac gtgatgtgaa gtttgtttca 1980
gcttcttaca catatgggga gttgcgaacc ctgctccaga ccaccacagt caagacttta 2040
ccactggttg actcaaaaga ttcaatgatc ctgctgggct cgggtggagcg gtcggaactg 2100
caggccctcc tgcagcgcca cctgtgtcct gagcgcagac tgcgcgcagc ccaagagatg 2160
gcgcggaagt tgtcggagct gccttacgac gggaaggcgc ggctggctgg ggaggggctc 2220
cccgcgcgcc ctccaggccg gcccgagtc ttcgcctttg tggatgagga tgaggacgaa 2280
gacctctctg gcaagagcga gcttcctctt tcccttgctc tccaccctc tactactgcc 2340
cctctgtccc cagaagagcc caatgggctt ctgcctggcc acaaacagca gccggaagca 2400
ccagagcctg cagggtcaaag accctccatc ttccagtccc tgcttcactg cttgctgggc 2460
agagctcgcc ccacaaagaa gaaaacaacc caggattcca cagatttagt ggataacatg 2520
tcacctgaag agattgagc ctgggagcag gagcagctga gccagcctgt ctgttttgat 2580
tctgtctgta ttgaccagtc tcccttcag ctggtggagc agacaaccct gcacaagact 2640
cataccctgt tttcactcct tggcctccac ctgccttacg tgaccagcat ggggaagctc 2700
agggcgctcc tggccctgga ggagctacag aaggccattg aggggcacac caagtctggg 2760
gtgcagctcc gccctccctc tgccagcttc cggaacacga cttcaactcg aaagagtacc 2820
ggggcacctc catcttctgc agagaactgg aacctgcctg aggacaggcc tggggccact 2880
ggaacagggg atgtgattgc tgcctcccca gagaccctg tgccatctcc tccccagag 2940
ccccctctct ccctggcccc aggcaaggta gagggcgagt tggaggagct ggagctggtg 3000
gagagtccag ggctggaaga ggagctggcc gacatcttgc agggccccag cctgcgatcc 3060

```

acagacgagg aggatgagga tgaactgata ctttgacccc ctcccacgac ctctcataa 3120
agaccgtgga gaggcccaaa aaaaaaaaaa aaaaaaaaaa 3159

<210> 90
<211> 1821
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 7505294CB1

<400> 90
gctgcctgcc ggtgctcttc gtggctctgg gcatggcctc ggaccccatc ttcacgctgg 60
cgcccccgct gcattgccac tacggggcct tccccctaa tgcctctggc tgggagcagc 120
ctcccaatgc cagcggcgctc agcgctcgcca gcgctgccct agcagccagc gccgccagcc 180
gtgtgcgccac cagtaccgac ccctcgtgca gcggcttcgc cccgccggac ttcaaccatt 240
gcctcaagga ttgggactat aatggccttc ctgtgctcac caccaacgcc atcggccagt 300
gggatctggg gtgtgacctg ggctggcagg tgatcctgga gcagatcctc ttcattcttg 360
gctttgcctc cggctacctg ttccctgggtt accccgcaga cagatttggc cgtcgcggga 420
ttgtgctgct gaccttgggg ctggtggggc cctgtggagt aggaggggct gctgcaggct 480
cctccacagg cgtcatggcc ctccgattcc tcttgggctt tctgcttgcc ggtgttgacc 540
tgggtgtcta cctgatgcgc ctggagctgt gcgacccaac ccagaggctt cgggtggccc 600
tggcagggga gttggtgggg gtgggagggc acttcctgtt cctgggcctg gcccttgtct 660
ctaaggattg gcgattccta cagcgaatga tcaccgctcc ctgcatcctc ttctgtttt 720
atggctggcc tggtttgttc ctggagtccg cacggtggct gatagtgaag cggcagattg 780
aggaggctca gtctgtgctg aggatcctgg ctgagcgaaa ccggcccatc gggcagatgc 840
tgggggagga ggcccaggag gccctgcagg cttcattgcc catgccattc gccactgcta 900
ccagcctgtg ggaggaggag ggagcccatc ggacttctac ctgtgctctc tgctggccag 960
cggcaccgca gccctggcct gtgtcttctt gggggtcacc gtggaccgat ttggccgccc 1020
gggcacacct cttctctcca tgacccttac cggcattgct tccctggctc tgctgggccc 1080
gtgggattat ctgaacgagg ctgccatcac cactttctct gtccctgggc tcttctctcc 1140
ccaagctgcc gccatcctca gcacctcctt tgctgctgag gtcacccca ccactgtccg 1200
gggcccgtgg ctgggcctga tcatggctct aggggcgctt ggaggactga gcggcccggc 1260
ccagcgcctc cacatgggca atggagcctt cctgcagcac gtgggtgctg cggcctgcgc 1320
cctcctctgc attctcagca ttatgctgct gccggagacc aagcgcaagc tccctgccga 1380
ggtgctccgg gacggggagc tgtgtcgccg gccttccctg ctgcggcagc caccacctac 1440
ccgctgtgac cacgtcccgc tgcttgccac ccccaacctt gccctctgag cggcctctga 1500
gtacctggc gggaggctgg ccacacaga aaggtggcaa gaagatcggg aagactgagt 1560
agggaaggca gggctgcca gaagtctcag aggcacctca cgcagccat cgcggagagc 1620
tcagagggcc gtccccacc tgcctcctcc ctgctgcttt gcattcactt ccttggccag 1680
agtcagggga caggagaga gctccacact gtaaccactg ggtctgggct ccatcctgcg 1740
cccaaagaca tccaccaga cctcattatt tcttgcctta tcattctgtt tcaataaaga 1800
catttggaat aaacagcaa a 1821

<210> 91
<211> 3526
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 7505631CB1

<400> 91
cacttggcgg ccatggcagc tgtagtatcg gcgactccgg gtcaaggccc ggtcagtgct 60


```

agtagcatgg gcagcaccgg gtatagggca gagacagctt tgtgtcaact ttgctgctga 120
acccttagga cccatcggtta gagacctgca ggactccttt cctcatccca ggctcggagg 180
agagtttgct gggactgggtg ggctgggttc ctgctctggg gggcggatca ccttcggggc 240
cgctctcttg agacaggggc gcctagggaa cgaacagggt cgcttgagtc acttaccgcg 300
cgccgcctaa gacattgtgc caccctcaat ccgacaatcg aagaaatcga tcattcgcac 360
atcttcccca ttgacttttc ccatctctgt taaccacga gaatctaag actggcatct 420
gagaaccag agcctgggac cttagattgc tgtaagcttt ctctgggtgt aatatcagca 480
aaaaggggtc gttgccgggt acgttcaaga ggaagggtgc tcgtgaacac atctgctggt 540
gggaaggcct aaagaactgg aaagcccact ctcttggaac caccacacct gtttaaagaa 600
cctaagcacc atttaaagcc actggaaatt tgggtgtctag tgggtgtggg tgaataaagg 660
agggcagaat ggatgatttc atctccatta gcctgctgtc tctggctatg ttgggtggat 720
gttacgtggc cggatcatt cccttggtgt ttaatttctc agaggaacga ctgaagctgg 780
tgactgtttt ggggtgctggc cttctctgtg gaactgctct ggcagtcac gtgcctgag 840
gagtacatgc cctttatgaa gatattcttg agggaaaaca ccaccaagca agtgaaacac 900
ataatgtgat tgcacagac aaagcagcag aaaaatcagt tgtccatgaa catgagcaca 960
gccacgacca cacacagctg catgcctata ttgggtgttc cctcgttctg ggcttcgttt 1020
tcatgttgct ggtggaccag attggtaact cccatgtgca ttctactgac gatccagaag 1080
cagcaaggte tagcaattcc aaaatcacca ccacgctggg tctgggtgtc catgctgcag 1140
ctgatggtgt tgctttggga gcagcagcat ctacttcaca gaccagtgtc cagttaattg 1200
gttttgtggc aatcatgcta cataaggcac cagctgcttt tggactggtt tccttcttga 1260
tgcatgctgg cttagagcgg aatcgaatca gaaagcactt gctgggtctt gcattggcag 1320
caccagttat gtccatggtg acatacttag gactgagtaa gagcagtaaa gaagcccttt 1380
cagagggtga cgccacggga gtggccatgc ttttctctgc cgggacattt ctttatgttg 1440
ccacagttag gaaagtagca caaataggat acagttgtat gtagtcattg gcaacaattg 1500
catacaattt tactaccaag agaaggata gtatggaaag tccaaatgac ttccttgatt 1560
ggatgttaac agctgactgg tgtgagactt gaggtttcat ctagtccctc aaaactatat 1620
ggttgcttag attctctctg gaaactgact ttgtcaaata aatagcagat tgtagtgtct 1680
ggtttggttt ggacagtagt gctttctatc atattgttgt gtgcaatggt aatttgttct 1740
actggccaaa gcctctttca gcagtgcctt gccatcatgc ttaaaagtgt ggctagtata 1800
tcttgctgga tggagccttg aactccggca aggattgaac catctgactt ccaaatttgc 1860
cttccctctt ggacctcact attaacaagc aaacctttca gggccctctt agctctcaga 1920
agctatgtat gggctttccc agatttttaa gctgctgcct cgagaactac tcatttctct 1980
cctggtcagc agacagaaat agccatacta atctcatagg gctcaaagtc atcttcaggc 2040
agcagggaac caagcagcgt ggcacaggcc ttcttgactg gaggaagagc ttgctggcat 2100
ggtgggcagt attccaggag aggccatgtc cgtgttctact tcttggcaca ttccagttcc 2160
gttttctctt tgtttaaaac tgcctcttta gatgtggatg ccttaatgct gtaacacatt 2220
tgaaaacatt ggcaatactt aagttgtctg catgattaca gatggaatta ttggctacca 2280
aagagacgca attgatgat agaagcatga ttcttgcttc catataacca aagttaatct 2340
taattgcaat ttgactccgt ttcttggta gggatagact ttcttcagat tccaagtgtc 2400
ctcttaaatg gcaaatgaat ttaagaata ctactgctcc attccctca cttattctcc 2460
agttaattgc ttgtcagttc catttcaaga aagcagtgat gttccagggt tgattcagtt 2520
ttctgtgca cactattgcc aaattttttt ttagcaaaga ttctgcactg gaacgtagac 2580
agtggaaac agtactacct acctagaggt tatgtgtttt ctctttctcc ccgctttcac 2640
ctctttcttt cccaattcaa aacagccaag tgagccctgt tctgggtatt tgaatcatta 2700
gagaaaagaa agggagtggc tgttttgagt tgtcctttct ttgcagaaag gagaaaatgt 2760
gattgtgttt tttttttacc agcctacttc taagtgtcac tgccgtggtt ttctcttttt 2820
caaggattag aactaagagg acacaccagc atcggagtgt attaagcccc tgaaacacat 2880
ggtagctagg gactgaacac aggaaccgta tgacagcagc acaaaccccc aaaggatgtt 2940
cctgccttgt gggccctga gccctttggg agactgagaa tcatgaccag attcatccag 3000
aactgtgca gtgttaagtg aaaatcctct gtagttgttc tgcagaggaa ccttccttcc 3060
attagaaaat ttctgtctcaa tacagaatgg tccacatcac ccaaagtga ctgttgagga 3120
tgctgtgaaa taaaacctc tttgtacctg agacatctag attcacctca ggaggcctga 3180
aggaaatgtg taacttgtgg gaaagaacta gacaaccatt taggaattct ctagatatac 3240
tcagcctaac ccagtggctt aacacaagga gattggcttt gatctttttt tcttggtgga 3300
tcttcagca agttagaagt ctcatgggat aagactgcag ttcccctggt tcaatagctg 3360
gaacagtgat tttaaatgtc ctttttctg gatccctgt aaacatgaaa tcattccatg 3420

```

gatggctgcc ttataat tttt gtctctttcc actttaattg tgaatgggta aaaaaatgct 3480
gttttctgat attaaat tttt tattagt gca taccttaaaa aaaaaa 3526

<210> 92

<211> 946

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7506561CB1

<400> 92

cacggagatt cggcagcagg aggaaaagca gcaaaccaga tggagaagga aggccaaaaa 60
gataagtaga aagctggacc atgagctcct tgagggcagg gactgaatgg ttactatgtc 120
cccagggccc agcatgacct tctcctggat tctcatctt ccttctgtga cctgtgtctc 180
catcagtttc tctccggca tctttttctt acaggattct tacctcagga atagatggac 240
atggcctggc agatgatgca gctgctgctt ctggcttttg tgactgctgc ggggagtgcc 300
cagcccagga gtgcgcgggc caggacggac ctgctcaatg tctgcatgaa cgccaagcac 360
cacaagacac agcccagccc cgaggacgag ctgtatggcc agtgacgtcc ctggaagaag 420
aatgcctgct gcacggccag caccagccag gagctgcaca aggacacctc ccgcctgtac 480
aactttaact gggatcactg tggtaacca gagctggcgc aaagagcgca ttctgaacgt 540
gccccgtgct aaagaggact gtgagcgtg gtgggaggac tgtcgcacct cctacacctg 600
caaaagcaac tggcacaag gctggaattg gacctcaggg attaatgagt gtccggcccg 660
ggccctctgc agcacctttg agtctactt cccactcca gccgccctt gtgaaggcct 720
ctggagccac tccttcaagg tcagcaacta tagtcgaggg agctgccgct gcatccagat 780
gtggtttgac tcagcccagg gcaaccccaa tgaggaggtg gccaaagttct atgctgcggc 840
catgaatgct ggggccccgt ctcgtgggat tattgattcc tgatccaaga agggctcctc 900
ggggttcttc caacaaccta ttctaataga caaatccaca tgaaaa 946

<210> 93

<211> 2737

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7510733CB1

<400> 93

agcgaacagg gaatgacagt tccaccagaa gacgattaag ccacagcctc taattggaac 60
ggcatttgta cagtcagaga ctcttaccag acatctccag gaatctgtga gccattgtca 120
aaacgtccat tttcatctgg ctgtgaaagt gaggaccaca acaggtaggt attggtagaa 180
acaggagtcc tcagagaagc cccaagatgc agcctgaggg agcagaaaaa ggaaaaagct 240
tcaagcagag actgggtcttg aagagcagct tagcgaaaga aaccctctct gaggttcttg 300
gcacgttcat cttgattgtc cttggatgtg gctgtgttgc ccaagctatt ctgagtcgag 360
gacgttttg agggttcac actatcaatg ttggattttc aatggcagtt gcaatggcca 420
tttatgtggc tggcgggtgc tctgatggac ttatgtcctt tgctgggtgga aaactgctga 480
tcgtgggaga aaatgcaaca gcacacattt ttgcaacata ccagctccg tatctatctc 540
tggcgaacgc atttgcagat caagtgggtg ccaccatgat actcctcata atcgtctttg 600
ccatttttga ctccagaaac ttgggagccc ccagaggcct agagccatt gccatcggcc 660
tctgattat tgtcattgct tctccctgg gactgaacag tggctgtgcc atgaacccag 720
ctcagacact gactcccaga cttttcactg ccttggcagg ctgggggttt gaagtcttca 780
gagctggaaa caacttctgg tggattcctg tagtgggccc tttgggttgt gctgtcattg 840
gaggcctcat ctatgttctt gtcattgaaa tccaccatcc agagcctgac tcagtcctta 900
aggcagaaca atctgaggac aaaccagaga aatatgaact cagtgtcatc atgtagtggc 960

```

atgctcagct ctggatttgc agtcagtttg ggattctctt cagaaagatg gcatctaagt 1020
gtctgtgttc ttgtaagcct gaggtggaat ccaccagtt ttgtctgcta gccatattggg 1080
acatctaatt ggaaaagcat ctgcataaaa gtttggaac aatgaccact tctctaccat 1140
tgtcccccac cccaccccc cagaataacg ctgactgtcc cctgaaacag ctttctctcc 1200
tgccctgttt atttcatcct cgatgggaat tcttgctagg taagcactaa taactcggca 1260
tcttgacgat agtcccatth ggggtggttc agctgcacta tctgtatgaa atgggtgtcac 1320
caaaaccctt ttcttcagta tcgacaaaaga ttacattctg agtaccaacc aaaccctaaa 1380
ttgaaagaca aaactatggg ttacgtcaac atattcatga attagggagc taatgggtta 1440
agcttccagt tcccgtatg ctactggatt tgtataaata ctgatattct ccaaaccatg 1500
tgggtgtaggg agcaagagaa tgcagctgga aggcacaagg ggaggacatt gtggcattca 1560
gaaactgcag gagacaagat gaatttgaga agccaaatgg aatttttaat ggaaaccatt 1620
tatcagatta atctcttgct ctctgtcatt ttagaggaca ccaattaatt tcctggtctt 1680
tagtatataa taacctaaaa taccattgta cctcagtcga tgaaaaatac atcactctgt 1740
cttttttagct caaatgtatt ttctaattg cccacttgag aacagacatt tgacaagtta 1800
tatcaacgac tgtgcttgtc cattatttta cacatgccct agaagccaaa actgaaagcc 1860
actggatcct ggtctagctg aatcttcaga gtgggagggtc tccaaaaaga tattacctta 1920
ttgggcttaa caattcacia ggcactttca caccattat ctaatttaat cctcataatg 1980
actatgtgag gcaaatgcc aattgcccatt ttttcagata aagaaacaaa atcttaggga 2040
agataagttg agttgtccaa gagcacactg aaagttgaat gttatcta atgcattcctct 2100
acctttcaga agatcagtag ctggctgaga atctttgcca aatcttcctt gctagccaga 2160
agtgaattg gcagcttcta gaatatgtac acctctggac aaaatgttcc tcaatcttaa 2220
gatacaaaaga cctcattgt ctgggtctat tcccacactt actgagtaca gatgaaggaa 2280
agtggtagca atttaatcat aactttcatt tgctgaaaaa cattatgaga aggcctccct 2340
tcctaagcca cctctggtct tgctaagtct tgatcttgct tcctgccagc accaaacatt 2400
acattcaggg gatttccctt ggctcagctt ttccccttg aagttctcta atagattta 2460
cttttgacaa aagatcgct atgagttaca agcaccagg gatgctctac atcaagggat 2520
gcaccttcag tcaaaactgtc aaaaagccca gaattcccaa aggcattagg tttcccaact 2580
gctttgtgct gatatcagaa cagcagaaat taaatgtgaa atgtttctga tgacttatgt 2640
tctacaatct atggacatac gggatttttt ttttcttgct ttgaagctac ctggatattt 2700
cctatttgaa ataaaattgt tcgggtcattg ttgaaaa 2737

```

<210> 94

<211> 2821

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7510734CB1

<400> 94

```

agcgaacagg gaatgacagt tccaccagaa gacgattaag ccacagcctc taattggaac 60
ggcattttgta cagtcagaga ctcttaccag acatctccag gaatctgtga gccattgtca 120
aaacgtccat tttcatctgg ctgtgaaagt gaggaccaca acaggtaggt attggtagaa 180
acaggagtcc tcagagaagc cccaagatgc agcctgaggg agcagaaaaag ggaaaaagct 240
tcaagcagag actgggtcttg aagagcagct tagcgaaaaga aaccctctct gagttcttgg 300
gcacgttcat cttgattgtc cttggatgtg gctgtgttgc ccaagctatt ctcagtcgag 360
gacgttttgg aggggtcatc actatcaatg ttggattttc aatggcagtt gcaatggcca 420
tttatgtggc tggcgggtgtc tctggtgtgc acatcaacc agctgtgtct ttagcaatgt 480
gtctcttttg acggatgaaa tggttcaaat tgccatttta tgtgggagcc cagttcttgg 540
gagcctttgt gggggctgca accgtctttg gcatttacta tgatggactt atgtcctttg 600
ctgggtgga aactgctgatc gtgggagaaa atgcaacagc acacattttt gcaacatacc 660
cagctccgta tctatctctg gcgaacgcat ttgcagatca aaaacttggg agccccaga 720
ggcctagagc ccattgccat cggcctcctg attattgtca ttgcttcctc cctgggactg 780
aacagtggct gtgccatgaa cccagctcga gacctgagtc ccagactttt cactgccttg 840
gcaggctggg ggtttgaagt cttcagagct ggaaacaact tctggtggat tcctgtagtg 900

```

```

ggcccttttg ttggtgctgt cattggaggc ctcctctatg ttcttgtcat tgaaatccac 960
catccagagc ctgactcagt ctttaaggca gaacaatctg aggacaaacc agagaaatat 1020
gaactcagtg tcatcatgta gtggcatgct cagctctgga ttgacagtca gtttgggatt 1080
ctcttcagaa agatggcatc taagtgtctg tgttcttgta agcctgaggt ggaatccacc 1140
cagttttgtc tgctagccat atgggacatc taattggaaa agcatctgca taaaagtttg 1200
gaaacaatga ccacttctct accattgtcc cccaccccca cccccagaa taacgctgac 1260
tgtccctga aacagccttc tctcctgccc tgtttatttc atcctcgatg ggaattcttg 1320
ctaggtaagc actaataact cggcatcttg acgatagtc catttgggtg gtttcagctg 1380
cactatctgt atgaaatggt gtcacaaaaa cccttttctt cagtatcgac aaagattaca 1440
ttctgagtag caaccaaaacc ctaaattgaa agacaaaact atggtttcag tcaacatatt 1500
catgaattag ggagctaatg ggttaagctt ccagttcccg ctatgctact ggatttgtat 1560
aaatactgat attctccaaa cctagtgggt tagggagcaa gagaatgcag ctggaaggca 1620
caaggggagg acattgtggc attcagaaac tgcaggagac aagatgaatt tgagaagcca 1680
aatggaattt ttaattgaaa ccattttatc gattaatctc ttgctctcct gcattttaga 1740
ggacaccaat taatttctct gctcttagta tataataacc taaaatacca ttgtaacctc 1800
agtcatgaaa aatacatcac tctgtctttt tagctcaaat gtattttcct aattgcccac 1860
ttgagaacag acatttgaca agttatatca acgactgtgc ttgtccatta ttttacacat 1920
gccctagaag ccaaaactga aagccactgg atcctgggtc agctgaatct tcagagtggg 1980
aggctctcaa aaagatatta ccttattggg cttaacaatt cacaaggcac tttcacaccc 2040
attatctaata ttaatcctca taatgactat gtgaggcaaa tgccacattg cccatttttc 2100
agataaagaa acaaaatctt agggaagata agttgagttg tccaagagca cactgaaagt 2160
tgaatgttat ctaatgcatt cctctacctt tcagaagatc agtagctggc tgagaatctt 2220
tgccaaatct tccttgctag ccagaagtgg aattggcagc ttctagaata tgtacacctc 2280
tggaacaaat gttctcaat cttaagatac aaagaccctc attgtctggg tctattccca 2340
cacttactga gtacagatga aggaagtgg tagcaattta atcataactt tcatttgctg 2400
aaaacacatta tgagaaggcc tcccttccca agccacctct ggtcttgcta agtcttgatc 2460
ttgcttctct ccagcaccaa acattacatt caggggattt cctctggctc agtcttttcc 2520
ccttgaagtt ctctaataga tgttactttt gacaaaagat cgcctatgag ttacaagcac 2580
caggggatgc tctacatcaa gggatgcacc ttcagtcaaa ctgtcaaaaa gccagaatt 2640
cccaaaggca ttaggtttcc caactgcttt gtgctgatat cagaacagca gaaattaaat 2700
gtgaaatgtt tctgatgact tatgttctac aatctatgga catacgggat ttttttttcc 2760
ttgctttgaa gctacctgga tatttcctat ttgaaataaa attgttcggt cattgttgaa 2820
a

```

<210> 95

<211> 3583

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7503977CB1

<400> 95

```

ctgggcttcg tgccccgacc tgggtgtgtca gtgctggggg gatcgggggg ccccgctctc 60
cagacctggc tgcaggacct gctgcgtcgt gggctgggtc gggctgcca gagcacagga 120
gcctggattg tcaactggggg tctgcacacg ggcacgggcc ggcatgttgg tgtggctgta 180
cgggaccatc agatggccag cactgggggc accaagggtg tggccatggg tgtggccccc 240
tggggtgtgg tccggaatag agacaccctc atcaacccca agggctcgtt ccctgcgagg 300
taccgggtgg gcggtgacct ggaggacggg gtccagtttc ccctggacta caactactcg 360
gccttcttcc tgggtggacga cggcacacac ggctgcctgg ggggcgagaa ccgcttccgc 420
ttgcgcctgg agtcctacat ctcacagcag aagacgggag tgggagggac tgggaattgac 480
atccctgtcc tgcctcctct gattgatggt gatgagaaga tgttgacgcg aatagagaac 540
gccaccagg ctcagctccc atgtctctc gtggctggct cagggggagc tgcggactgc 600
ctggcgagga ccctggaaga cactctggcc ccagggagtg ggggagccag gcaaggcgaa 660
gcccagagatc gaatcaggcg tttctttccc aaaggggacc ttgaggtcct gcaggccag 720

```

```

gtggagagga ttatgacccg gaaggagctc ctgacagtct attcttctga ggatgggtct 780
gaggaattcg agaccatagt tttgaaggcc cttgtgaagg tccttccatc tcgaagcttc 840
cctcatggac gccctgctga atgaccggcc tgagttcgtg cgcttgctca tttccacagg 900
cctcagcctg ggccacttcc tgaccccgat gcgcctggcc caactctaca gcgcggcgcc 960
ctccaactcg ctcatccgca accttttgga ccaggcgctc cacagcgag gcaccaaaagc 1020
cccagcccta aaagggggag ctgaggagct ccggccccct gacgtggggc atgtgctgag 1080
gatgctgctg ggggaagatgt gcgcgcgag gtacccctcc gggggcgcc tggaccctca 1140
cccaggccag ggcttcgggg agagcatgta tctgctctcg gacaaggcca cctcgccgct 1200
ctcgctggat gctggcctcg ggcaggcccc ctggagcgac ctgcttcttt gggcactggt 1260
gctgaacagg gcacagatgg ccatgtactt ctgggagatg ggttccaatg cagtttcttc 1320
agctcttggg gctgttttgc tgctccgggt gatggcacgc ctggagcctg acgctgagga 1380
ggcagcacgg aggaaagacc tggcgttcaa gtttgagggg atgggcggtg acctctttgg 1440
cgagtgtat cgagcagtg aggtgagggc tgcccgccct ctcctccgtc gctgcccgt 1500
ctggggggat gccacttgcc tccagctggc catgcaagct gacgcccgct ccttctttgc 1560
ccaggatggg gtacagtctc tgctgacaca gaagtgggtg ggagatatgg ccagcactac 1620
acctatctgg gccctggttc tcgccttctt ttgccctcca ctcatctaca ccgcctcat 1680
caccttcagg aaatcagaag aggagccac acgggaggag cttagagttt acatggatag 1740
tgtcattaat ggggaagggc ctgtcgggac ggcggacca gccgagaaga cgccgctggg 1800
ggtcccgcc cagtcgggcc gtccgggttg ctgccccggc cgctcgggg ggcgcgggtg 1860
cctacgccgc tggttccact tctggggcgc gccggtgacc atcttcatgg gcaacgtggt 1920
cagctacctg ctgttccctg tgcttttctc gcgggtgctg ctcggtgatt tccagccggc 1980
gccgccccgc tccctggagc tgctgctcta tttctgggct ttcacgctgc tgtgcgagga 2040
actgcgccag ggcctgagcg gaggcggggg cagcctcgcc agcgggggcc ccgggcctgg 2100
ccatgcctca ctgagccagc gcctgcgcct ctacctcgcc gacagctgga accagtgcga 2160
cctagtggct ctcacctgct tcctcctggg cgtgggctgc cggctgacct cgggtttgta 2220
ccacctgggc cgactgtcc tctgcatcga cttcatgggt ttacagggtc ggctgcttca 2280
catcttcacg gtcaacaaac agctggggcc caagatcgct atcgtagca agatgatgaa 2340
ggacgtgttc ttcttctct tcttccctcg cgtgtggctg gtagcctatg gcgtggccac 2400
ggaggggctc ctgaggccac gggacagtga cttcccaagt atcctgcgcc gcgtcttcta 2460
ccgtccctac ctgcagatct tcgggcagat tccccaggag gacatggacg tggccctcat 2520
ggagcacagc aactgctcgt cggagcccg cttctgggca caccctcctg gggcccaggc 2580
gggcacctgc gtctcccagt atgccaaact gctgggtggt ctgctcctcg tcatcttct 2640
gctcgtaggc aacatcctgc tggtaactt gctcattgcc atgttcagtt acacattcgg 2700
caaagtacag ggcaacagcg atctctactg gaaggcgag cgttaccgcc tcatccggga 2760
attccactct cggcccgcc tgcccccgcc ctttatcgct atctccact tgcgcctcct 2820
gctcaggcaa ttgtgcaggc gaccccgag cccccagcg tcctccccgg ccctcgagca 2880
tttccgggtt tacctttcta aggaagccga gcggaagctg ctaacgtggg aatcgggtga 2940
taaggagaac tttctgctgg cacgcgctag ggacaagcgg gagagcgact ccgagcgct 3000
gaagcgacag tcccagaagg tggacttgcc actgaaacag ctgggacaca tccgcgagta 3060
cgaacagcgc ctgaaagtgc tggagcggga ggtccagcag tgtagccgcg tcctgggggtg 3120
ggtggccgag gccctgagcc gctctgcctt gctgccccca ggtgggcccgc caccctctga 3180
cctgcctggg tccaaagact gagccctgct ggcggaactc aaggagaagc cccacaggg 3240
gattttgctc cttagagtaag gctcatctgg gcctcgcccc ccgcacctgg tggccttgct 3300
cttgaggtga gccccatgtc catctgggcc actgtcagga ccacctttgg gagtgtcatc 3360
cttacaacc acagcatgcc cggctcctcc cagaaccagt cccagcctgg gaggatcaag 3420
gcctggatcc cgggccgtta tccatctgga ggctgcaggg tccttggggg aacaggggacc 3480
acagaccctt caccactcac agattcctca cactggggaa ataaagccat ttcagaggaa 3540
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aag 3583

```

<210> 96

<211> 2125

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7505084CB1

<400> 96

```
gagaacttta cgcttgatc tcactaact gacacagaaa ccctgtaagg atccagaggt 60
ctcgttcagg accatggaga gcggcaccag cagccctcag cctecacagt tagatcccct 120
ggatgcgttt cccagaagg gcttgagacc tggggacatc gcggtgctag ttctgtactt 180
cctctttgtc ctggctgttg gactatggtc cacagtgaag accaaaagag acacagtga 240
aggctacttc ctggctggag gggacatggg gtgggtggcca gtgggtgcat ccttgtttgc 300
cagcaatggt ggaagtggac atttcattgg cctggcaggg tcaggtgctg ctacgggcat 360
ttctgtatca gcttatgaac ttaatggctt gttttctgtg ctgatgttg cctggatctt 420
cctaccatc tacattgctg gtcagggtcac cacgatgcca gaatacctac ggaagcgctt 480
cgggtggcatc agaatcccca tcactcctggc tgtactctac ctatttatct acatcttcac 540
caagatctcg gtagacatgt atgcagggtc catcttcac cagcagtctt tgcacctgga 600
tctgtacctg gccatagttg ggctactggc catcactgct gtatacacgg ttgctggttg 660
cctggctgct gtgatctaca cggatgccct gcagacgctg atcatgctta taggagcgct 720
caccttgatg ggctacagtt tcgcccggtt tgggtgggat gaaggactga aggagaagta 780
cttcttggcc ctggctagca accggagtga gaacagcagc tgcgggctgc cccgggaaga 840
tgccttccat attttccgag atccgctgac atctgatctc ccgtggccgg gggtcctatt 900
tggaatgtcc atcccatccc tctggtactg gtgcacggat caggtgattg tccagcggac 960
tctggctgcc aagaacctgt cccatgcca aggaggtgct ctgatggctg catacctgaa 1020
gggtgctgcc ctcttcataa tgggtgtccc tgggatggct agccgcatcc tcttcccaga 1080
tcaagtggcc tgtgcagatc cagagatctg ccagaagatc tgcagcaacc cctcaggctg 1140
ttcggacatc gcgtatccca aactcgtgct ggaactcctg cccacagtgc cagcaccatc 1200
ttcaccatgg acctctggaa tcacctccgg cctcgggcat ctgagaagga gctcatgatt 1260
gtgggcaggg tgtttgtgct gctgctggtc ctggtctcca tcctctggat ccctgtggtc 1320
caggccagcc agggcgcca gctcttcac tatatccagt ccatcagctc ctacctgcag 1380
ccgcctgtgg cgggtgtctt catcatggga tgtttctgga agaggacca tgaagggt 1440
gccttctggg gcctgatctc gggcctgctc ctgggcttgg ttaggctggg cctggacttt 1500
atttacgtgc agcctcgtg cgaccagcca gatgagcgcc cggctcctgg gaagagcatt 1560
cactacctct acttctccat gatcctgtcc acggtcaccc tcactactgt ctccaccgtg 1620
agctggttca cagagccacc ctccaaggag atggtcagcc acctgacctg gtttactcgt 1680
cacgaccccg tgggtccagaa ggaacaagca ccaccagcag ctcccttgct tcttaccctc 1740
tctcagaacg ggatgccaga ggccagcagc agcagcagcg tccagttcga gatggttcaa 1800
gaaaacacgt ctaaaaccca cagctgtgac atgaccccaa agcagttcaa agtgggtgaag 1860
gccatcctgt ggtctgttg aatacaggag aagggcaagg aagagctccc ggccagagca 1920
gaagccatca tagtttccct ggaagaaaac cccttggtga agaccctcct ggacgtcaac 1980
ctcattttct cgtgagctg cgccatcttt atctgggct attttgctta gtgtggggtg 2040
aaccagggg tccaaactct gtttctcttc agtgctccat ttttttaatg aaagaaaaa 2100
taataaagct tttgtttacc aaaaa 2125
```

<210> 97

<211> 1517

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7506950CB1

<400> 97

```
gaagaaaaca ccgaattctg cttgccgttt cagagcggcg gtgatgaaga caaaattgaa 60
catctacaac atgcagttcc tgctttttgt tttcttggtg tgggaccctg ccaggttggg 120
gctggctaac atccaagaag atgaggctaa aaataacatt accatcttta cgagaattct 180
tgacagactt ctggatgggt acgataatcg gcttagacca ggactgggag acagtattac 240
tgaagtcttc actaacatct acgtgaccag ttttggccct gtctcagata cagatatgga 300
atatacaatt gatgttttct ttcgacaaaa atggaaagat gaacgtttta aatttaaagg 360
```

```

tcctatgaat atccttcgac taaacaattt aatggctagc aaaatctgga ctccagatac 420
ctttttttcac aatgggaaaa aatcagtagc tcataaatatg acaatgccaa ataagttgct 480
tcgaattcag gatgatggga ctctgctgta taccatgagg agtaacaact gtcctaacaa 540
tgacaactct aagcatcagt gctcggaatt ctctcccaa agtggcttat gcaactgcc 600
tggaactggt tattgctgtt tgttatgcat ttgtgttctc tgccctaatt gaatttgcaa 660
ctgttaatta cttcaccaaa agaggatggg cttgggatgg gaagagtgtg gtaaatgaca 720
agaaaaaaga aaaggcttcc gttatgatac agaacaacgc ttatgcagtg gctgttgcca 780
attatgcccc gaatctttca aaagatccag ttctctccac catctccaag agtgcaacca 840
cgccagaacc caacaagaag ccagaaaaca agccagctga agcaaagaaa actttcaaca 900
gtgttagcaa aattgacaga atgtccagaa tagtttttcc agttttgtt ggtaccttta 960
atttagttta ctgggtctaca tatttaaaca gagaacctgt attaggggtc agtccctgaa 1020
ttgagaccca tgttatcttt gggatgtata gcaacattaa atttggtttg ttttgctatg 1080
tacagtctga ctaataactg ctaatttgtg atccaacatg tacagtatgt atatagtga 1140
atagcttacc agtagacctt taatggagac atgcatttgc taactcatgg aactgcagac 1200
agaaagcact ccatgcgaaa acagccattg ccttttttaa agatttacc taggacctga 1260
tttaaagtga atttcaaatg acctgattaa tttctattc ttccaaatga gatgaaaatg 1320
gggatcctgt acaacctttt gtggacactt ttggtttagc tcttaagtag gggtattttc 1380
tactgttgcc taatatgatg gaagtaacat tgtcattcta gatgaatctt tgaagtacca 1440
acattgttct ggaatcagct cgggtccagat gctcaaggct cctgtaatgt attggaagct 1500
ggtaccctaa gaaaaaca
1517

```

<210> 98

<211> 1694

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7506951CB1

<400> 98

```

gaagaaaaaca ccgaattctg cttgccgttt cagagcggcg gtgatgaaga caaaattgaa 60
catctacaac atgcagttcc tgctttttgt tttcttggtg tgggacctg ccaggttggt 120
gctggctaac atccaagaag atgaggctaa aaataacatt accatcttta cgagaattct 180
tgacagactt ctggatgggt acgataatcg gcttagacca ggactgggag acagtattac 240
tgaagtcttc actaacatct acgtgaccag ttttggccct gtctcagata cagatatgga 300
atatacaatt gatgttttct ttcgacaaaa atggaaagat gaacgtttaa aatttaaagg 360
tcctatgaat atccttcgac taaacaattt aatggctagc aaaatctgga ctccagatac 420
ctttttttcac aatgggaaga aatcagtagc tcataaatatg acaatgccaa ataagttgct 480
tcgaattcag gatgatggga ctctgctgta taccatgagg cttacagttc aagctgaatg 540
cccaatgcac ttggaggatt tcccaatgga tgcctattca tgtcctctga aatttggcag 600
ctatgcatat acaacttcag aggtcactta tatttggact tacaatgcat ctgattcagt 660
acaggttgct cctgatggct ctagggttaa tcaatatgac ctgctgggcc aatcaatcgg 720
aaaggagaca attaaatcca gtacagggtga atatactgta atgacagctc atttccacct 780
gaaaagaaaa attgggtatt ttgtgattca aacctatctg ccttgcatca tgactgtcat 840
tctctcccaa gtttcattct ggcttaacag agaatctgtg cctgcaagaa ctgtgtttga 900
aaaaagaaaa ggcttccgtt atgatacaga acaacgctta tgcaagtggc gttgccaatt 960
atgccccgaa cttttcaaaa gatccagttc tctccaccat ctccaagagt gcaaccacgc 1020
cagaacccaa caagaagcca gaaaacaagc cagctgaagc aaagaaaact ttcaacagt 1080
ttagcaaaaat tgacagaatg tccagaatag tttttccagt tttgtttggg acctttaatt 1140
tagtttactg ggctacatat ttaaacagag aacctgtatt aggggtcagt ccttgaattg 1200
agacctatgt tatctttggg atgtatagca acattaaatt tggtttgggt tgctatgtac 1260
agtctgacta ataactgcta atttgtgatc caacatgtac agtatgtata tagtgacata 1320
gcttaccagt agacctttaa tggagacatg catttgctaa ctcatggaac tgcagacaga 1380
aagcactcca tgcgaaaaca gccattgcct tttttaaaga tttaccctag gacctgattt 1440
aaagtgaatt tcaaatgacc tgattaattt cctattcttc caaatgagat gaaaatgggg 1500

```

```

atcctgtaca accctttgtg gacacttttg gtttagctct taagtagggg tattttctac 1560
tggtgcctaa tatgatggaa gtaacattgt cattctagat gaatctttga agtaccaaca 1620
ttgttctgga atcagctcgg tccagatgct caaggtccct gtaatgtatt ggaagctggg 1680
accctaagaa aaca                                     1694

```

<210> 99

<211> 1102

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7506954CB1

<400> 99

```

ctctctctct ctctctctct ctctctctct ctctctctct ctcccaagtt tcctatctcg 60
tcaagatcag ggcaaaagaa gaaaacaccg aattctgctt gccgtttcag agcggcggtg 120
atgaagacaa aattgaacat ctacaacatg cagttcctgc tttttgtttt cttgggtgtg 180
gacctgcca gggtgtgtgt ggctaacatc caagaagatg aggctaaaaa taacattacc 240
atctttacga gaattcttga cagacttctg gatggttacg ataatcggct tagaccagga 300
ctggggagaaa aaagaaaagg cttccggtat gatacagaac aacgcttatg cagtggctgt 360
tgccaattat gcccgaatc tttcaaaaga tccagttctc tccaccatct ccaagagtgc 420
aaccacgcca gaaccaaca agaagccaga aaacaagcca gctgaagcaa agaaaacttt 480
caacagtgtt agcaaaattg acagaatgtc cagaatagtt tttccagttt tgtttggtac 540
ctttaattta gtttactggg ctacatatat aaacagagaa cctgtattag gggtcagtcc 600
ttgaattgag acccatgtta tctttgggat gtatagcaac attaaatttg gtttgttttg 660
ctatgtacag tctgactaat aactgctaat ttgtgatcca acatgtacag tatgtatata 720
gtgacatagc ttaccagtag acctttaatg gagacatgca tttgctaact catggaactg 780
cagacagaaa gcactccatg cgaaaacagc cattgccttt tttaaagatt taccctagga 840
cctgatttaa agtgaatttc aaatgacctg attaatctcc tattcttcca aatgagatga 900
aaatggggat cctgtacaac cctttgtgga cacttttggg ttagctctta agtaggggta 960
ttttctactg ttgcctaata tgatggaagt aacattgtca ttctagatga atctttgaag 1020
taccaacatt gttctggaat cagctcgggc cagatgtcca aggtccctgt aatgtattgg 1080
aagctggtac cctaagaaaa ca                                     1102

```

<210> 100

<211> 1744

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7506956CB1

<400> 100

```

gaagaaaaca ccgaattctg cttgccgttt cagagcggcg gtgatgaaga caaaattgaa 60
catctacaac atgcagttcc tgctttttgt tttcttggtg tgggaccctg ccaggttggg 120
gctggctaac atccaagaag atgaggctaa aaataacatt accatcttta cgagaattct 180
tgacagactt ctggatggtt acgataatcg gcttagacca ggactgggag acagtattac 240
tgaagtcttc actaacatct acgtgaccag ttttgccct gtctcagata cagatatgga 300
atatacaatt gatgttttct ttcgacaaaa atggaaagat gaacgtttta aatttaaagg 360
tcctatgaat atccttcgac taaacaattt aatggctagc aaaatctgga ctccagatac 420
cttttttcac aatgggaaga aatcagtagc tcataatatg acaatgccaa ataagttgct 480
tcgaattcag gatgatggga ctctgctgta taccatgagg cttacagtcc aagctgaatg 540
cccaatgcac ttggaggatt tcccaatgga tgctcattca tgtcctctga aatttggcag 600
ctatgcatat acaacttcag aggtcactta tatttggtac tacaatgcat ctgattcagt 660

```



```

acaggttgct cctgatggct ctaggttaaa tcaatatgac ctgctgggcc aatcaatcgg 720
aaaggagaca attaaatcca gtacaggagt aacaactgtc ctaacaatga caactctaag 780
catcagtgct cggaattctc tccccaaagt ggcttatgca actgccatgg actgggttat 840
tgctgtttgt tatgcatttg tggtctctgc cctaattgaa tttgcaactg ttaattactt 900
caccaaaaaga ggatgggctt gggatgggaa gagtgtagta aatgacaaga aaaaagaaaa 960
ggcttccggt atgatacaga acaacgctta tgcagtggtt gttgccatt atgccccgaa 1020
tctttcaaaa gatccagttc tctccaccat ctccaagagt gcaaccacgc cagaacccaa 1080
caagaagcca gaaaacaagc cagctgaagc aaagaaaact ttcaacagt ttagcaaaat 1140
tgacagaatg tccagaatag tttttccagt tttgtttggt acctttaatt tagtttactg 1200
ggctacatat ttaaacagag aacctgtatt aggggtcagt ccttgaattg agacccatgt 1260
tatctttggg atgtatagca acattaaatt tgggtttgtt tgctatgtac agtctgacta 1320
ataactgcta atttgtgatc caacatgtac agtatgtata tagtgacata gcttaccagt 1380
agacctttaa tggagacatg catttgctaa ctcatggaac tgcagacaga aagcactcca 1440
tgcgaaaaca gccattgcct tttttaaaga tttaccctag gacctgattt aaagtgaatt 1500
tcaaatgacc tgattaattt cctattcttc caaatgagat gaaaatgggg atcctgtaca 1560
accctttgtg gacacttttg gtttagctct taagtagggg tattttctac tgttgccata 1620
tatgatggaa gtaacattgt cattctagat gaatctttga agtaccaaca ttgttctgga 1680
atcagctcgg tccagatgct caaggtccct gtaatgtatt ggaagctggt accctaagaa 1740
aaca 1744

```

<210> 101

<211> 1753

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7506959CB1

<400> 101

```

gaagaaaaca ccgaattctg cttgccgttt cagagcggcg gtgatgaaga caaaattgaa 60
catctacaac atgcagttcc tgctttttgt tttcttggtg tgggaccctg ccagggttgg 120
gctggctaac atccaagaag atgaggctaa aaataacatt accatcttta cgagaattct 180
tgacagactt ctggatgggt acgataatcg gcttagacca ggactgggag acagtattac 240
tgaagtcttc actaacatct acgtgaccag ttttggccct gtctcagata cagatatgga 300
atatacaaat gatgttttct ttcgacaaaa atggaaagat gaacgtttta aatttaaagg 360
tcctatgaat atccttcgac taaacaattt aatggctagc aaaatctgga ctccagatac 420
cttttttcac aatgggaaga aatcagtagc tcataatatg acaatgcaa ataagttgct 480
tcgaattcag gatgatggga ctctgctgta taccatgagg cttacagttc aagctgaatg 540
cccaatgcac ttggaggatt tcccaatgga tgctcattca tgctcctctga aatttggcag 600
ctgtgaatat actgtaatga cagctcattt ccacctgaaa agaaaaattg ggtattttgt 660
gattcaaacc tatctgcctt gcacatgac tgtcattctc tcccaagttt cattctggct 720
taacagagaa tctgtgcctg caagaactgt gtttggagta acaactgtcc taacaatgac 780
aactctaagc atcagtgctc ggaattctct ccccaaagtg gcttatgcaa ctgccatgga 840
ctggtttatt gctgtttggt atgcatttgt gttctctgcc ctaattgaat ttgcaactgt 900
taattacttc accaaaagag gatgggcttg ggtgggaag agtgtagtaa atgacaagaa 960
aaaagaaaag gcttccgtta tgatacagaa caacgcttat gcagtggctg ttgccaat 1020
tgccccgaat ctttcaaaag atccagttct ctccaccatc tccaagagtg caaccacgcc 1080
agaacccaac aagaagccag aaaacaagcc agctgaagca aagaaaactt tcaacagtgt 1140
tagcaaaatt gacagaatgt ccagaatagt tttccagtt ttgtttggta cctttaattt 1200
agtttactgg gctacatatt taaacagaga acctgtatta ggggtcagtc cttgaattga 1260
gacccatggt atctttggga tgtatagcaa cattaaattt ggtttgtttt gctatgtaca 1320
gtctgactaa taactgctaa tttgtgatcc aacatgtaca gtatgtatat agtgacatag 1380
cttaccagta gacctttaat ggagacatgc atttgctaac tcatggaact gcagacagaa 1440
agcactccat gcgaaaacag ccattgcctt ttttaaagat ttaccctagg acctgattta 1500
aagtgaattt caaatgacct gattaatttc ctattcttcc aaatgagatg aaaatgggga 1560

```

```

tcctgtacaa ccccttgtgg acacttttgg tttagctctt aagtaggggt attttctact 1620
gttgccaat atgatggaag taacattgtc attctagatg aatccttgaa gtaccaacat 1680
tgttctggaa tcagctcggg ccagatgctc aaggccctg taatgtattg gaagctggta 1740
ccctaagaaa aca 1753

```

<210> 102

<211> 1609

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7506960CB1

<400> 102

```

ctctctctct ctctctctct ctctctctct ctctctctct ctcccaagtt tcctatctcg 60
tcaagatcag ggcaaaagaa gaaaacaccg aattctgctt gccgtttcag agcggcggtg 120
atgaagacaa aattgaacat ctacaacatg cagttcctgc tttttgtttt cttgggtgtg 180
gaccctgcca gggttggtgct ggctaacatc caagaagatg aggctaaaaa taacattacc 240
atctttacga gaattcttga cagacttctg gatggttacg ataatcggct tagaccagga 300
ctgggaggaa tatacaattg atgttttctt tcgacaaaaa tggaaagatg aacgtttaaa 360
atttaaaggc cctatgaata tccttcgact aaacaattta atggctagca aaatctggac 420
tcagataacc ttttttcaca atgggaagaa atcagtagct cataatatga caatgccaaa 480
taagttgctt cgaattcagc atgatgggac tctgctgtat accatgaggc ttacagttca 540
agctgaatgc ccaatgcact tggaggattt cccaatggat gctcattcat gtcctctgaa 600
atttggcagc tgagtaacaa ctgtcctaac aatgacaact ctaagcatca gtgctcgga 660
ttctctcccc aaagtggctt atgcaactgc catggactgg tttattgctg ttgtttatgc 720
atttgtgttc tctgccctaa ttgaatttgc aactgttaat tacttcacca aaagaggatg 780
ggcttgggat gggaagagt tagtaaatga caagaaaaaa gaaaaggctt ccgttatgat 840
acagaacaac gcttatgcag tggctgttgc caattatgcc ccgaatcttt caaaagatcc 900
agttctctcc accatctcca agagtgeaac cacgccagaa cccaacaaga agccagaaaa 960
caagccagct gaagcaaaga aaactttcaa cagtgttagc aaaattgaca gaatgtccag 1020
aatagttttt ccagttttgt ttggtacctt taatttagtt tactgggcta catatttaa 1080
cagagaacct gtattagggg tcagtccttg aattgagacc catgttatct ttgggatgta 1140
tagcaacatt aaatttggtt tgttttgcta tgtacagtct gactaataac tgctaatttg 1200
tgatccaaca tgtacagtat gtatatagt acatagctta ccagtagacc tttaatggag 1260
acatgcattt gctaactcat ggaactgcag acagaaagca ctccatgcga aaacagccat 1320
tgctttttt aaagatttac cctaggacct gatttaaagt gaatttcaa tgacctgatt 1380
aatttcctat tcttccaaat gagatgaaaa tggggatcct gtacaaccct ttgtggacac 1440
ttttggttta gctcttaagt aggggtattt tctactgttg cctaatatga tggaaagtaac 1500
attgtcattc tagatgaatc tttgaagtac caacattgtt ctggaatcag ctcggtccag 1560
atgctcaagg tcctgtaat gtattggaag ctggtaccct aagaaaaa 1609

```

<210> 103

<211> 1930

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7510540CB1

<400> 103

```

attgacagga ctcccaacta gtacaatgac agaagataag gtcactggga ccctggtttt 60
cactgtcatc actgctgtgc tgggttcctt ccagtttgga tatgacattg gtgtgatcaa 120
tgcacctcaa cagaatcaaa gccatgttag tagcaaacat tctgtcatta gttggagctc 180

```

```

tcttgatggg gttttcaaaa ttgggacccat ctcatatact tataattgct ggaagaagca 240
tatcaggact atattgtggg ctaatttcag gcctgggtcc tatgtatata ggtgaaattg 300
ctccaaccgc tctcagggga gcacttggca cttttcatca gctggccatc gtcacgggca 360
ttcttattag tcagattatt ggtcttgaat ttatcttggg caattatgat ctgtggcaca 420
tcctgcttgg cctgtctggt gtgcgagcca tccttcagtc tctgctactc tttttctgtc 480
cagaaagccc cagatacctt tacatcaagt tagatgagga agtcaaagca aaacaaagct 540
tgaaaagact cagaggatat gatgatgtca ccaaagatat taatgaaatg agaaaagaaa 600
gagaagaagc atcgagttag cagaaagtct ctataattca gctcttcacc aattccagct 660
accgacagcc tattctagtg gcaactgatgc tgcattgtggc tcagcaattt tccggaatca 720
atggcatttt ttactactca accagcattt ttcagacggc tgggtatcagc aaacctgttt 780
atgcaacccat tggagttggc gctgtaaaca tggttttcac tgctgtctct gtattccttg 840
tggagaaggc agggcgacgt tctctctttc taattggaat gagtgggatg tttgtttgtg 900
ccatcttcat gtcagtggga cttgtgtgtc tgaataagtt ctcttggatg agttatgtga 960
gcatgatagg catcttcctc tttgtcagct tctttgaaat tggggccaggc ccgatcccc 1020
ggttcatggg ggctgagttt ttcagtcaag gaccacgtcc tgctgcttta gcaatagctg 1080
cattcagcaa ttggacctgc aatttcattg tagctctgtg tttccagtac attgaggact 1140
tctgtggacc ttatgtgttt ttctcttttg ctggagtgtc cctggccttt accctgttta 1200
cattttttta agttccagaa accaaaggaa agtcttttga ggaaattgct gcagaattcc 1260
aaaagaagag tggctcagcc cacaggccaa aagctgtgtg agaaatgaaa ttcctaggag 1320
ctacagagac tgtgtaaaaa aaaaaccctg ctttttgaca tgaacagaaa caataaggga 1380
accgtctgtt tttaaatgat gattccttga gcattttata tccacatctt taagtattgt 1440
tttattttta tgtgctctca tcagaaatgt catcaaatat taccaaaaaa gtattttttt 1500
aagttagaga atatattttt gatggtaaga ctgtaattaa gtaaaccaaa aaggctagtt 1560
tattttgtta cactaaaggg caggtgggtc taataatttt agctctgttc tttataacaa 1620
ggttcttcta aaattgaaga gatttcaaca tatcattttt ttaacacata actagaacc 1680
tgaggatgca acaaatattt atatatttga atatcattaa attggaattt tcttaccat 1740
atatcttatg ttaaaggaga tatggctagt ggcaataagt tccatgttaa aatagacaac 1800
tcttccattt attgcactca gcttttttct tgagtactag aatttgtatt ttgcttaaaa 1860
ttttactttt gttctgtatt ttcattgtga atggattata gagtatacta aaaaatgtct 1920
atagagaaaa                                     1930

```

<210> 104

<211> 1205

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7510545CB1

<400> 104

```

cttggcggag gcgaggaggc cgcgggggacg ggaggcgagg ccggccgggc ccccgaagcc 60
atggagaacg cgcacaccaa gacgggtggag gaggtgctgg gccacttcgg cgtcaacgag 120
agtgaatctg tctctgtcat caagcacact gatcccgtcc ctgaccacag agctgtcaac 180
caagataaaa agaacatgct gttttctgtg gccctggctg tagcagccat tcctgaaggt 240
ctgcctgcag tcatcaccac ctgcctggct cttggaactc gcagaatggc aaagaaaaat 300
gccattgttc gaagcctccc gtctgtggaa acccttgggt gtacttctgt tatctgtctc 360
gacaagactg gtacacttac aacaaaccag atgtcagttc gcaggatgtt cattctggac 420
agagtggag atcacaccgc tgaacgtgac ccagtggctg atggtgctga aaatctcctt 480
gcccgatgatt ctcattggatg agacgctcaa gtttggggcc cgcaactacc tggaaacctg 540
taaagaggtg gtgcagcctg ccaccaaatc ctgctcgctc tcggcatgca ccgatgggat 600
ttcctggcgg tttgtgtgtc tcataatgcc cctggtgatc tgggtctata gcacagacac 660
taacttttagc gatatgttct ggtcttgact gacagttttc cataaagaag atgtttaact 720
taatcaatta atttttttat tgtttaaagc aactgtctat ttctgtgtaa ttttcacatg 780
aacatactgg ctggtgatgg aggtttcata ctctagattt tgttttgctt tttctgactc 840
cagtggggca agattttcct tttttatata cataattaaa gtgtocattg acatgtacag 900

```

```
agaactaaca ctatatttatg caaatatttt tttgtagatg aaaaagcatg tacagtgttc 960
tgtttaatac tcatccttgt ataaaaaaaa tagttgagcc agcagacatt gtcagcaaat 1020
taattggcag cagatttttag gaaatgaatg tgtgtggttt tttttctaaa actaaatagc 1080
atgtattgtg tcttttgcac gatgatccgg atttaatttg atatcacagt ctaattttta 1140
ttcataagcc attttcgcac ggcagagtct gcactcatca gatgtttggt gcactcgcac 1200
cactg 1205
```

<210> 105

<211> 1790

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7510654CB1

<400> 105

```
cgggcggttca ggcgccagag ctggccgatc ggcgttggcc gccgacatga cgcccgagga 60
cccagaggaa acccagccgc ttctggggcc tcctggcgcc agcgcgcccc gcggccgccg 120
cgtcttcctc gccgccttcg ccgctgccct gggccactc agcttcggct tcgcgctcgg 180
ctacagctcc ccggccatcc ctacgctgca gcgcgcgcgc ccccgggccc cgcgccctgga 240
cgacgccgcc gcctcctggt tcggggctgt cgtgacctg ggtgccgcgc cggggggagt 300
gctgggcggc tggctggtgg accgcgccgg gcgcaagctg agcctcttg tgtgctccgt 360
gcccttcgtg gccggctttg ccgtcatcac cgcggcccag gacgtgtgga tgctgctggg 420
ggggccgcctc ctaccggcc tggcctgcgg tgttgccctc ctagtggccc cggtctacat 480
ctccgaaatc gcctaccag cagtcggggg gttgctcgcc tcctgtgtgc agctaattgt 540
cgctgctggc atcctcctgg cctacctggc aggtggtgt ctggagtggc gctggctggc 600
tgtgctgggc tgcgtgcccc cctccctcat gctgcttctc atgtgcttca tgcccagagc 660
cccgcgcttc ctgctgactc agcacaggcg ccaggaggcc atggccgccc tgcggttcct 720
gtggggctcc gagcagggtc gggaagaccc cccatcgagg gctgagcaga gctttcacct 780
ggccctgctg cggcagcccg gcatctacaa gcccttcac atcggcgtct ccctgatggc 840
cttcagcag ctgtcggggg tcaacgccgt catgttctat gcagagacca tctttgaaga 900
ggccaagttc aaggacagca gcctggcctc ggtcgtcgtg ggtgtcatcc aggtgctgtt 960
cacagctgtg gcggctctca tcatggacag agcaggggcg aggtgctcc tggctctgtc 1020
aggaggtcct caggccctat ggagccttct ggcttgctc cgctttctgc atcttcagt 1080
tccttttcac tttgttctgt gtccctgaaa cttaaaggaaa gactctggaa caaatcacag 1140
ccattttga gggcgcatga cagccactca ctaggggatg gagcaagcct gtgactccaa 1200
gctgggcccc agcccagagc ccctgcctgc ccaggggag ccagaatcca gcccttggga 1260
gccttgggtc gcagggtccc tccttcctgt catgctccct ccagcccatg acccggggct 1320
aggaggctca ctgcctcctg ttccagctcc tgctgctgct ctgaggactc aggaacacct 1380
tcgagctttg cagacctgcg gtcagccctc catgcgcaag actaaagcag cggaagagga 1440
ggtgggcctc taggatcttt gtcttctggc tggaggtgct tttggaggtt ggggtgctggg 1500
cattcagctg ctctctcac gggctgcct tatcggaag gaaatttgt tgccaaataa 1560
agactgacac agaaaatcag gtcagtgtct ctgggctttg tgcaagctca gtttgaaaag 1620
ggtttattcc catcactgcc caggacaccc tgtggcttta cttgctcatg gtcagccaag 1680
cttacccttc aactgagaa gtcatttctg gctacttctc tgggctcagt tccctgggtc 1740
atcagccatc aaatcttgtt gagttaaaaa aataaacagc aaaaaaaaaa 1790
```

<210> 106

<211> 3824

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7510660CB1

<400> 106

```

gccagcctgt tctgttgccc tggctcttcc tagtccaggc tgccatggcg gcgctcaggg 60
cttaccggaa gtaaaacttc ggaagtgagg cgttcctctg cccggaagtg agcgcgggcg 120
taggaaagat ggcggcagcg gcggcggtgg gcaacgcggt gccctgcggg gcccggcctt 180
gcgggggtccg gcctgacggg cagcccaagc ccggggccgca gccgcgcgcg ctcccttgccg 240
ccggggccggc gctcatagcg aacggtgacg agctgggtggc tgccgtgtgg ccgtaccggc 300
ggttggcgct gttgcggcgc ctcacggtgc tgccattcgc cgggctgctt taccggcgct 360
ggttgggtgc cgcagccgct ggctgctggg gctggggcag cagttgggtg cagatccccg 420
aagctgcgct gctcgtgctt gccaccatct gcctcgcgca cgcgctcact gtccctctcg 480
ggcatttggtc tgtgcacgcg cattgcgcgc tcacctgcac cccggagtac gaccccgca 540
aagcgacctt tgtgaagggt gtgccaaccc ccaacaatgg ctccacggag ctcggtggcc 600
tgcaccgcaa tgagggcgaa gacgggcttg aggtgctgtc cttcgaattc cagaagatca 660
agtattccta cgatgccctg gagaagaagc agtttctccc cgtggccttt cctgtgggaa 720
acgccttctc atactatcag agcaacagag gcttccagga agactcagag atccgagcag 780
ctggaagaaa atttgggagc aacaaggccg agatgggtgg gcctgacttc tcggagcttt 840
tcaaggagag agccacagcc cccttctttt tatttcagggt gttctgtgtg gggctctggt 900
gcctggatga gtactggtac tacagcgtct ttacgctatc catgctgggt gcgttcgagg 960
cctcgctggt gcagcagcag atgcggaaca tgtcggagat ccggaagatg ggcaacaagc 1020
cccacatgat ccaggctctac cgaagccgca agtggaggcc cattgccagt gatgagatcg 1080
taccagggga catcgtctcc atcggccgct cccacagga gaacctgggt ccatgtgacg 1140
tgcttctgct gcgaggccgc tgcacgttag acgaggccat gctcacgggg gagtccgtgc 1200
cacagatgaa ggagcccatc gaagacctca gccagaccg ggtgctggac ctccaggctg 1260
attcccggtc gcacgtcatc ttccggggca ccaagggtgt gcagcacatc cccccacaga 1320
aagccaccac gggcctgaag ccggttgaca gcgggtgcgt ggcctacgtc ctgcggaccg 1380
gattcaacac atcccagggc aagctgctgc gcaccatcct cttcggggtc aagagggtga 1440
ctgcgaacaa cctggagacc ttcattctca tcctcttctc cctgggtgtt gccatcgctg 1500
cagctgccta tgtatggatt gaaggtagca aggacccag ccggaaccgc tacaagctgt 1560
ttctggagtg caccctgatc ctcacctcgg tcgtgcctcc tgagctgccc atcgagctgt 1620
ccctggcgtc caacacctcc ctcacgtccc tggccaagct ctacatgtac tgacagagc 1680
ccttcgggat cccctttgct ggcaaggctc aggtgtgctg ctttgacaag acggggacgt 1740
tgaccagtga cagcctgggt gtgcgcgggt tggccgggct gagagacggg aaggagggtga 1800
ccccagtgtc cagcatccct gtagaaacac accgggccct ggcctcgtgc cactcgctca 1860
tgcagctgga cgacggcacc ctcggtgggt accctctaga gaaggccatg ctgacggccg 1920
tggtactggac gctgacaaa gatgagaaa tattcccccg aagtattaaa actcaggggc 1980
tgaaaattca ccagcgcttt cattttgcca gtgccctgaa gcgaatgtcc gtgcttgct 2040
cgtatgagaa gctgggctcc accgacctct gctacatcgc ggccgtgaag ggggcccccg 2100
aaactctgca ctccatgttc tcccagtgc cggccgacta ccaccacatc cacaccgaga 2160
tctcccgga aggagccgc gtccctggcg tggggtacaa ggagctggga cacctcactc 2220
accagcaggt ggtcatgatc acgggagaca acccgctcac tgcatgccac gtggcccagg 2280
agctgcactt cattgaaaag gccacacgc tgatcctgca gcctccctcc gagaaaggcc 2340
ggcagtgcga gtggcgctcc attgacggca gcatcgtgct gccctggcc cggggctccc 2400
caaaggcact ggccctggag tacgcactgt gcctcacagg cgacggcttg gccacctgc 2460
aggccaccga ccccgagcag ctgctccgcc tcatcccca tgtgcagggt ttcgcccgtg 2520
tggctcccaa gcagaaggag tttgtcatca ccagcctgaa ggagctgggc tacgtgacct 2580
tcatgtgtgg ggtggcacc aacgacgtgg gcgccctgaa gcatgctgac gtgggtgtgg 2640
cgctcttggc caatgcccct gagcgggttg tcgagcggcg acggcgggcc cgggacagcc 2700
caacctgag caacagtggc atcagagcca cctccaggac agccaagcag cggtcggggc 2760
tccctocctc cgaggagcag ccaacctccc agagggaccg cctgagccag gtgctgcgag 2820
acctcgagga cgagagtacg cccattgtga aactggggga tgccagcatc gcagaccct 2880
tcacctcaa gctctcatcc atccagtga tctgccagc gatcaagcag ggccgtgca 2940
cgctgggtgac cagctacag atgttcaaga tctggcgct caatgccctc atcctggcct 3000
acagccagag gtcctctac ctggaggag tcaagttcag tgacttccag gccacctac 3060
aggggctgct gctggccggc tgcttctct tcatctcccg ttccaagccc ctcaagacct 3120
tctcccgaga acggccctg cccaacatct tcaacctgta caccatcctc accgtcatgc 3180
tccagttctt tgtgcacttc ctgagccttg tctacctgta ccgtgaggcc caggcccgga 3240
gccccgagaa gcaggagcag ttcgtggact tgtacaagga gtttgagcca agcctggtca 3300

```

```

acagcaccgt ctacatcatg gccatggcca tgcagatggc caccttcgcc atcaattaca 3360
aaggcccgcc cttcatggag agcctgcccg agaacaagcc cctggtgtgg agtctggcag 3420
tttcaactcct ggccatcatt ggctgtctcc tcggctcctc gcccgacttc aacagccagt 3480
ttggcctcgt ggacatccct gtggaggtcc tgctcctgga cttctgcctg gcgctcctgg 3540
ccgaccgcgt cctgcagttc ttcctgggga cccgaagct gaaagtgcct tcctgagatg 3600
gcagtgtctg tacccactgc ccacctggc tgcgctggg cggaacccc aacagggccc 3660
cgggagggaa ccctgcccc aacccccac agcaaggctg tacagtctcg cccttggaag 3720
actgagctgg gacccccaca gccatccgct ggcttggcca gcagaaccag cccaagcca 3780
gcacctttgg taaataaagc agcatctgag attttaaaaa aaaa 3824

```

<210> 107

<211> 3770

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7510661CB1

<400> 107

```

gccagcctgt tctgttgccc tggctcttcc tagtccaggc tgccatggcg gcgctcaggg 60
cttaccggaa gtaaaacttc ggaagtgagg cgttcctctg cccggaagtg agcgcggcgc 120
taggaaagat ggcggcagcg gcggcggtgg gcaacgcggt gccctgcggg gcccgccctt 180
gcggggtccg gcctgacggg cagcccaagc ccgggcccga gccgcgcgcg ctcttgcgcg 240
ccgggcccgc gctcatagcg aacgggtgacg agctgggtggc tgccgtgtgg ccgtaccggc 300
ggttggcgct gttgcggcgc ctacgggtgc tgccattcgc cgggctgctt taccggcct 360
ggttggtgct cgcagccgct ggctgctggg gctggggcag cagttgggtg cagatccccg 420
aagctgcgct gctcgtgctt gccaccatct gcctcgcgca cgcgctcact gtcctctcgg 480
ggcattggtc tgtgcacgcg cattgcgcgc tcacctgcac cccggagtac gaccccagca 540
aagcgacctt tgtgaagggt gtgccaaccc ccaacaatgg ctccacggag ctctggccc 600
tgcaccgcaa tgagggcgaa gacgggcttg aggtgctgtc cttcgaattc cagaagatca 660
agtattccta cgatgccttg gagaagaagc agtttctccc cgtggccttt cctgtgggaa 720
acgccttctc atactatcag agcaacagag gcttcagga agactcagag atccgagcag 780
ctgagaagaa atttgggagc aacaaggccg agatgggtgg gcctgacttc tcggagcttt 840
tcaaggagag agccacagcc cccttctttg tatttcaggt gttctgtgtg gggctctggg 900
gcctggatga gtactggtac tacagcgtct ttacgctatc catgctggtg gcgttcgagg 960
cctcgtggtg gcagcagcag atgcggaaca tgtcggagat ccggaagatg ggcaacaagc 1020
cccacatgat ccaggtctac cgaagccgca agtggaggcc cattgccagt gatgagatcg 1080
taccagggga catcgtctcc atcgccgct cccacagga gaacctggtg ccatgtgacg 1140
tgcttctgct gcgaggccgc tgcatcgtag acgaggccat gctcacgggg gagtccgtgc 1200
cacagatgaa ggagcccatc gaagacctca gccagaccg ggtgctggac ctccaggtcg 1260
attcccggct gcacgtcatc ttccgggggca ccaaggtggt gcagcacatc cccccacaga 1320
aagccaccac gggcctgaag ccggttgaca gcgggtgctg ggccctacgtc ctgcccggaccg 1380
gattcaacac atcccagggc aagctgctgc gcaccatcct cttcgggggtc aagaggggtga 1440
ctgccaacaa cctggagacc ttcattctca tcctcttctc cctgggtgtt gccatcgctg 1500
cagctgccta tgtatggatt gaaggtacca aggaccccag ccggaaccgc tacaagctgt 1560
ttctggagtg caccctgatc ctacctcgg tcgtgcctcc tgagctgccc atcgagctgt 1620
ccctggccgt caacacctcc ctcatcgccc tggccaagct ctacatgtac tgcacagagc 1680
ccttccggat cccctttgct ggcaaggctg aggtgtgctg ctttgacaag acggggacgt 1740
tgaccagtga cagcctggtg gtgcgcggtg tggccgggct gagagacggg aaggaggtga 1800
ccccagtgtc cagcatccct gtagaaacac accgggccct ggccctcgtg cactcgtcga 1860
tgcagctgga cgacggcacc ctctggtgtg acctctaga gaaggccatg ctgacggccg 1920
tggactggac gctgacaaa gtgccctgaa gcgaatgtcc gtgcttgctt cgtatgagaa 1980
gctgggctcc accgacctct gctacatcgc ggccgtgaag ggggcccccg aaactctgca 2040
ctccatgttc tcccagtgcc cgcccagacta ccaccacatc cacaccgaga tctcccggga 2100
aggagccccg gtcctggcgc tggggtacaa ggagctggga cacctcactc accagcaggt 2160

```

```

ggtcacgatc acgggagaca acccgctcac tgcacgccac gtggcccagg agctgcactt 2220
cattgaaaag gccacacgc tgatcctgca gectcctcc gagaaaggcc ggcagtgca 2280
gtggcgctcc attgacggca gcatcgtgt gcccctggcc cggggctccc caaaggcact 2340
ggccctggag tacgcactgt gcctcacagg cgacggcttg gccacctgc aggccaccga 2400
ccccagcag ctgctccgcc tcatcccca tgtgcaggtg ttcgcccgtg tggctcccaa 2460
gcagaaggag tttgtcatca ccagcctgaa ggagctgggc tacgtgacct tcatgtgtgg 2520
ggatggcacc aacgacgtgg gcgcctgaa gcatgctgac gtgggtgtgg cgctcttggc 2580
caatgccctt gagcgggttg tcgagcggcg acggcgccc cgggacagcc caacctgag 2640
caacagtggc atcagagcca cctccaggac agccaagcag cggctcggggc tccctccctc 2700
cgaggagcag ccaacctccc agagggaccg cctgagccag gtgctgcgag acctcgagga 2760
cgagagtacg ccatttgtga aactggggga tgccagcatc gcagcaccct tcacctcaa 2820
gctctcatcc atccagtga tctggcacgt gatcaagcag ggccgctgca cgctggtgac 2880
cacgctacag atgttcaaga tccctggcgt caatgccctc atcctggcct acagccagag 2940
cgctctctac ctggaggagg tcaagtccag tgacttccag gccaccctac aggggtgtgt 3000
gctggccggc tgcctcctct tcatctcccg ttccaagccc ctcaagacct tctcccgaga 3060
acggcccttg cccaacatct tcaacctgta caccatcctc accgtcatgc tccagttctt 3120
tgtgcacttc ctgagccttg tctacctgta ccgtgaggcc caggcccgga gcccagaga 3180
gcaggagcag ttcgtggact tgtacaagga gtttgagcca agcctggtca acagcaccgt 3240
ctacatcatg gccatggcca tgcagatggc cacttctgcc atcaattaca aaggcccgc 3300
cttcatggag agcctgcccg agaacaagcc cctggtgtgg agtctggcag tttactcct 3360
ggccatcatt ggcctgtctc tcggctcctc gccgacttc aacagccagt ttggcctcgt 3420
ggacatccct gtggagtcca agctggtcat tgcccaggtc ctgctcctgg acttctgcct 3480
ggcgctcctg gccgaccgcg tcttgacgtt cttcttgggg accccgaagc tgaaagtgcc 3540
ttcctgagat ggcagtgtgt gtaccactgt cccacctgg ctgccgctgg gcgggaacct 3600
caacagggcc ccgggagggg accctgcccc caaccccca cagcaaggct gtacagtctc 3660
gcccttgga gactgagctg ggacccccc acccatccgc tggcttggcc agcagaacca 3720
gcccgaagcc agcacctttg gtaaataaag cagcatctga gattttaaaa 3770

```

<210> 108

<211> 1978

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7510680CB1

<400> 108

```

cctcctacct ggggtcttgg gccctcagcc tggctcatgc acaactgtct gaagtgtctt 60
ggactatggt gatgaacagc gcccttcaga cgcgaggctg gggaggaatc gtcggggttt 120
ttattatttt tgccgtattt gctgtcctga cagtagccat cttctgatc atggagggcc 180
tctctgcttt cctgcacgcc ctgcgactgc actgggaagc tgtttgggga acttgagcta 240
tttagaagat ggcaaccaag ccaacagagc ctgtcacgat cctcagcctt cggaaattga 300
gcctggggac cgagagacca caggttaaag agccaaagac gttcacctgt gaagatgcag 360
tgagactat cggttcggg cgtttcaca ttgccctctt tctgatcatg ggcagtactg 420
gggtggttga ggcatggag atcatgttga tagctgtgt gtctcctgtc atccgctgtg 480
aatggcaact ggagaattgg caggtggcat tagtaaccac gatggtgttt tttggctaca 540
tggttttcag tatcctcttt ggcctcctgg ctgacagata tggccgctgg aagattctgc 600
tcactctggt cctgtgggga gcctatttct ccttgcgtac ctcgtttgc cttctgata 660
tctggtttgt cttcctgcgg acgatggtgg gctgtggtgt gtccggccac tcgcaagggg 720
taatcataaa gactgaattt ttgccacga aataccgagg ctatatgtta ccctgtctc 780
aggtgttctg gcttgcgggc tccctgtcga tcattggctt ggcctctgtg atcatcccca 840
ccatcggttg gcgctggctc attcgcgtcg cctccatccc gggcatcatc ctcatcgtgg 900
ccttcaagtt tattcctgaa tctgcccggt tcaatgtctc cactgggaac actcgggctg 960
ccctggccac tctggagcgc gttgccaaga tgaaccgctc ggtcatgccg gaggggaagc 1020
tggtggagcc cgtcctggaa aaaagaggaa gatttgcaga cctattggat gctaaatatt 1080

```

```

tacggaccac attacagatc tgggtcatat ggcttggaat ctcttttgcc tactatgggg 1140
ttatcctggc cagtgtgag ctgctggagc gggacttggg ctgtgggtca aagtcagact 1200
ctgcggtggg ggtgactggg ggggactcag gggagagcca gagcccctgc tactgccaca 1260
tgttttgcacc ctctgactat cggaccatga tcatcagcac catcgggtgaa attgctttga 1320
atccttttaa tatactgggc atcaatttcc tgggaagacg gctgagcctt tctattacca 1380
tgggatgcac ggctttattc ttccttctcc tcaacatttg cacttcaagt gccggcctga 1440
ttggcttcct ctcatgctg agggctctgg tagctgcaaa cttoaacacc gtctacattt 1500
acacagctga ggttcttatg agtgcacaa tactgggggc cctgtgtctc ttctcatctg 1560
tctgtgttgt atgcgccatt tctgcattca ctctcccat cgaaaccaa ggacggggcc 1620
tccagcaaat taaatgaaga cctgcaaagc tatgtctacc agatgagaaa aatgaattct 1680
atcttcagaa ctgcggtgca tttttttaa acttggtttt acttctgtat gctactcggg 1740
aattgataaa gtgatttttt ttttaaaggc atatatggga atggggtagg taactgtata 1800
ttgatctctt ccttgaggaa caatatata agtactttta taaaatataa ttttaagctt 1860
caaaggggtg tgagaggag atggtggggg ggaagatggc ttttcttcat tgaaatcaag 1920
tctgtaaac tttatatgaa taaatactaa attttaact tacaaaaaa aaaaaagg 1978

```

<210> 109

<211> 1622

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7505145CB1

<400> 109

```

tgcttgggtgc cctgttccgc gtctgtgcga ccgtccgtcc cgagcgcgca ccggggcagg 60
ccaggctcaga gcagcccacc atgggatggg gaggggggtg aggtgcacc ccgcgccacc 120
ccatccacca gcagccgccg gagcgccgcg tgggtaccgt tgtctttctc ggctcctgc 180
tggaacctct ggcccttcacg ctgctgtctg ccctgtctgc cgggctgttg gagagccacg 240
gccgtgcccc cgacccctc tatggctcct ggcagggcgg ggtggactgg tttgccaccg 300
ccatcgggat gccagtggag aagaggtaaa acagtgtcct gttcggagggt ctcatgtggt 360
cggcattctc tgcctgcag tttctgtgtg cgccactcac tggggccacc tctgactgct 420
tggggaggcg cccgggtgat ctgctgtgcc tgatgggtgt ggccacctca tatgcagtct 480
ggggccacct tcggagcttt gcggccttcc tggcctccag gctgattggg ggcatcagca 540
aagggaacgt cagcctctcc acggccatcg ttgctgacct gggctcgcct ctggcccgcg 600
gtcaaggcat ggcggtcatt ggggtggcct tctcactggg cttcaccctg ggccctatgc 660
tcggagcctc cctgcccctg gaaatggcac cctggtttgc cctgctcttc gcagcctccg 720
acctgctgtt catcttctgc ttcctgccag agacgtgcc cctggagaaa cgggcgccct 780
ctatcgccct ggggttccgt gatgcggctg atctgtctag cccctggcc ctgctgcgct 840
tctcggctgt cgctcgtggc caggaccac cctctggaga caggctcagc agcctgcgcc 900
gcctgggcct agtctacttc ctctacctct tctgttctc gggcctggag tacacgctga 960
gcttcctcac acaccagcgc ttccagttca gtaggcctc ctgctgctgg tgccgcctt 1020
cctctcatc ggctggggac gttctctgcc cgtgctggg ctggggctgc tgcctactc 1080
ctttgccgcc gccgttgttg tgcctgect gtcctcctg gtcgctggct atggctcacc 1140
agggcagaag ggcacggtca tgggtacact gcgcagccta ggtgctctgg ccagggccgc 1200
ggggcccctg gtggccgctt cagtgtactg cctggccggg gccaggcct gcttcaccac 1260
gtggtccggg ctctttttgc tccccttctt cctcctgcag aagctgagtt acccggcaca 1320
gacgtcaag gctgagtagc tgagccactg tgcccaggct gtgggcacca ggcagagtgg 1380
gagcctaggt caggcccctg cccactgcct gacccacc ccccgccagt ccaggagac 1440
cctgtgggtg ggggcccggc cctaagcagg aagctcaggc agctcctcca gacttactta 1500
ctccttcagt gactccgagc tgcagcactc caaggctgtc agggcttctg tttgtttttt 1560
aaactatgca ccagggttct gatgatgaaa taaagcacct gtttgtttta taaaaaaaa 1620
aa 1622

```

<210> 110

<211> 1982

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7505162CB1

<400> 110

```

ggctccccgcc tctgttcagg acactgggtc cccttggagc ctccccaggc ttaatgattg 60
tccagaaggc ggctataaag ggagcctggg aggctgggtg gaggagggag cagaaaaaac 120
ccaactcagc agatctggga actgtgagag cggcaagcag gaactgtggt cagaggctgt 180
gogtcttggc tggtagggcc tgcctctttc taccatggca gccagggt atggctatta 240
tcgcactgtg atcttctcag ccattgttgg gggctacagc ctgtattact tcaatcgcaa 300
gaccttctcc ttgtcatgc catcattggt ggaagagatc ctttggaca aggatgattt 360
ggggttcac accagcagcc agtcggcagc ttatgctatc agcaagtgtg tcagtgggt 420
gctgtctgac cagatgagt ctcgctggct cttctcttct gggctgctcc tggttggcct 480
gggtcaacata ttctttgcct ggagctccac agtacctgtc tttgctgcc tctggttcct 540
taatggcctg gccaggggc tgggctggcc cccatgtggg aaggctctgc ggaagtgtt 600
tgagccatct cagtttggca cttgggtggc catcctgtca accagcatga acctggctgg 660
agggtgggc cctatcctgg caaccatcct tgcccagagc tacagctggc gcagcacgct 720
ggccctatct ggggcactgt gtgtggtgt ctccttcctc tgtctcctgc tcatccacaa 780
tgaacctgct gatgttgac tccgcaacct ggaccccatg ccctctgagg gcaagaagg 840
ctccttgaag gaggagagca ccctgcagga gctgctgctg tccccttacc tgtgggtgct 900
ctccactggt taccttgtgg tgttggagt aaagacctgc tgtactgact ggggccagtt 960
cttcttctc caggagaaa gacagtcagc cctttagggc gggactgtcc aactacggga 1020
accctcgcca tggcctgtt ctgttcata tggctggcat gacagtgtcc atgtacctct 1080
tccggtaac agtgaccagt gactccccca agctctggat cctggtattg ggagctgtat 1140
ttggtttctc ctgtatggc cccattggcc tgttggagt catagccaac gagagtggc 1200
ctcccaactt gtgtggcacc tcccagcca ttgtgggact catggccaat gtgggcggct 1260
ttctggctgg gctgccctc agcaccattg ccaagcacta cagttggagc acagccttct 1320
gggtggctga agtgattgt gggccagca cggctgcctt cttctccta cgaaacatcc 1380
gcaccaagat gggccgagt tccaagaag ctgagtgaag agagtccagg ttccggagca 1440
ccatccacg gtggccttcc ccctgcacgc tctgcgggga gaaaaggagg ggcctgcctg 1500
gctagccctg aacctttcac ttccatttc tgccctttt ctgtcaccgg ggtggcgctg 1560
gaagtatatca gtggctagt aggtcccagc tccctgatcc tatgctctat ttaaaagata 1620
acctttggcc ttagactccg ttagctccta tttctgcct tcagacaaac aggaaacttc 1680
tgcagttagg aaggctcctg tacccttctt ctttctctag gccctgtcct gccgcctcc 1740
taccctatcc ccacctgaag tgaggctatc cctgcagctg cagggcacta atgaccttg 1800
acttctgctg ggtcctaagt cctctcagca tgggtgact gctgttgcca atacctcaga 1860
ctccagggaa agagaggagg ccattattct cactgtacca ctaggcgagc ttggatatag 1920
gtgggaagaa aagggtgact gttatagaag attaaaacta gatttgatac tgaaaaaaa 1980
aa 1982

```

<210> 111

<211> 2231

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7505469CB1

<400> 111

```

ggcttatgaa agtgtgatgt tcgcgtatct cttgccaggc agtggcgtga tcttggctca 60
ctgcaacctc cgactccctg gttcaagcga ttctcctgcc tcagcctcct gagtggggat 120

```

```

tacaggccac agcaaacaca ggtgtgcagg aaccgtttgt catggaagcc agggagcctg 180
ggaggccac acccacctac catcttgtcc ctaacaccag ccagtcccag gtggaagaag 240
atgtcagctc gccacctcaa aggtcctccg aaactatgca gctgaagaag gagatctccc 300
tgctgaatgg ggtcagcctg gtggtgggca acatgatcgg ctgagggatc tttgtctcac 360
ccaaggggtg gctggtacac actgcctcct atgggatgtc actgattgtg tgggccattg 420
gtgggctctt ctctgtttgt ggtgcccttt gttatgcaga gctggggacc accatcacca 480
agtcgggagc cagctacgct tatattctag aggcctttgg gggcttcatt gccttcaccc 540
gcctgtgggt ctcaactgta gttgttgagc ccaccgggtca ggccatcatc gccatcacct 600
ttgccaacta catcatccag ccgctccttc ccagctgtga tccccatac ctggcctgcc 660
gtctcctggc tgtgcttgc atatgtctgc tgacatttgc gaactgtgcc tatgtcaagt 720
ggggcacacg tgtgcaggac acgttcactt acgccaaggt cgtagcgtc attgccatca 780
ttgtcatggg ccttgtttaa ctgtgccagg aaatttgccc ttggccattg ggatttctat 840
gccaattgtg acgtcatct acatcctgac caatgtggcc tattacacag tgctgaacat 900
ttcagatgtc cttagcagtg atgctgtggc tgtgacattt gctgaccaga cgtttggcat 960
gttcagctgg accatcccca ttgctgttgc cctgtcctgc tttggggggc tcaatgcac 1020
catctttgct tcatcaaggt tgttcttctg gggctcccg gagggccacc taccggacct 1080
tctgtccatg atccacattg agcgttttac acctatccct gctttactgt tcaattgcac 1140
catggcactc atctacctca tctgtggagga tgttttccag cttatcaact acttcagctt 1200
cagctactgg ttcttctgtg gcctgtctgt tgttgacag ctctacctcc gctggaagga 1260
gccaagcgg ccccgccctc tcaagctgag cgtgtttttc cccatcgtgt tctgcatatg 1320
ctccgtgttt ctggtgatag tgccctctt cactgacacc attaatccc tcattggcat 1380
cggtattgcc ctttctggag tcccttctta ctcatgggt gtttacctgc cagagtcccg 1440
gaggccattg tttattcgga atgtcctggc tgctatcacc agaggcacc agcagctttg 1500
cttttgtgtc ctgactgagc ttgatgtagc cgaagaaaaa aaggatgaga ggaaaactga 1560
ctagaggtca gagtggtctt tctgaggcct ggaaggcagg ccaaccagca aaatcctgat 1620
aacaagactc tgtgggcca actctcctga attaaaggag ctttttgacc caatcatata 1680
gtggggctca gggccagtgc tcaactctat tggtttgtt tacacttga gccaccttg 1740
tgtgggtcac cgggacagt tactctctc ctgccagcct ccccttcccc gaggtgtggt 1800
ggctgcagtc tcaggaagag cttggtactt gtggggactt ctgttttct cctgtggaga 1860
tcagtgaaga ctgggaggaa agctgcttca acctgagtc ggctcttcag caggctgcac 1920
aagtgaagc aactaattct ggtgctcagg ctgggtctc caccgaagt aggcctgtc 1980
tggcctaatt gatcttactg tatgagcagg acggctgcat tggattgtac aactgtttg 2040
tgatgcccc agacactgtc atcctaggcc gagaagaacc tgctagcttg acatacccca 2100
tgggcttatc cttagggtttt ggaattggtc aacagtgagg cagtctccct tcctgacct 2160
tcttctccac ccagtcacag ataagggaat aaccttgcc atatatattgc tcaataaaga 2220
ttgaaggaag c 2231

```

<210> 112

<211> 5170

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7505475CB1

<400> 112

```

agctgctgga gtaggcaccc atttaaagaa aaaatgaaga agcagcaata aagaagttgt 60
aatcgttacc tagacaaaca gagaactgggt tttgacagt tttctagagt gctttttatt 120
attttcttga cagttgtgtt ccaccatgat tactttctcc ttcagcgaat aggctaaatg 180
aatatgaaac agaaaagcgt gtatcagcaa accaaagcac ttctgtgcaa gaattttctt 240
aagaaatgga ggatgaaaag agagagctta ttggaatggg gcctctcaat acttctagga 300
ctgtgtattg ctctgttttc cagttccatg agaaatgtcc agtttctctg aatggctcct 360
cagaatctgg gaagggtaga taaatttaaat agctcttctt taatggttgt gtatacacca 420
atatctaatt taaccagca gataatgaat aaaacagcac ttgctcctct tttgaaagga 480
acaagtgtca ttggggcacc aaataaaaca cacatggacg aaatacttct ggaaaattta 540

```

ccatatgcta tgggaatcat ctttaaatgaa acttttctctt ataagttaat atttttccag 600
 ggatataaca gtccactttg gaaagaagat ttctcagctc attgctggga tggatatggt 660
 gagttttcat gtacattgac caaatactgg aatagaggat ttgtggcttt acaaacagct 720
 attaatactg ccattataga aatcacacc aatcacctg tgatggagga gttgatgtca 780
 gttactgcta taactatgaa gacattacct ttcataacta aaaatcttct tcacaatgag 840
 atgtttatctt tattcttctt gcttcatttc tccccacttg tatattttat atcactcaat 900
 gtaacaaaag agagaaaaaa gtctaagaat ttgatgaaa tgatgggtct ccaagattca 960
 gcattctggc tctcctgggg tctaacttat gctggcttca tctttattat ttccatattc 1020
 attacaatta tcataacatt cacccaaatt atagtcata ctggcttcat ggtcatattt 1080
 ataccctttt ttttatatgg cttatctttg gtatctttgg tgttctctgt gagtgtgctg 1140
 ttaaagaaag ctgtcctcac caatttggtt gtgtttctcc ttaccctctt ttggggatgt 1200
 ctgggattca ctgtatttta tgaacaactt cttcatctc tggagtggat tttgaatatt 1260
 tgtagccctt ttgcctttac tactggaatg attcagatta tcaaactgga ttataatttg 1320
 aatgggtgtaa tttttcctga cccttcagga gactcatata caatgatagc aactttttct 1380
 atgttgcttt tggatgggtc catctacttg ctattggcat tatactttga caaaatttta 1440
 ccctatggag atgagcgcca ttattctcct ttatttttct tgaattcatc atcttgtttc 1500
 caacaccaa ggactaatgc taaggttatt gagaaagaa tcatgctga gcatccctct 1560
 gatgattatt ttgaaccagt agctcctgaa ttccaaggaa aagaagccat cagaatcaga 1620
 aatgttaaga aggaatataa aggaaaatct ggaaaagtgg aagcattgaa aggcttgcct 1680
 tttgacatat atgaaggta aatcacggca atcctgggtc acagtggagc tggcaaatct 1740
 tcaactgctaa atattcttaa tggattgtct gttccaacag aaggatcagt taccatctat 1800
 aataaaaatc tctctgaaat gcaagacttg gaggaatca gaaagataac tggcgtctgt 1860
 cctcaattca atgttcaatt tgacatactc accgtgaagg aaaacctcag cctgtttgct 1920
 aaaataaaa ggattcatct aaaggaagtg gaacaagagg tacaacgaat attattggaa 1980
 ttggacatgc aaaacattca agataacctt gctaaacatt taagtgaagg acagaaaaa 2040
 aagctgactt ttgggattac catttttagga gatcctcaaa tagaaaagtg atcatgtcca 2100
 atgggagact gaagtgtgca ggttcttcta tgtttttgaa aagaaggtgg ggtcttggat 2160
 atcacctaag tttacatagg aatgaaatat gtaaccaga acaataaaca tcttcatata 2220
 ctcacacat ccccgatgct aaattaaaaa cagaaaacaa agaaaagctt gtatatactt 2280
 tgccactgga aaggacaaat acatttccag atcttttcag tgatctggat aagtgttctg 2340
 accagggagt gacaggttat gacatttcca tgtcaactct aaatgaagtc tttatgaac 2400
 tggaaggaca gtcaactatc gaacaagatt tcgaacaagt ggagatgata agagactcag 2460
 aaagcctcaa tgaaatggag ctgggtcact cttccttctc tgaaatgcag acagctgtga 2520
 gtgacatggg cctctggaga atgcaagtct ttgccatggc acggctccgt ttcttaaagt 2580
 taaaacgtca aactaaagt ttattgacct tattattggt atttggaatc gcaatattcc 2640
 ctttgattgt tgaataatata atatatgcta tgttaaatga aaagatcgat tgggaattta 2700
 aaaacgaatt gtattttctc tctcctggac aacttcccca ggaacccgt accagcctgt 2760
 tgatcatcaa taacacagaa tcaaatattg aagattttat aaaatcactg aagcatcaaa 2820
 atatactttt ggaagtagat gactttgaaa acagaaatgg tactgatggc ctctcataca 2880
 atggagctat catagtttct ggtaaacaaa aggattatag attttcagtt gtgtgtaata 2940
 ccaagagatt gcaactgttt ccaattctta tgaatattat cagcaatggg ctacttcaaa 3000
 tgtttaatca cacacaacat attcgaattg agtcaagccc atttctctct agccacatag 3060
 gactctggac tgggttgccg gatggttctt ttttcttatt tttggttcta tgtagcattt 3120
 ctccttatat caccatgggc agcatcagtg attacaagaa aaatgctaag tcccagctat 3180
 ggatttcagg cctctacact tctgcttact ggtgtgggca ggcactagtg gacgtcagct 3240
 tcttcatttt aattctcctt ttaatgtatt taattttcta catagaaac atgcagtacc 3300
 ttcttattac aagccaaatt gtgtttgctt tggttatagt tactcctggt tatgcagctt 3360
 ctcttgcctt cttcatatat atgatatcat ttatttttct caaaaggaga aaaaacagtg 3420
 gcctttgggtc attttacttc ttttttgcct ccaccatcat gttttccatc acttttaatca 3480
 atcatattga cctaagtata ttgattacca ccatgggtatt ggttccttca tatacttgc 3540
 ttggatttaa aacttttttg gaagtgaag accaggagca ctacagagaa tttccagagg 3600
 caaattttga attgagtgc actgattttc tagtctgctt cataccctac tttcagactt 3660
 tgctattcgt ttttgttcta agatgcattg aactaaaatg tggaaagaaa agaatgcgaa 3720
 aagatcctgt tttcagaatt tcccccaaa gtagagatgc taagccaaat ccagaagaac 3780
 ccatagatga agatgaagat attcaaacag aaagaataag aacagccact gctctgacca 3840
 cttcaatctt agatgagaaa cctgttataa ttgccagctg tctacacaaa gaatatgcag 3900

```

gccagaagaa aagttgcttt tcaaagagga agaagaaaat agcagcaaga aatatctctt 3960
tctgtgttca agaaggtgaa attttgggat tgctaggacc cagtgggtgct ggaaaaagtt 4020
catctattag aatgatatct gggatcacaa agccaactgc tggagaggtg gaactgaaag 4080
gctgcagttc agttttgggc cacctggggg actgccctca agagaacgtg ctgtggccca 4140
tgctgacgtt gagggaacac ctggaggtgt atgctgccgt caaggggctc aggaaagcgg 4200
acgcgaggct cgccatcgca agattagtga gtgctttcaa actgcatgag cagctgaatg 4260
ttcctgtgca gaaattaaca gcaggaatca cgagaaagtt gtgttttgtg ctgagcctcc 4320
tgggaaactc acctgtcttg ctctggatg aaccatctac gggcatagac cccacagggc 4380
agcagcaaat gtggcaggca atccaggcag tcgttaaaaa cacagagaga ggtgtcctcc 4440
tgaccaccca taacctggct gaggcggaag ccttgtgtga ccgtgtggcc atcatggtgt 4500
ctggaaggct tagatgcatt ggctccatcc aacacctgaa aaacaaactt ggcaaggatt 4560
acattctaga gctaaaagtg aaggaaacgt ctcaagtga tttgggtccac actgagattc 4620
tgaagctttt cccacaggct gcagggcagg aaaggatttc ctctttgtta acctataagc 4680
tgcccggtggc agacgtttac cctctatcac agacctttca caaattagaa gcagtgaagc 4740
ataactttta cctggaagaa tacagccttt ctgagtcac actggagaag gtattcttag 4800
agcttttctaa agaacaggaa gtaggaatt ttgatgaaga aattgataca acaatgagat 4860
ggaaactcct ccctcattca gatgaacctt aaaacctcaa acctagtaat tttttgttga 4920
tctcctataa acttatgttt tatgtaataa ttaatagtat gtttaatttt aaagatcatt 4980
taaaattaac atcaggtata ttttgtaa attagttaaca aatacataaa ttttaaaatt 5040
attcttcctc tcaaacatag gggatgtagc aaacctgtga taaaggcaat acaaaatatt 5100
agtaaagtca ccaaagatt caggcactgg aattatggac taaaacggta tatctagttt 5160
tagcctcttc                                     5170

```

<210> 113

<211> 1876

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7505568CB1

<400> 113

```

gccttggcag agtctggggg ccctggactg agccatcagc tgggtcactg agacccatgg 60
caaggaacaa aaataggaat tccaaggaac tgggcctagt tcccctcaca gatgacacca 120
gccacgcagg gcctccaggg ccaggaggag cactgctgga gtgtgaccac ctgaggagtg 180
gggtgccagg tgggaaggaga agaaaggact ggtcctgctc gctcctcgtg gcctccctcg 240
cgggcgcctt cggtcctctc ttctctacg gctacaacct gtcgggtggg aatgccccca 300
ccccggaagc acactttgct ggccaataat gggtttgcaa tttctgctgc attgctgatg 360
gcctgctcgc tccaggcagg agcctttgaa atgctcatcg tgggacgctt catcatgggc 420
atagatggag gcgtcgccct cagtgtgctc cccatgtacc ttagtgagat ctacccaag 480
gagatccgtg gctctctggg gcaggtgact gccatcttta tctgcattgg cgtgttcact 540
gggcagcttc tgggcctgcc cgagctgctg ggaaaggaga gtacctggcc atacctgttt 600
ggagtgattg tgggtccctgc cgttgtccag ctgctgagcc ttccctttct cccggacagc 660
ccacgtacc tgctcttgga gaagcacaa gaggcaagag ctgtgaaagc cttccaaacg 720
ttcttgggta aagcagacat ttcccaagag gtagaggagg tccctggctga gagccgcgtg 780
cagaggagca tccgcctggg gtccgtgctg gagctgctga gagctcccta cgtccgctgg 840
caggtggtca ccgtgattgt caccatggcc tgctaccagc tctgtggcct caatgcaatt 900
tggttctata ccaacagcat ctttggaata gctgggatcc ctccggcaaa gatcccatat 960
gtcaccttga gtacaggggg catcgagact ttggctgccg tcttctctgg tttggtcatt 1020
gagcacctgg gacggagacc cctcctcatt ggtggctttg ggctcatggg cctcttcttt 1080
gggaccctca ccatcacgct gaccctgcag gaccacgcc cctgggtcc cctacctgag 1140
tatcgtgggc attctggcca tcatcgctc tttctgcagt gggcccagggt ggcacccgt 1200
tcatcttgac tgggtgagttc ttccagcaat ctgagcgcc ggctgcctc atcattgcag 1260
gcaccgtcaa ctggctctcc aactttgctg ttgggtcct cttcccatte attcagaaaa 1320
gtctggacac ctactgtttc ctagtctttt ctacaatttt tatcacaggt gctatctacc 1380

```

```

tgtattttgt gctgcctgag accaaaaaca gaacctatgc agaaatcagc caggcatttt 1440
ccaaaaggaa caaagcatac ccaccagaag agaaaatcga ctcagctgtc actgatgcag 1500
ctcaaaggaa ctaagacaaa gatcatggag accatcgggt gagtctcaag acttccccca 1560
gctctgcttg gctgggtctcc tgctggtatt ttctgtctgt agagaggaaac aagaacttcc 1620
attttatctt gcttacctgc acttatgaaa agtcaaactg agtcatgctg agagccaggg 1680
aacataggag tcagttcttc tgcagcagca ctcagccagt tgaaggcaat gtggagtgat 1740
ggaaggagag cagtgatgca gtgatgctgg caccaactcc ttactatgg catccattgt 1800
accagctgcc atacaccagg caacttctac actttatctc taatcatcct agaataagta 1860
ttagtttccc catctt 1876

```

<210> 114

<211> 1602

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7506953CB1

<400> 114

```

ctctctctct ctctctctct ctctctctct ctctctctct ctcccaagtt tcctatctcg 60
tcaagatcag ggcaaaagaa gaaaacaccg aattctgctt gccgtttcag agcggcggtg 120
atgaagacaa aattgaacat ctacaacatg cagttcctgc tttttgtttt cttgggtgtg 180
gacctgcca ggttggtgct ggctaacatc caagaagatg aggctaaaaa taacattacc 240
atctttacga gaattcttga cagacttctg gatggttacg ataatcggct tagaccagga 300
ctgggagatg catatacaac ttcagaggtc acttatattt ggacttacia tgcatctgat 360
tcagtacagg ttgctcctga tggctctagg ttaaataaat atgacctgct gggccaatca 420
atcggaagg agacaattaa atccagtaca ggtgaatata ctgtaatgac agctcatttc 480
cacctgaaaa gaaaaattgg gtattttgtg attcaaactc atctgccttg catcatgact 540
gtcattctct cccaagtttc attctggctt aacagagaat ctgtgcctgc aagaactgtg 600
tttgagtaa caactgtcct aacaatgaca actctaagca tcagtgtctg gaattctctc 660
cccaaagtgg cttatgcaac tgccatggac tgggtttatt ctgtttgtta tgcatttgtg 720
ttctctgccc taattgaatt tgcaactgtt aattacttca ccaaaagagg atgggcttgg 780
gatgggaaga gtgtagtaaa tgacaagaaa aaagaaaagg cttccgttat gatacagaac 840
aacgcttatg cagtggctgt tgccaattat gccccgaatc tttcaaaaga tccagttctc 900
tccaccatct ccaagagtgc aaccacgcca gaaccaaca agaagccaga aaacaagcca 960
gctgaagcaa agaaaacttt caacagtgtt agcaaaattg acagaatgtc cagaatagtt 1020
tttccagttt tgtttggtac ctttaattta gtttactggg ctacatatatt aaacagagaa 1080
cctgtattag gggctcagtc ttgaattgag acccatgtta tctttgggat gtatagcaac 1140
attaaatttg gtttgttttg ctatgtacag tctgactaat aactgctaatt ttgtgatcca 1200
acatgtacag tatgtatata gtgacatagc ttaccagtag acctttaatg gagacatgca 1260
tttgctaact catggaactg cagacagaaa gcactccatg cgaaaacagc cattgccttt 1320
tttaaagatt taccctagga cctgatttaa agtgaatttc aaatgacctg attaatcttc 1380
tattcttcca aatgagatga aaatggggat cctgtacaac cctttgtgga cacttttggt 1440
ttagctctta agtaggggta ttttctactg ttgcctaata tgatggaagt aacattgtca 1500
ttctagatga atctttgaag taccaacatt gttctggaat cagctcggtc cagatgtctc 1560
aggtccctgt aatgtattgg aagctggtac cctaagaaaa ca 1602

```

<210> 115

<211> 2173

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7510176CB1

<400> 115

```

cactattgaa gccacctgct caggacaatg aaattcttca gttacattct ggtttatcgc 60
cgatttctct tcgtgggttt cactgtgttg gttttactac ctctgcccat cgtcctccac 120
accaagctta ttctgacttt tccaagatga agatgaagag caggccagtg gcatgggcca 180
gatgcagtca gatgactgac tgaccaggag ggcctccgtc cagtgaccag tctcagaatt 240
taaaggaccc ttccccctta cttatgcttg tactcagccc aggaagcaga atgtgcctac 300
acactctttg tggtcgccac attttggtc acagaagcat tgcctctgtc ggtaacagct 360
ttgtaccta gtttaatgtt acccatgttt gggatcatgc cttctaagaa ggtggcatct 420
gcttatttca aggattttca cttactgcta attggagtta tctgttttag aacatccata 480
gaaaaatgga atttgcacaa gagaattgct ctgaaaatgg tgatgatggt tgggtgtaa 540
cctgcatggc tgacgtggg gttcatgagc agcactgcct ttttgtctat gtggctcagc 600
aacacctcga cggctgccat ggtgatgcc attgctggag ctgtagtgc gcagatcatc 660
aatgcagaag cagaggtcga ggccactcag atgacttact tcaacggatc aaccaaccac 720
ggactagaaa ttgatgaaag tgttaatgga catgaaataa atgagaggaa agagaaaaca 780
aaaccagttc caggatacaa taatgataca gggaaaattt caagcaagggt ggagttggaa 840
aagaactcag gcatgagaac caaatatcga acaaagaagg gccacgtgac acgtaaactt 900
acgtgtttgt gcattgccta ctcttctacc attggtggac tgacaacaat cactgggtacc 960
tccaccaact tgatctttgc agagtatttc aatacacgct atcctgactg tcgttgacct 1020
aactttggat catggtttac gttttccttc ccagctgcc ttatcattct actcttatcc 1080
tggatctggc ttcagtggct tttcctagga ttcaatttta aggagatggt caaatgtggc 1140
aaaacaaaa cagccaaca aaaagcttg gctgagggtga ttaagcaaga atacaaaag 1200
cttgggcaa taaggatat agaaattgtg acctgggtcc tcttcattat aatggctctg 1260
ctatggttta gtcgagacc cggatttgtt cctggttggt ctgcactttt ttcagagtac 1320
cctggttttg ctacagattc aactgttgct ttacttatag ggctgctatt ctttcttacc 1380
ccagctaaga cactgactaa aactacacct acaggagaaa ttgttgcttt tgattactct 1440
ccactgatta cttggaaaga attccagtca ttcattgccct gggatatagc cattcttggt 1500
ggtggagggt ttgccctggc agatgggtgt gaggagtctg gattatctaa gtggatagga 1560
aataaattat ctctctggg ttcattacca gcatggctaa taattctgat atcttctttg 1620
atggtgacat ctttaactga ggtagccagc aatccagcta ccattacact ctttctccca 1680
atattatctc cattggccga agccattcat gtgaacctc tttatattct gataccttct 1740
actctgtgta cttcatttgc attcctccta ccagtagcaa atccaccaa tgctattgtc 1800
tttcatatg gtcactgaa agtcattgac atgggttaaag ctggacttgg tgtcaacatt 1860
tttgggtgtg ctgtgggtat gcttggcata tgtacttggg ttgtacccat gtttgacctc 1920
tacacttacc cttcgtgggc tctgtctatg agtaatgaga ccatgccata ataagcaca 1980
aatttctgac tatcttgcgg taatttctgg aagacattaa tgattgactg taaaatgtgg 2040
ctctaaataa ctaatgacac acatttaaat cagttatggt gtagctgctg caattcccgt 2100
gaatacccg aacctgctgt tataactcag agtccatatt tgttattgca gtgcaactaa 2160
agagcatcta tgt

```

2173

<210> 116

<211> 1826

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7510541CB1

<400> 116

```

cccacgcgtc cgcccacgcg tccgccacg cgtccgcagc cgagttcagc cgggagcaga 60
gcgaaccgca ccggcccag cggagcgcg caggttccca accgcgaggc cagacatctg 120
actgttggtg tgagaccagt gtcctggtg gtgtgccctg agccatggag gcgcctttgc 180
agacagagat ggtggagctg gtgcccact gcaaactc agaggggctg ctcccggtca 240
tcaccccat ggcaggcaac cagagggtcg aggacctgc acggagctgt atggagggca 300
agagcttct acagaaaagt cccagcaagg agccacact cactgacttc gaggggaaga 360
catcattcgg gatgtcagtg ttcaacctca gcaatgccat catgggcagc ggcatcctgg 420

```

```

gactgccta tgccatggcc aatacgggca ttatcctttt cctgcatccg tgcctatgag 480
cagctgggct accgtgcctt tgggacccca ggaaagctgg cagcagcctt ggccatcacg 540
ctccagaaca tcggagccat gtccagctac ctgtacatca tcaagtctga gctgccactt 600
gtcatacaga ccttcctgaa cctggaggag aaaacctcgg actggtacat gaacgggaac 660
tacctggtaa tccttgtctc tgtcaccatc attctgcccc tggcactgat gcggcagctt 720
ggctacctgg gctactccag cggcttctct cttagctgca tgggtgttct cctaattgca 780
gtcatctaca aaaagttcca cgtgccctgc ccactgcccc ccaacttcaa caacaccaca 840
ggcaacttca gccacgtgga gatcgtgaag gagaagggtg agctgcaggt cgagcctgag 900
gcttcagcct tctgcatccc cagctacttc acgctcaact cacagacagc atacaccatc 960
cccatcatgg ccttcgcctt cgtctgccac ccgaggtgac tgcccatcta tactgagctc 1020
aaggaccctt ccaagaagaa gatgcagcac atctccaacc tgtccatcgc tgtcatgtac 1080
atcatgtact tcctggctgc cctcttcggc tacctcacct tctacaacgg ggtggagtcg 1140
gagctgctgc acacctacag caaggtggac ccgtttgacg tcctgatcct gtgtgtgcgc 1200
gtggccgtgc tgacagcagt cacgctcaca gtgcccacgc ttctgttccc ggtgcgcgcg 1260
gccatccagc agatgctggt tccaaaccag gatttcagct ggctgcggca tgtgtttatt 1320
gccgttggcc tgctcacttg tatcaacctg ctggtcatct ttgcccccaa catcctgggc 1380
atctttgggg tcacgggtgc cacatctgcc ccattcctca tcttcatctt ccctgccatc 1440
ttctacttcc gaatcatgcc caccggagaag gagcctgcaa gatccacccc caaaatcctg 1500
gccctgtggt ttgctatgct tggcttcttg ctgatgacca tgagcttgag cttcatcatc 1560
attgactggg cctcagggac cagccggcat ggaggaaacc actagggtga ccctcatcct 1620
gttctgtcta ctcaccctag cagccctgcc cagactcttc agccctgct cccatccagt 1680
ggccagtcgg gggaggagaa agacgcgatt aacactgtgg cattcagcca ggcccatgt 1740
cctctctgtg gaaggttttt gttcaagagc caggaccaag gcccttgggc cactaccctg 1800
ctaggctctg gagctgtaga ggcttc 1826

```

<210> 117

<211> 2052

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7510923CB1

<400> 117

```

cccacgcgtc cggccacgcg tccgcccacg cgtccgcagc cgagttcagc cgggagcaga 60
gcgaaccgca ccggcccagc cggagcgccg cacgttgcca accgcgaggc cagacatctg 120
actgttggtg tgagaccagt gtccttggtg gtgtgcccct agccatggag gcgcctttgc 180
agacagagat ggtggagctg gtgcccacat gcaaacactc agaggggctg ctcccggcca 240
tcacccccat ggagggcaac cagagggctg aggaccctgc acggagctgt atggagggca 300
agagcttcct acagaaaagt cccagcaagg agccacactt cactgacttc gaggggaaga 360
catcattcgg gatgtcagt ttcaacctca gcaatgccat catgggcagc ggcatcctgg 420
gactgccta tgccatggcc aatacgggca ttatcctttt cctgttcctg ttgacagctg 480
tcgccttgct ctccagctac tccatccacc tgctactcaa gtcctcaggg gtcgtgggca 540
tccgtgccta tgagcagctg ggctaccgtg cctttgggac cccaggaaag ctggcagcag 600
ccctggccat cagctccag aacatcggag ccatgtccag ctacctgtac atcatcaagt 660
ctgagctgcc acttgtcata cagaccttcc tgaacctgga ggagaaaacc tcggactggt 720
acatgaacgg gaactacctg gtaatccttg tctctgtcac catcattctg ccctggcac 780
tgatgcggca gcttggtac ctgggctact ccagcggctt ctctcttagc tgcattggtg 840
tcttcctaat tgcagtcac tacaaaaagt tccacgtgcc ctgcccactg cccccaact 900
tcaacaacac cacaggcaac ttcagccacg tggagatcgt gaaggagaag gtgcagctgc 960
aggctgagcc tgaggcttca gccttctgca ctcccagcta cttcacgctc aactcacagg 1020
ttctgacagg tcagggcaag gcggggggcc aatgagagtg gcagactgcc ttgacacagc 1080
cccgtgtttc cccagacagc atacaccatc cccatcatgg ccttcgcctt cgtctgccac 1140
cccgaggtgc tgcccatcta tactgagctc aaggaccctt ccaagaagaa gatgcagcac 1200
atctccaacc tgtccatcgc tgtcatgtac atcatgtact tcctggctgc cctcttcggc 1260

```

```

tacctcacct tctacaacgg ggtggagtcg gagctgctgc acacctacag caaggtggac 1320
ccgtttgacg tcctgacccg gtgtgtgctg gtggccgtgc tgacagcagt cacgctcaca 1380
gtgcccacgc ttctgttccc ggtgcccgcg gccatccagc agatgctgtt tccaaaccag 1440
gagttcagct ggctgcccga tgtgcttatt gccgttggcc tgctcacttg tatcaacctg 1500
ctgggtcatct ttgcccccaa catcctgggc atctttgggg tcatcggtgc cacatctgcc 1560
ccattcctca tcttcatctt ccctgccatc ttctacttcc gaatcatgcc cacggagaag 1620
gagcctgcaa gatccacccc caaaatcctg gccctgtgtt ttgctatgct tggcttcttg 1680
ctgatgacca tgagcttgag cttcatcatc attgactggg cctcaggggc cagccggcat 1740
ggaggaaacc actaggggtga ccctcatcct gttctgtcta ctcaccctag cagccctgcc 1800
cagactcttc agcccctgct cccatccagt ggccagtcgg gggaggagaa agacgcgatt 1860
aacactgtgg cattcagcca ggccccatgt cctctctgtg gaagggtttt gttcaagagc 1920
caggaccaag gcccttgggc cactaccctg ctaggctctg gagctgtaga ggcttcttga 1980
aactgggagc agggtagggc tgtgcctt agatcccgcc caagccccct cattccctcc 2040
tttgacaga tg 2052

```

<210> 118

<211> 5056

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7510984CB1

<400> 118

```

cgcgcggagc cagcggagcc agctgagccc gagcccagcc cgcgcccgcg ccgccatgcc 60
cctggccttc tgcggcagcg agaaccactc ggccgcctac cgggtggacc agggggctct 120
caacaacggc tgctttgtgg acgcgctcaa cgtggtgccg cacgtcttcc tactcttcat 180
caccttcccc atctcttca ttggatgggg aagtcagagc tccaagggtg acatccacca 240
cagcacatgg cttcatttcc ctgggcacaa cctgcggtgg atcctgacct tcatgctgct 300
cttcgtcctg gtgtgtgaga ttgcagaggg catcctgtct gatgggggtga ccgaatccca 360
ccatctgcac ctgtacatgc cagccgggat ggcgttcatg gctgctgtcg cctccgtggg 420
ctactatcac aacatcgaga cttccaactt ccccaagctg ctaattgccg tgctggtgta 480
ttggaccctg gccttcatca ccaagaccat caagtttgtc aagttcttgg accacgccat 540
cggcttctcg cagctacgct tctgcctcac agggctgctg gtgacctct atgggatgct 600
gtcctcgtg gagtcaatg tcatcagggg gagagatac atcttcttca agacaccgag 660
ggagggtgaag cctcccaggg acctgcaaga cctgggggta cgcttcttgc agcccttctg 720
gaatctgctg tccaaaggca cctactggtg gatgaacgcc ttcataaga ctgccacaa 780
gaagcccatc gacttgcgag ccacgggaa gctgcccatc gccatgaggg ccctcaccaa 840
ctaccaacgg ctctgcgagg cctttgacgc ccagggtcgg aaggacattc agggcactca 900
aggtgcccgg gccatctggc aggcactcag ccacgcttcc gggaggcgcc tggctctcag 960
cagcactttc cgcattctgg ccgacctgct gggcttcgcc gggccactgt gcatcttctg 1020
gatcgtggac cacttggga aggagaacga cgtcttccag cccaagacac aatttctcgg 1080
ggtttacttt gtctcatccc aagagttcct tgccaatgcc tacgtcttag ctgtgcttct 1140
gttccttgcc ctctactgc aaaggacatt tctgcaagca tcctactatg tggccattga 1200
aactggaatt aacttgagag gagcaataca gaccaagatt tacaataaaa ttatgcacct 1260
gtccacctcc aacctgtcca tgggagaaat gactgctgga cagatctgta atctggttgc 1320
catcgacacc aatcagctca tgtgggtttt cttcttctgc ccaaacctct gggctatgcc 1380
agtacagatc attgtgggtg tgattctcct ctactacata ctcggagtca gtgccttaat 1440
tggagcagct gtatcattc tactggctcc tgtccagtag ttcgtggcca ccaagctgtc 1500
tcaggcccag cggagcacac tggagtattc caatgagcgg ctgaagcaga ccaacgagat 1560
gctccgcgcc atcaagctgc tgaagctgta cgcctgggag aacatcttcc gcacgcggtg 1620
ggagacgacc cgcaggaagg agatgaccag cctcaggggc tttgccatct atacctccat 1680
ctccattttc atgaacacgg ccaccccat tgcagctgtc ctcataactt tcgtgggcca 1740
cgtcagcttc ttcaaagagg ccgacttctc gcctccgtg gcctttgcct ccctctccct 1800
cttccatata ttggtcacac cgtgttctct gctgtccagt gtggtccgat ctaccgtcaa 1860

```


(19) World Intellectual Property Organization
International Bureau(43) International Publication Date
9 October 2003 (09.10.2003)

PCT

(10) International Publication Number
WO 2003/083085 A3

(51) International Patent Classification:

A61K 38/00 (2006.01) C07K 16/00 (2006.01)
 A61K 39/00 (2006.01) C12N 1/20 (2006.01)
 C07H 21/04 (2006.01) C12N 5/00 (2006.01)
 C07K 1/00 (2006.01) C12N 15/09 (2006.01)
 C07K 14/00 (2006.01) C12P 21/00 (2006.01)

(21) International Application Number:

PCT/US2003/009797

(22) International Filing Date: 27 March 2003 (27.03.2003)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

60/368,840 28 March 2002 (28.03.2002) US
 60/375,637 26 April 2002 (26.04.2002) US

(71) Applicant (for all designated States except US): INCYTE CORPORATION [US/US]; 3160 Porter Drive, Palo Alto, CA 94304 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): MARQUIS, Joseph, P. [US/US]; 4428 Lazy Lane, San Jose, CA 95135 (US). LEE, Soo, Y. [KR/US]; 40 Westdale Avenue, Daly City, CA 94015 (US). EMERLING, Brooke, M. [US/US]; 833 W. Buena Avenue #2108, Chicago, IL 60613 (US). HAFALIA, April, J.A. [US/US]; 15 Midvale Drive, Daly City, CA 94015 (US). KHARE, Reena [IN/US]; 12650 Orella Court, Saratoga, CA 95070 (US). KABLE, Amy, E. [US/US]; 2345 Polk Street #4, San Francisco, CA 94109 (US). RICHARDSON, Thomas, W. [US/US]; 616 Canyon Road #107, Redwood City, CA 94062 (US). SWARNAKAR, Anita [CA/US]; 8 Locksley Avenue #5D, San Francisco, CA 94122 (US). CHAWLA, Narinder, K. [US/US]; 33 Union Square, #712, Union City, CA 94587 (US). BECHA, Shanya, D. [US/US]; 1 Saint Francis #5508, San Francisco, CA 94107 (US). MASON, Patricia, M. [US/US]; 360 Clarke Lane, Morgan Hill, CA 95014 (US). ELLIOTT, Vicki, S. [US/US]; 3770 Polton Place Way, San Jose, CA 95121 (US). RAMKUMAR, Jayalaxmi [IN/US]; 34359 Maybird Circle, Fremont, CA 94555 (US). GRIFFIN, Jennifer, A. [US/US]; 33691 Mello Way, Fremont, CA 94555 (US). TRAN, Uyen,

K. [US/US]; 2638 Mabury Square, San Jose, CA 95133 (US). ISON, Craig, H. [US/US]; 1242 Weathersfield Way, San Jose, CA 95118 (US). LINDQUIST, Erika, A. [US/US]; 2394 Mariner Square Drive #C-121, Alameda, CA 94501 (US). JIANG, Xin [US/US]; 14371 Elva Avenue, Saratoga, CA 95070 (US). JACKSON, Alan, A. [US/US]; 1541 Elwood Drive, Los Gatos, CA 95032 (US). WILSON, Amy, D. [US/US]; 1056 Continentals Way, #27, Belmont, CA 94002 (US). JIN, Pei [US/US]; 320 Curtner Avenue #D, Palo Alto, CA 94306 (US). CHANG, Hsin-Ru [US/US]; 326 Treasure Island Drive, Belmont, CA 94002 (US).

(74) Agent: FOLEY & LARDNER LLP; Washington Harbour, 3000 K Street, N.W., Suite 500, Washington, D.C. 20007-5143 (US).

(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

— with international search report
 — before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments

(88) Date of publication of the international search report:

23 March 2006

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: TRANSPORTERS AND ION CHANNELS

(57) Abstract: Various embodiments of the invention provide human transporters and ion channels (TRICH) and polynucleotides which identify and encode TRICH. Embodiments of the invention also provide expression vectors, host cells, antibodies, agonists, and antagonists. Other embodiments provide methods for diagnosing, treating, or preventing disorders associated with aberrant expression of TRICH.

WO 2003/083085 A3

```

agctctagtg agcgtgcaaa agctaagcga gttcctgtcc agtgacagaga tccgtgagga 1920
gcagtggtgcc ccccatgagc ccacacctca gggcccagcc agcaagtacc aggcgggtgcc 1980
cctcaggggtt gtgaaccgca agcgtccagc ccgggaggat tgtcggggcc tcaccggccc 2040
actgcagagc ctgggtcccca gtgcagatgg cgatgtgtgac aactgctgtg tccagatcat 2100
gggagggtac ttcacgtgga cccagatgg aatccccaca ctgtccaaca tcaccattcg 2160
tatccccga gggcagctga ctatgatcgt ggggcaggtg ggctgcggca agtcctcgct 2220
ccttctagcc gcactggggg agatgcagaa ggtctcaggg gctgtcttct ggagcagcag 2280
ccttctgac agcgagatag gagaggaccc cagcccagag cgggagacag cgaccgactt 2340
ggatatcagg aagagaggcc ccgtggccta tgcttcgcag aaaccatggc tgctaaatgc 2400
cactgtggag gagaacatca tctttgagag tcccttcaac aaacaacggg acaagatggg 2460
cattgaagcc tgctctctgc agccagacat cgacatcctg ccccatggag accagaccca 2520
gattggggaa cggggcatca acctgtctgg tggtaacgc cagcgaatca gtgtggcccg 2580
agccctctac cagcacgcca acgttgtctt ctggatgac cccttctcag ctctggatat 2640
ccatctgagt gaccacttaa tgcaggccgg catccttgag ctgctccggg acgacaagag 2700
gacagtggtc ttagtgaccc acaagctaca gtacctgccc catgcagact ggatcattgc 2760
catgaaggat ggcaccatcc agaggagggg taccctcaag gacttccaga ggtctgaatg 2820
ccagctcttt gagcactgga agaccctcat gaaccgacag gaccaagagc tggagaagga 2880
gactgtcaca gagagaaaag ccacagagcc accccagggc ctatctcgtg ccatgtcctc 2940
gagggatggc cttctgcagg atgaggaaga ggaggaagag gaggcagctg agagcgagga 3000
ggatgacaac ctgtcgtcca tgctgcacca gcgtgctgag atcccatggc gagcctgcgc 3060
caagtacctg tcctccgccg gcacccctgct cctgtcgttg ctggtcttct cacagctgct 3120
caagcacatg gtctgggtgg ccacgcacta ctggctggcc aagtggaccg acagcgccct 3180
gaccctgacc cctgcagcca ggaactgctc cctcagccag gagtgcaccc tcgaccagac 3240
tgtctatgcc atgggtgttca cgggtgctctg cagcctgggc attgtgctgt gcctcgtcac 3300
gtctgtcact gtggagtgga cagggctgaa ttttgagacc acgccccttg ggagcatcct 3420
aaaccggatc atcctagccc ccatgagggt cgaccagcac atcccatcca cgctggagtg 3480
gaacagattt tcatctgact gtaacacccat agccctggcc gtcatctcct atgtcacacc 3540
cctgagccgc tccacctgc tctgtgtctc agccctggcc gtcatctcct atgtcacacc 3600
tgtgttctct gtggccctct tgccctggc catcgtgtgc tacttcatcc agaagtactt 3660
ccgggtggcg tccagggacc tgcagcagct ggatgacacc acccagcttc cacttctctc 3720
acactttgcc gaaaccgtag aaggactcac caccatccgg gccttcaggt atgagggccg 3780
gttccagcag aagcttctcg aatacacaga ctccaacaac attgcttccc tcttctcac 3840
agctgccaac agatggctgg aagtccgaat ggagtacatc ggtgcatgtg tgggtctcat 3900
cgcagcgggtg acctccatct ccaactccct gcacaggag ctctctgctg gcctgggtgg 3960
cctgggcccct acctacgccc taatggtctc caactacctc aactggatgg tgaggaacct 4020
ggcagacatg gagctccagc tgggggctgt gaagcgcac catgggctcc tgaaaaccga 4080
ggcagagagc tacgaggggc tccctgggtga gaggtcagg gagaggggtg ggaagagtc 4140
caaggaggag tgtgtctggg ttgggggcca caaggagacc tggggatggg gtggcacttt 4200
cggatactag ctgtggccca tgccctgggtg ctgagcccag cccggccccc agcaccatcg 4260
ctgatcccaa agaactggcc agaccaaggg aagatccaga tccagaacct gagcgtgcgc 4320
tacgacagct ccctgaagcc ggtgctgaag cacgtcatgc cctcatcgcc ctggacagaa 4380
gatcggggtc tgccggccgca ccggcagtg gaagtcctcc ttctctcttg ccttcttccg 4440
catggtggac acgttcgaag ggcacatcat cattgatggc attgacatcg ccaaactgcc 4500
gctgcacacc ctgcgctcac gcctctccat catcctgcag gaccccgcc tcttcagcgg 4560
caccatccga tttaacctgg accctgagag gaagtgtca gatagcacac tgtgggaggc 4620
cctggaaatc gccagctga agctgggtgt gaaggcactg ccaggaggcc tcgatgccat 4680
catcacagaa ggcggggaga atttcagcca gggacagagg cagctgttct gcctggcccc 4740
ggccttctgt aggaagacca gcatcttcat catggacgag gccacggctt ccattgacat 4800
ggccacggaa aacatcctcc aaaagggtgt gatgacagcc ttgcagacc gcactgtggt 4860
caccatcgcg catcgagtgc acaccatcct gagtgcagac ctggtgatcg tctgaagcg 4920
gggtgccatc cttgagttcg ataagccaga gaagctgctc agccggaagg acagcgtctt 4980
cgcctccttc gtccgtgcag acaagtgacc tgccagagcc caagtgccat cccacattcg 5040
gaccctgccc ataccctgc ctgggttttc taactgtaaa tcacttgtaa ataaatagat 5056
ttgattatct cctaaa

```

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US03/09797

A. CLASSIFICATION OF SUBJECT MATTER

IPC(8) : A61K 38/00, 39/00; C07H 21/04; C07K 1/00, 14/00, 16/00; C12N 1/20, 5/00, 15/09; C12P 21/00;
 US CL : 424/85.1, 130.1, 184.1; 435/4, 7.1, 69.1, 70.1, 252.3, 320.1, 325; 514/2, 12; 530/300, 350, 387.1

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
 U.S. : Please See Continuation Sheet

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
 Please See Continuation Sheet

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X — A	SHEN et al. Identification of a novel folate receptor, a truncated receptor, and receptor type beta in hematopoietic cells: cDNA cloning, expression, immunoreactivity, and tissue specificity. Biochemistry 1994, Vol. 33, pages 1209-1215, especially Figure 2 and pages 1210-1211 and 1213 (col 2); 95.8% identical to SEQ ID NO: 1 of the instant application.	1, 3, 6-7, 9, 11, 13, 17, 32, 36-38, 44 2, 4-5, 8, 10, 12, 14-16, 18-31, 33-35, 39-43, 45-173

☐ Further documents are listed in the continuation of Box C.☐ See patent family annex.

* Special categories of cited documents:	
"A" document defining the general state of the art which is not considered to be of particular relevance	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"E" earlier application or patent published on or after the international filing date	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"O" document referring to an oral disclosure, use, exhibition or other means	"&" document member of the same patent family
"P" document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

01 December 2005 (01.12.2005)

Date of mailing of the international search report

07 FEB 2006

Name and mailing address of the ISA/US

Mail Stop PCT, Attn: ISA/US
 Commissioner of Patents
 P.O. Box 1450
 Alexandria, Virginia 22313-1450

Facsimile No. (571) 273-3201

Authorized officer

Bridget E. Bunne

Telephone No. (571) 272-1600

INTERNATIONAL SEARCH REPORT

PCT/US03/09797

Continuation of B. FIELDS SEARCHED Item 1:

424/85.1, 130.1, 184.1; 435/4, 7.1, 69.1, 70.1, 252.3, 320.1, 325; 514/2, 12; 530/300, 350, 387.1; 536/23.1, 23.5; 800/8

G01N 33/53; A01K 67/00

Continuation of B. FIELDS SEARCHED Item 3:

EAST, DIALOG (file biosci), MEDLINE, PALM
serach terms: inventors' names, transporter, TRICH